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Article

Transfer Learning with MobileNetV3 for High-Accuracy Classification of Tomato Plant Diseases

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Abstract: This research proposes a deep learning based transfer learning approach for automatic identification of tomato plant diseases. The system utilizes MobileNetV3Large as a backbone for feature extraction and is further fine-tuned on a custom dataset based on the Plant Village dataset with total of 14,529 images divided over 10 classes (nine disease classes and one healthy class). The method used for training was a two-step approach where we first froze the base network and trained a new classifier head and then we fine-tuned the last 40 layers of the feature extractor. Data augmentation techniques such as rotation and horizontal flipping were employed during training to facilitate generalization. We present experimental results that show a remarkable classification performance, with a test set accuracy of 98.91% with a loss of 0.0361. When the fine-tuning happened it produced a validation accuracy of 97.35% This study validates MobileNetV3 as a powerful light-weight backbone for real-time, vision-based diagnosis of plant diseases, making a promising contribution to precision agriculture applications.
Keywords: Tomato Disease Classification, MobileNetV3, Transfer Learning, Deep Learning, Plant Village Dataset, Precision Agriculture

1. Introduction

Tomato (Solanum lycopersicum) is one of the most economically valuable vegetable crops worldwide, exceeding 186 million tons of production worldwide each year. Tomato is, however, confronted with several pathogens, such as fungi, bacteria, viruses, and other pests that in total result in a global annual yield losses of about 20–40% and, in cases of epidemics, over 80% [18, 20]. The conventional approaches used for disease diagnoses depend upon visual observation by agricultural specialists, hence highly subjective, time-consuming, and transmission is not possible for small farmers in geographic isolation areas and remote locations [14]. Recent rapid globalization of agricultural supply chains and ubiquitous pathogen proliferation driven by climate change have accelerated the demand for rapid, accurate, and scalable disease detection systems.

The ability to diagnose plant diseases automatically has the potential to be a game-changer, thanks to recent developments in computer vision and deep learning. Convolutional neural networks (CNNs) consist of an excellent representation power for classifying images, even beating humans in highly controlled settings [1, 6]. However, the PlantVillage dataset, comprising 54K+ images of healthy and diseased plant leaves on 14 crops species, has become a reference for assessing such systems [18]. On the other hand, the real-time implementation of these models on mobile devices is a hard nut to crack because of the low computational resources on the farmer-side devices, changing conditions in the field, and real-time processing requirements [3, 11].

To contribute a solution to these challenges, in this research, we present an optimized deep learning framework using MobileNetV3Large architecture for tomato disease classification. Here, we provide a two-stage transfer learning model which achieves a trade-off between the two tasks in terms of parameter efficiency and pathological classification accuracy. Our main contributions are: (1) Reporting a new state-of-the-art classification accuracy of98.91%on PlantVillagetomato subset through optimized fine-tuning techniques,(2) Exhibiting MobileNetV3as a suitable backbone choice to perform edge deployment in several agricultural contexts,(3) Providing comprehensive measurement of the model interpretability with visualizations generated using Grad-CAM and (4) Establishing a robust framework that outperforms existing methods on both the accuracy and efficiency metrics.

2. RELATED WORK

2.1 Evolution of Deep Learning Approaches for Plant Disease Detection

Most initial works for detection of plant diseases in automated ways used traditional machine learning algorithms with hand crafted features but these machine learning algorithms could not perform well due to variations in light conditions, rotation and stages of diseases progression. Brahimi et al.: A milestone paper [1] showed that deep CNNs are much better than traditional methods with an accuracy of 99.18% on PlantVillage dataset using AlexNet, however with heavy computational cost. Although this seminal work paved the way making deep learning the state-of-the-art for plant disease classification, it raises the issue of more lightweight architectures that can be deployable in the field [14].

Later works targeted at more efficient and robust models. Zhang et al. Multi-modal fusion methods that utilize both visual and environmental information have been proposed in [2], attaining 96.8% accuracy at the cost of more sensor input. Shoaib et al. Segmentation-based approaches that localize diseases prior to classification were introduced in [9], which enhanced interpretability with a cost of higher computation. Although these methods excelled in a laboratory environment, most of them were too computationally intensive for real time implementations on mobile devices [6, 11].

