Enhancing Plant Disease Detection with Transfer Learning and Ensemble Techniques Based on Plant Families

A. Mohamed Aslam Sujah[1][0000-0002-2582-831X], Asanka P. Sayakkara[2][0000-0001-9558-7913] and H.B.P. Sandani[3][0000-0002-3546-5233]

[1] South Eastern University of Sri Lanka, Oluvil, Sri Lanka
[2] University of Colombo School of Computing, Colombo, Sri Lanka
[3] Open University of Sri Lanka, Nugegoda, Sri Lanka
ameersujah@seu.ac.lk

Abstract. This research presents a comprehensive study on the development of an efficient and accurate plant disease prediction system using transfer learning models. The objective is to provide a reliable and accessible solution for farmers and agronomists to identify and address plant diseases in a timely manner, leading to improved crop yields and sustainable farming practices. The study analyzes five transfer learning models: Efficientnet_v2, Inception_v3, Mobilenet_v2, Resnet_v2, and Nasnet. Among these models, Efficientnet_v2, Resnet_v2, and Mobilenet_v2 demonstrate superior performance and are selected for further analysis. The research evaluates different experimental conditions: Global Model, Crop-Specific Approach, Disease-Specific Approach, and Plant-Family Based Approach. The Plant-Family Based Approach, focusing on the Nightshade plant family, exhibits superior accuracy in disease detection. An ensemble model combining three transfer learning models is developed using the Plant-Family Based Approach. The ensemble model shows exceptional performance and accuracy. Extensive testing and validation using diverse datasets demonstrate the system's high accuracy and efficiency in detecting diseases in various plant species. Future work includes expanding the dataset, fine-tuning hyperparameters, enabling real-time disease monitoring, and collaborating with agricultural experts to incorporate domain knowledge.

Keywords: Plant Disease Prediction, Transfer Learning Models, Ensemble Model, Plant Family, Agricultural Management, Nightshade Family.

1 Introduction

Agriculture plays a crucial role in economic development, providing food security, employment, and contributing to overall growth. However, crop diseases pose a significant threat to agricultural productivity, resulting in economic losses. Timely and accurate identification of crop diseases is essential for effective control measures. Unfortunately, farmers and agricultural professionals face challenges in disease iden-

tification and management, which can lead to extensive crop damage and reduced profitability [1].

Motivated by the growing trend of home gardening and the need for effective disease management in large-scale crop production systems, this research aims to address the lack of accessible solutions for early detection and identification of crop diseases. The objective is to develop a user-friendly solution leveraging machine learning and image recognition technologies to enable easy and precise disease detection based on plant families.

The proposed solution aims to democratize disease identification and empower individuals with limited resources and expertise to detect and manage crop diseases effectively. By training a robust and accurate crop disease identification model using transfer learning and ensemble learning techniques, this research aims to enhance agricultural productivity, reduce crop losses, and contribute to sustainable food production [2].

The research questions directly interconnected with this study are as follows: RQ1: Which transfer learning algorithms output high performance for predicting crop diseases using leaf images? RQ2: How does the family-based plant disease detection model differ from other existing approaches in terms of performance? RQ3: How does the integration of ensemble learning techniques enhance the performance and accuracy of the family-based plant disease detection model?

The research scope focuses on developing and evaluating a family-based plant disease detection model using transfer learning and ensemble learning techniques, with a specific emphasis on the Nightshade biological family. The dataset used for training and validation is the PlantVillage dataset [3]. The research's contribution to the field includes advancements in crop disease prediction techniques, exploration of transfer learning algorithms, integration of ensemble learning techniques, and practical implementation with real-world impact. These contributions have implications for improving agricultural practices, optimizing resource management, and promoting sustainable farming.

2　Related Work

Crop disease recognition is crucial for agricultural productivity and food security. Traditional methods like visual inspection and symptom observation have limitations in terms of subjectivity, time consumption, and expertise requirements. Automated techniques are needed for accurate and efficient disease recognition [4].

2.1　Computer Vision-Based Techniques for Crop Disease Recognition

Computer vision-based techniques, particularly deep learning-based approaches using convolutional neural networks (CNNs), have shown promise in crop disease recognition. CNNs can extract features from crop images and classify diseases without explicit feature engineering [5]. Several CNN-based models have achieved high accuracy in detecting diseases in various crops.

Agarwal and their team propose a simplified CNN model with 8 hidden layers for tomato crop disease identification [6]. The model surpasses traditional machine learning approaches and pretrained models, achieving an accuracy of 98.4% on the PlantVillage dataset. Image pre-processing techniques and augmentation are used to improve performance. Furthermore, the model achieves a high accuracy of 98.7% on datasets other than PlantVillage. In another study, Bharathi and colleagues combine CNN and an autoencoder for crop leaf disease detection, achieving an impressive accuracy of 99.82% on the PlantVillage dataset. The optimized approach outperforms existing methods in detecting crop leaf infections. This research highlights the potential of CNN-based techniques for accurate and efficient crop disease recognition in agriculture [7]. Additionally, Mohanty et al. address the challenge of rapid crop disease identification by leveraging deep learning and smartphone usage. Their deep CNN model trained on a large dataset achieves a remarkable accuracy of 99.35% on the test set, enabling smartphone-assisted crop disease diagnosis on a global scale using publicly available image datasets [8].

2.2   Transfer Learning in Crop Disease Recognition

Transfer learning is a technique that transfers knowledge from pre-trained models to new tasks. In crop disease recognition, transfer learning addresses the challenge of limited annotated data and reduces training time [9]. Various transfer learning architectures, such as EfficientNet, Inception, MobileNet, ResNet, and NasNet, have been applied to crop disease recognition tasks, achieving high accuracy in different crop species. Researchers have investigated these structures in conjunction with various crop species in order to improve the accuracy and efficiency of plant disease prediction. Table 1 provides a complete overview of the individual architectural and crop species to which they have been applied.

Table 1. Architecture and crop species with model accuracy.

Reference	TL Architecture	Crop Species	Accuracy
[16]	Efficientnet	Corn	98.85%
[17]	Inception	Banana	90%
[18]	Mobilenet	open-source dataset	99.13%
[19]	VGGNet	Rice	92%
[20]	ResNet	Tomato	97.28%
[21]	Nasnet	38 Crop Species	99.31%
[22]	VGGNet	Tomato	89%
[1]	ResNet50	Potato, Tomato, Corn	98.7%
[23]	DenseNet	Tomato (10 classes)	97.11%

EfficientNet_v2: An advanced CNN architecture that optimizes depth, width, and resolution simultaneously, achieving state-of-the-art results [10]. Inception_v3: Introduces the Inception module for multi-scale feature extraction and incorporates techniques like factorized convolution and batch normalization [11]. MobileNet_v2: Designed for resource-constrained environments, it employs depth-wise separable convolutions to reduce computational complexity while maintaining accuracy [12].

VGGNet: Known for its simplicity and uniformity, it uses deeper networks with smaller filters for accurate feature extraction [13]. ResNet_v2: Introduces residual connections to alleviate the vanishing gradient problem and enables training of deeper networks [14]. NasNet: Based on neural architecture search, it automatically discovers optimal network architectures for specific tasks using reinforcement learning or evolutionary algorithms [15].

2.3 Existing Crop Disease Recognition Approaches

Existing plant disease prediction approaches can be categorized into three modeling strategies. The first involves models designed for a single crop, capable of detecting multiple diseases with high accuracy. The second focuses on models trained to detect a specific disease across different crops, ensuring effective recognition regardless of the crop type. The third employs a global model that identifies multiple diseases across various crops, treating crop-disease combinations as class labels.

While individual models for specific crops and diseases have achieved high accuracy, developing separate models for each combination is resource intensive. To address this, some studies have explored global models that leverage shared knowledge and unified datasets, successfully detecting multiple crops and diseases. However, integrating a large number of crops and diseases into a single model presents challenges, highlighting the need for alternative approaches. Table 2 provides an overview of different crop disease prediction strategies.

Table 2. Crop disease prediction approaches.