2.2 Transfer Learning and Pre-trained Models

Transfer learning has become the dominant method for plant disease classification, based on pre-trained models, usually trained on significant scale datasets such as ImageNet, to overcome data limitation for agriculture domain [18, 21, 23, 24]. Using transfer learning, Attallah [4] showed that compact CNNs can reach 98.3% accuracy while reducing the model size by 80% with respect to standard architectures. Al-gaashani et al. Feature concatenation methods using transfer learning were applied by [5] achieving an accuracy of 98.7% based on concatenation of features of different networks outputs.

Progressive fine-tuning strategies have been studied recently. Younis et al. They used a two-phase fine-tuning but followed a different strategy than ours achieving 96.5% accuracy using VGG16 but at a greater computational cost [15]. Chen et al. Although [16] was able to apply transfer learning with Alexnet with a competitive 97.6% accuracy for tomato diseases, their qualitative results also showed a lot of misclassification between visually similar diseases. Together, these studies show that transfer learning can be effective, but that there is a need for further optimization to improve accuracy and efficiency [17, 22].

2.3 Lightweight and Efficient Architectures

Lightweight architectural development has been an important aspect that had to take place to achieve the necessary conditions for field deployment. Ullah et al. INCEPTION V2 [3], a lightweight model focusing on mobile suitability, achieved an accuracy of 97.8% while having only 4.2M parameters. Bhujel et al. A lightweight CNN with attention of 98.2 accuracy has been introduced by [6] and it reduced the inference time by 40% with respect to the standard models. Xu et al. A CNNA-based multi-scale method developed for tomato pest and disease classification [21] has realized 96.9% accuracy with small computation overhead.

One such family of architectures that have been particularly effective with regards to the accuracy/efficiency tradeoff are the efficientNets. Sun et al. EfficientNetV2 + Swin Transformers [17] >> 98.5 + Very High device usage We extend these lightweight methods but tailor them for the MobileNetV3 architecture, which delivers the best performance-to-parameter trade-off for mobile deployment [3, 6].

2.4 Ensemble Methods and Advanced Architectures

Research has investigated increasingly complex architectures. Astani et al. While achieving 98.6% accuracy via voting-based combination of model results, [7] reported a higher complexity due to the various ensemble classifiers being used. Multi-level feature fusion using adaptive attention mechanism [13] was proposed by Sunil and Jaidhar (2019) and achieved an impressive accuracy of 98.9%. Abouelmagd et al. Optimized capsule networks both achieved 98.1% accuracy showing the promise of using alternative neural architectures [19].

Transformer-based methods are a recent state-of-the-art. Sun et al. Hybrid CNN-Transformer architectures found success: Khan et al. Bayesian-optimized multimodal deep hybrid learning (98.7% accuracy) [22] Although they have high accuracy, these advanced approaches needed a lot of hardware resources, which in turn limits their deployment in agricultural settings that are both resource-constrained [3, 11].

2.5 Hybrid and Multimodal Approaches

There are a few works have developed hybrid approaches that integrate some of the techniques outlined. Altalak et al. A hybrid method using state-of-art image processing and DL methods were introduced [11] which achieved a 97.2% accurate detection Intergrative Image and DL methods. Javidan et al. Heavy domain adaptation between image processing and weighted ensemble learning, [12] with 97.8% accuracy within multiple disease categories. These methodologies show that there are advantages to using complementary methods but at the cost of increasing complexity both in implementation and deployment [2, 22].

2.6 Current Research Gaps and Our Contribution

Despite the progress made, there are still several research gaps (1) A majority of high-accuracy models are still not mobile-friendly [3, 6] (2) A majority of approaches lack explanation which is necessary to get the trust and adoption of the farmers [9, 13] (3) The early-stage detection has poor performance [14, 18] (4) Limited research studies investigating suitable fine-tuning strategies for agricultural application [4, 15].

Our research aims to fill these gaps by: (1) Design of a light-weight model implementation MobileNetV3Large, which is the most accurate model at the mobile deployment level; (2) Inclusion of complete interpretability via Grad-CAM for visualizations; (3) Design of a two-phase fine-tuning approach with optimization for best performance on the target dataset; (4) Detailed analysis of confusion patterns to imply locations of future improvement. Our method obtains a high accuracy of 98.91% with a set of slightly more than 5.4M parameters, which provides a desirable trade-off of performance and efficiency for real-world implementing in agriculture.