Reference	Crop/Disease	Approach
[24]	Rice	Crop Specific
[25]	Potato	Crop Specific
[26]	Maize	Crop Specific
[27]	Potato Blight	Diseases Specific
[28]	Blight Disease	Diseases Specific
[29]	Late Blight Disease	Diseases Specific
[30]	Multiple Plants	Global Model
[31]	Multiple Plants	Global Model
[32]	Multiple Plants	Global Model
[8]	Multiple Plants	Global Model

2.4 Plant Family-Based Approach (Proposed Approach)

This approach in crop disease recognition considers the evolutionary relationships and genetic similarities among crop species within the same plant family. This approach recognizes that closely related crops share common characteristics and vulnerabilities to specific diseases. Table 3 discloses the Nightshade family plants, diseases and responsible pathogens. By utilizing this knowledge, disease recognition models can leverage similarities between crops to enhance accuracy and efficiency.

This approach offers several advantages. It allows for the transfer of knowledge and insights gained from one crop to another within the same family, reducing the need for extensive training data for each individual crop. It enables targeted interventions based on shared disease characteristics and improves disease recognition accuracy, especially for diseases that have not been extensively studied in certain crops.

Crop species belonging to the same plant family often exhibit similar growth patterns and nutrient requirements, making them susceptible to the same pathogens. For example, the Nightshade family includes crops like pepper and tomato, which are affected by the *Geminivirus* pathogen causing Yellow Leaf Curl disease. When a disease emerges in one crop within a family, there is a high probability of its spread to other crops within the same family. Farmers often cultivate crops from same family in specific geographic locations due to their compatibility with local weather conditions.

By adopting this approach, the challenges associated with the vast diversity of crop species and their diseases can be addressed. Instead of trying to develop a single global model for all crops, focusing on plant family-based models provides a more targeted and efficient approach to crop disease recognition and management. This approach aligns with the practical realities of crop cultivation and offers a framework for improving disease diagnosis and prevention strategies on a broader scale.

Table 3. Nightshade family plants, diseases and responsible pathogens.

Plant	Disease	Pathogen
Tomato	Late blight	*Phytophthora infestans*
Tomato	Early blight	*Alternaria solani*
Tomato	Tobacco mosaic disease	*Tobacco mosaic virus*
Tomato	Verticillium wilt	*Verticillium dahliae*
Potato	Late blight	*Phytophthora infestans*
Potato	Early blight	*Alternaria solani*
Potato	Verticillium wilt	*Verticillium dahlia*
Eggplant	Early blight	*Alternaria solani*
Eggplant	Verticillium wilt	*Verticillium dahlia*
Pepper	Early blight	*Alternaria solani*
Pepper	Tobacco mosaic disease	*Tobacco mosaic virus*
Pepper	Verticillium wilt	*Verticillium dahliae*
Tobacco	Tobacco mosaic disease	*Tobacco mosaic virus*

2.5   Ensemble Learning Techniques

Ensemble learning has gained popularity as a strategy to improve prediction accuracy and generalization performance in machine learning [33]. It involves combining multiple models to make predictions and can be categorized into bagging and boosting techniques.

Bagging methods, such as Random Forest and Extra Trees, train independent models on different subsets of data and aggregate their predictions to enhance accuracy and address overfitting. Random Forest combines decision trees, while Extra Trees further increases diversity among the trees by randomizing the tree-building process. Boosting algorithms, such as AdaBoost and Gradient Boosting, sequentially train

models and give more importance to misclassified instances. AdaBoost assigns weights to instances based on difficulty and combines the predictions of weak classifiers using weighted voting. Gradient Boosting builds an ensemble iteratively by minimizing the loss function [34]. Ensemble learning techniques have been successfully applied in various domains. In image classification, they are effective in handling complex visual patterns.

3   Methodology

3.1   Initial Phase

In this study, a dataset consisting of manually collected images of Nightshade family plants and the publicly accessible Plant Village dataset was used. The dataset includes a total of 54,309 leaf images from 14 different crop species, representing 38 distinct diseased and healthy classifications. The images were collected from experimental research stations associated with Land Grant Universities in the USA [3]. The dataset was focused specifically on Nightshade family plants, including Tomato, Potato, and Pepper crops. It consisted of 15,000 instances of healthy and diseased images, resulting in a balanced dataset with 15 initial classes. The dataset was split into training and validation folders, with an 8:2 ratio. A manually collected set of 450 images, expert reviewed and labeled, was used to assess the model's performance.

The original dataset primarily focuses on tomato plants, while the dataset used in this study includes a more limited representation of potato and pepper crops. However, this dataset configuration is sufficient to evaluate the proposed approach, and the experimental strategies employed in the research, ensuring that they are tailored to the specific characteristics and requirements of Nightshade family crops.

Image pre-processing method was used to enhance the quality of input images and facilitate subsequent processing. The method included image resizing, normalization, and data augmentation techniques. To ensure consistency in the dataset, all images were resized to a stable size of 224 x 224 pixels. This standardization allowed for easier processing and analysis by ensuring that all images had the same dimensions.

Data normalization was applied to ensure consistent distribution of data across each pixel of the images. This step involved extracting the mean value of each pixel and normalizing the values by dividing them by the standard deviation. This normalization process improved convergence during network training.

Image augmentation techniques were used to create a robust image classifier. By applying techniques such as rotation, zooming, and flipping, new data was generated from existing images. This augmentation process expanded the dataset and introduced more variations, enabling the classifier to learn and generalize better from a wider range of image samples.

A literature review is conducted to identify transfer learning models that have shown excellent performance in previous crop disease prediction research using various approaches. Based on the review, five models are chosen for analysis: Efficient-

net_v2, Inception_v3, Mobilenet_v2, Resnet_v2, and Nasnet. These models have demonstrated their effectiveness in similar tasks.

Several factors were considered to assess the selected transfer learning models. The first factor was the computational efficiency of the models, specifically their training time. The second factor was the models' training accuracy over 10 epochs, which measured their ability to learn from the dataset. The third factor was their prediction accuracy on a new dataset, which evaluated their overall performance. Lastly, the variation between training and validation accuracy was examined to determine the stability of the models.

The analysis was conducted using high-performance computing devices provided by Microsoft Azure, which featured a specific configuration including an Intel(R) Xeon(R) Platinum 8370C CPU 2.80GHz processor, 8 vCPUs, 64GB RAM, and Premium SSD storage. Maintaining stable conditions throughout the analysis was crucial to ensure consistency in the dataset, the number of images, the number of classes, and other relevant factors.

3.2   Experiment Design

In the experiment phase, four different experimental conditions were designed to evaluate the performance of different crop disease detection approaches using three transfer learning architectures. Balanced datasets were used for each experimental condition, and stable conditions were maintained for assessing efficiency and effectiveness.

Experimental Condition 1 focused on a global model where crop-disease combinations were treated as individual classes. It included 15 classes representing tomato, potato, and pepper crops. Experimental Condition 2 employed a crop-specific approach, focusing on the tomato crop with multiple diseases as class labels. It consisted of 10 classes of tomatoes, including diseased and healthy samples. Experimental Condition 3 considered disease-specific approaches for Bacterial Spot and Early Blight diseases, involving multiple crops. Each disease had 4 classes representing pepper and tomato, as well as potato and tomato, respectively. Experimental Condition 4 implemented a plant-family based approach, defining classes based on disease names and selecting samples from Nightshade family crops. It included 10 classes representing various diseases.

3.3   Evaluation and Implementation Phase

The four experimental conditions are thoroughly analyzed with the real dataset to determine the most efficient and effective approach. Using the previously selected top three transfer learning architectures and the plant-family based approach, transfer learning models are developed. These models incorporate the stable conditions maintained throughout the analysis phase. The output transfer learning models are subjected to ensemble learning techniques, specifically using the average function. The ensemble model is obtained as the final output, combining the strengths and knowledge of the individual models. The proposed system is illustrated in Fig. 1, which presents

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the flow chart depicting the various steps and processes involved. This visual representation outlines the sequential flow of operations and decisions within the system.
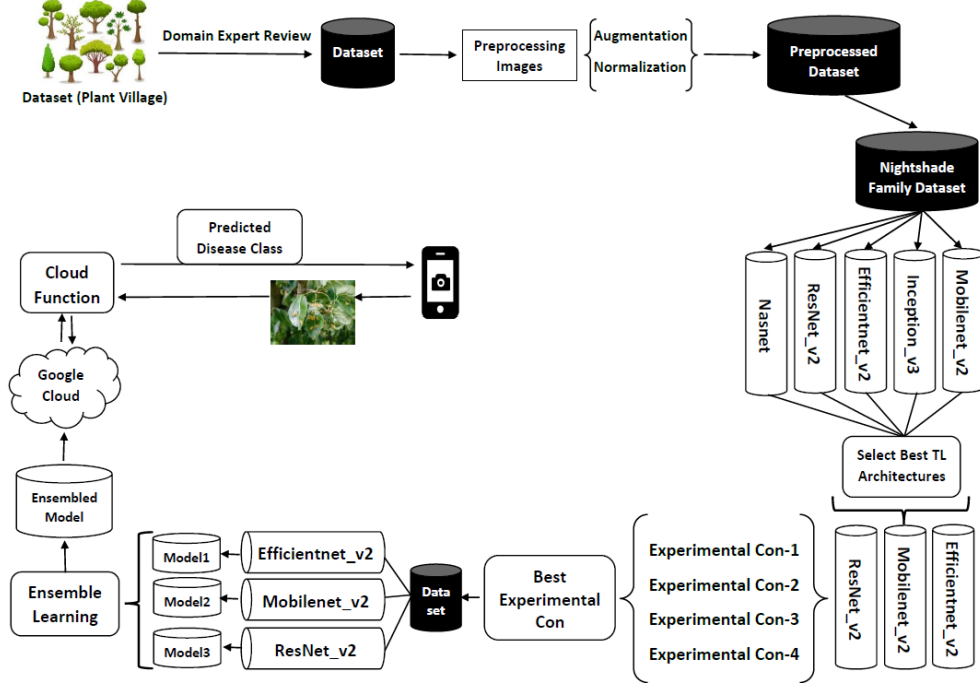

Fig. 1. Proposed System's Flow Chart.

4 Results and Discussion

4.1 Evaluation of Transfer Learning Models

Thoroughly evaluated five transfer learning models: Efficientnet_v2, Inception_v3, Mobilenet_v2, Resnet_v2, and Nasnet. We conduct a detailed analysis under stable conditions to ensure consistency in the dataset, image counts, classes, and training epochs. We consider the factors of evaluation metrics to evaluate. The objective of this comprehensive evaluation is to identify the top-performing models that achieve high accuracy while being computationally efficient. More detailed information about these models can be found in Table 4. Efficientnet_v2, Mobilenet_v2, and Resnet_v2 emerged as the top-performing models with high training accuracy, minimal variation, and excellent generalization capabilities. Efficientnet_v2 stood out with the highest accuracy and stability, while Mobilenet_v2 offered a balanced combination of accuracy and shorter training time. Resnet_v2 also performed well across all criteria. These models ensure reliable predictions considering computational efficiency and practical constraints.

Table 4. Transfer Learning model selection experiment results.

TL Model	Training Time (S)	Accuracy	Variation	Performance (New Dataset)
Efficientnet_v2	2408	96.98%	1.98%	95.00%
Inception_v3	5368	89.78%	2.41%	87.37%
Mobilenet_v2	1755	90.80%	3.23%	87.57%
Resnet_v2	3676	92.66%	3.73%	88.93%
Nasnet	3265	85.28%	2.55%	82.73%

4.2 Experimental Conditions and Results

In this section, we present the results obtained from the four experimental conditions: Global Model, Crop-Specific Approach, Disease-Specific Approach, and Plant-Family Based Approach.

Experimental Condition 1: Global Model: Each crop-disease combination is treated as a separate class (15 Classes). The results showed that all three models performed well in this approach. When considering the accuracy of the global model at the class level. Classes are designated L1 through L15. Table 5 contains the relevant information. The results highlight variations in the models' accuracy across different classes. Efficientnet_v2 generally achieved higher accuracy across multiple classes, followed by Mobilenet_v2 and Resnet_v2.

Table 5. Class level accuracy of global model.

TL Model	L1	L2	L3	L4	L5	L6	L7	L8	L9	L10	L11	L12	L13	L14	L15
Efficientnet_v2	99.5	99.0	98.9	100.0	95.1	93.6	79.2	98.4	95.8	94.8	91.1	98.1	89.0	99.0	93.8
Mobilenet_v2	98.0	95.9	100	96.7	87.2	95.5	56.8	86.5	86.5	86.9	71.4	78.8	85.2	94.6	93.3
Resnet_v2	92.1	97.9	100	97.8	81.3	94.1	78.1	98.4	76.0	68.6	92.7	94.2	80.0	93.2	93.8

Experimental Condition 2: Crop-Specific Approach: It focused on the tomato crop and its 10 distinct classes. When considering the accuracy of the crop-specific model at the class level. Classes are designated L1 through L10. Table 6 contains the relevant information. Efficientnet_v2 consistently demonstrated the highest accuracy across most classes, indicating its effectiveness in classifying the specific disease types. Mobilenet_v2 showed decent performance but had slightly lower accuracy in some classes. Resnet_v2 exhibited mixed results, with varying levels of accuracy across different classes.

Table 6. Class level accuracy of crop-specific model.

TL Model	L1	L2	L3	L4	L5	L6	L7	L8	L9	L10
Efficientnet_v2	95	79.3	100	92.7	94.5	87.6	93.5	97.5	99.1	97.5
Mobilenet_v2	92.8	65.3	93.2	92.2	77	71.8	80.5	84.3	90.7	98
Resnet_v2	86.1	67.9	97.6	81.3	74.7	89.6	90	90.9	85	88.9

Experimental Condition 3: Disease-Specific Approach: We investigated two specific diseases: Bacterial Spot disease with pepper and tomato crops, and Early Blight disease with potato and tomato crops. The evaluation metrics were used to measure the performance of the model with 4 distinct classes for bacterial spot disease. Classes are designated L1 - L4, accordingly. Pepper_Bacterial_Spot, Pepper_Healthy, Tomato_Bacterial_Spot, Tomato_Healthy. Similarly used 4 distinct classes for early blight disease. Classes are designated L5 - L8, accordingly. Potato_Early_Blight, Potato_Healthy, Tomato_Early_Blight, Tomato_Healthy. Table 7 discloses the summary of evaluation metrics for the disease-specific approach. All three models showcased strong performance in accurately identifying Bacterial Spot and Early Blight Disease.

Table 7. Evaluation metrics of disease-specific model.

TL Model	Bacterial Spot Disease				Early Blight Disease			
	Accuracy	Precision	Recall	F1-Score	Accuracy	Precision	Recall	F1-Score
Efficientnet_v2	99.36	99.42	99.34	99.37	99.63	99.62	99.62	99.62
Mobilenet_v2	98.38	98.37	98.41	98.38	98.25	98.38	98.16	98.22
Resnet_v2	98.00	98.13	97.93	98.01	99.38	99.38	99.39	99.38

Experimental Condition 4: Plant-Family Based Approach: This approach focused on constructing classes based solely on disease names within the Nightshade plant family. The evaluation metrics were used to measure the models' ability to detect diseases within this plant family with 10 distinct classes. Classes are designated L1 - L10, accordingly. Bacterial_Spot, Early_Blight, Healthy, Late_Blight, Leaf_Mold, Mosaic_Virus, Septoria_Leaf_Spot, Spider_Mites, Target_Spot, and Yellow_Leaf_Curl_Virus. Table 8 contains the relevant information.

4.3 Discussion of Experiment Results

In experimental condition 3, the EfficientNet_V2 model demonstrates the highest performance, establishing it as the optimal scenario for detecting a specific disease. However, despite its high accuracy, its focus on a single disease restricts its applicability to a broader range of diseases and crops. Based on evaluation metrics, experimental condition 1 is the second-best scenario, with the EfficientNet_V2 model achieving the highest scores. While MobileNet_V2 and ResNet_V2 perform slightly lower, they still demonstrate strong results. This condition offers a broader approach by predicting multiple diseases across various crops, enhancing versatility. However, the large number of class-labels and potential imbalances may challenge accuracy and precision.

Experimental condition 4 ranks as the third-best scenario, with the EfficientNet_V2 model achieving strong yet slightly lower performance than condition 1. MobileNet_V2 and ResNet_V2 also perform well, though slightly below EfficientNet_V2. This condition leverages shared characteristics within plant families to group diseases, simplifying classification and reducing class labels. This approach balances

specificity and generalization, enhancing prediction while mitigating challenges associated with numerous class labels.

Experimental condition 2 ranks as the fourth-best scenario, with all models achieving lower scores across all metrics. This condition focuses on predicting multiple diseases for a single crop, providing targeted disease detection beneficial for farmers. However, its limited generalization to other crops may necessitate separate models for different crops.

Considering the strengths and limitations of each experimental condition, the plant-family-based approach (experimental condition 4) offers notable advantages. By leveraging shared characteristics within plant families, it balances specificity and generalization, simplifying classification and reducing challenges associated with numerous class labels. This approach enhances prediction accuracy while accounting for disease relatedness within similar pathogens. Based on the results, the plant-family-based model, focused on detecting diseases within the Nightshade family, outperforms the Global Model, Crop-Specific Model, and Disease-Specific Model.

Table 8. Class level accuracy for plant family-based model.

TL Model	L1	L2	L3	L4	L5	L6	L7	L8	L9	L10
Efficientnet_v2	95.6	77.7	98	93.8	94.5	100	96.5	94.4	90.7	97.5
Mobilenet_v2	86.7	72.5	89.3	88.1	85.7	90.6	75	81.8	82.7	96
Resnet_v2	84.4	80.8	92.2	81.3	78.3	95	86.5	88.9	89.3	88.4

4.4 Ensemble Model Development

To create our ensemble model, we have chosen three effective transfer learning models from the plant-family based approach: Efficientnet_v2, Mobilenet_v2, and Resnet_v2. These models have shown excellent performance in accurately detecting Nightshade plant family diseases. By combining their strengths, our ensemble model aims to improve predictive capability and robustness. We expect the ensemble model to achieve even higher accuracy than the individual models through training. By leveraging the collective intelligence of multiple models, the ensemble model can make more informed disease predictions within the Nightshade plant family. Fig. 2 illustrates the training & validation accuracy and loss of ensemble model over 15 epochs. After the ensemble model development, we evaluate the model with randomly selected 2000 images of PlantVillage dataset which are not previously used in this research. The below Fig. 3 shows the confusion matrix of this evaluation.

5 Conclusion

In summary, this research aimed to develop an efficient and accurate plant disease prediction system using transfer learning models. Various experimental conditions, including the Global Model, Crop-Specific, Disease-Specific, and Plant-Family-Based approaches, were evaluated. The Plant-Family-Based approach, focused on the Nightshade family, demonstrated the highest accuracy, precision, recall, and F1-score.

Building on this, an ensemble model combining three transfer learning models was developed, achieving superior performance.
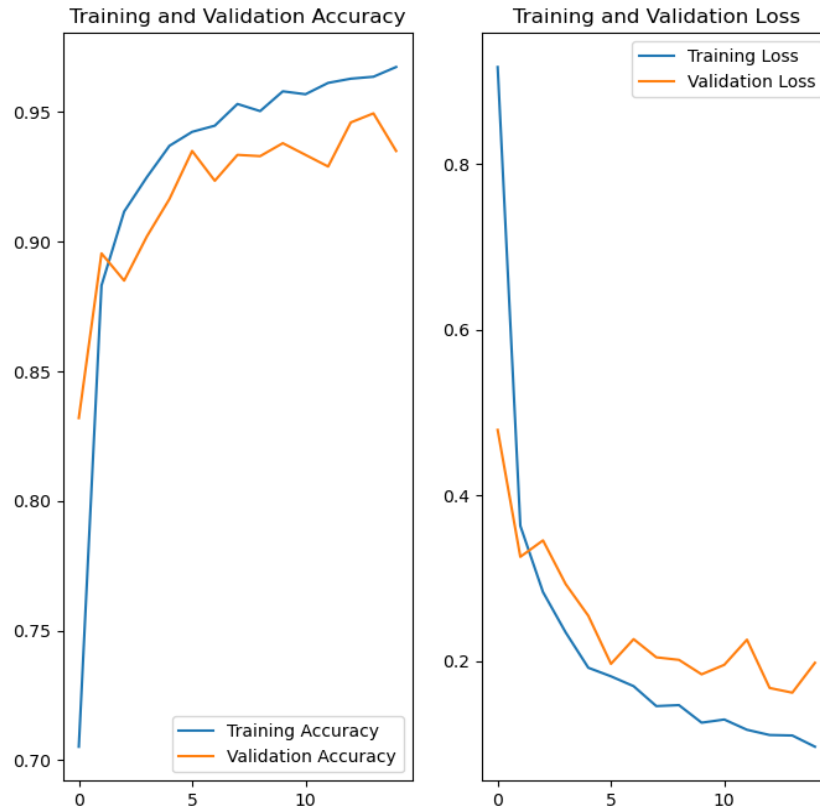

Fig. 2. Training and Validation Accuracy and Loss of Ensemble Model Training.

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