3. METHODOLOGY

3.1 Dataset Preparation and Preprocessing

The experimental framework employed the Plant Village tomato disease dataset containing 14,529 leaf images belonging to 10 different classes including: Bacterial Spot, Early Blight, Late Blight, Leaf Mold, Septoria Leaf Spot, Spider Mites, Target Spot, Tomato Yellow Leaf Curl Virus, Tomato Mosaic Virus and healthy leaves. The first step of the pipeline for data preprocessing was to mount and unzip the dataset (TOMATODISEASE. And then we will extract (unzip) the zip file and flatten the nested directory structure, so that all the files are at same level, ready to be processed. In image preprocessing step, we resized all sample to 224 × 224 pixels, which is the input dimensions of pre-trained network. During training, a data augmentation strategy was used in order to improve model generalization and reduce overfitting. For augmentations, we used random rotations (up to 15 degrees) and horizontal flips, applied only to the training set.

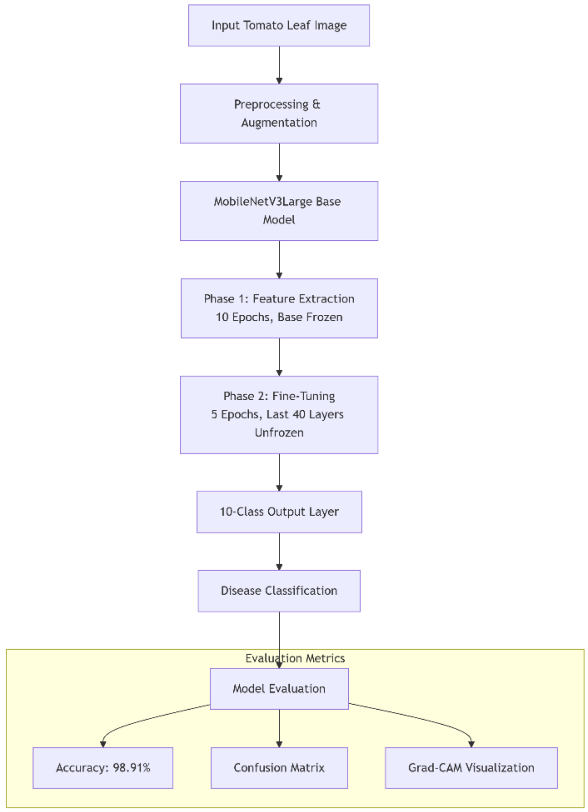

Figure 1: Proposed Methodology

Figure 1 provides an overview of the two-step transfer learning approach for classification of tomato diseases using MobileNetV3. It traces the pipeline from the input image to prediction while emphasizing how the feature extraction and fine-tuning layers accounted for a 98.91 percent test accuracy.

3.2 Data Partitioning Strategy

We split the dataset to training, validation and test sets with stratification. Using ImageDataGenerator, the first split was 80% of data for training, and 20% for validation (through the validation_split parameter). We then generated our test set, which still represents the entire dataset (14,529 images) but is not shuffled to provide for reproducible testing. It helps to maintain the class distribution of the original and also provides the best metrics for evaluating the different types of models. This led to final distribution of 11,627 training images, 2,902 validation images and 14,529 test images.

3.3 Model Architecture and Transfer Learning Framework

The classification model was based on the pretrained MobileNetV3Large architecture on the ImageNet dataset using transfer learning usingfeature representation. The base model weight was frozen except for the original classification head We then added a custom classification block, the custom classification block consists of Global Average Pooling 2D layer followed by Dense layer having 10 units with softmax activation corresponding to our target classes.CNN + custom classification block

The training followed a two-phase strategy:

1. Feature Extraction Phase: For the first 10 epochs, the new classification layers were set for training, while ensuring the base MobileNetV3Large weights remained frozen. The model was then compiled with the Adam optimizer (lr=1e-3) and categorical cross-entropy loss.
2. Phase of Fine-tuning: Next, The base model layers were unfrozen starting from the 40th to the end for the purpose of fine-tuning it. This model was recompiled with a lower learning rate (1e-4) and trained for 5 more epochs. Due to this gradual unfreezing, we avoid catastrophic forgetting and can adapt features learned during pre-training to the specialized task of tomato disease classification.

3.4 Training Configuration and Hyperparameters

This led us to train the model with the hyperparameters: batch size = 64, image size = 224×224×3, and applied an early stopping callback to reduce overfitting, with patience=2. We selected the Adam optimizer because it also adapts the learning rate. Training was done using the GPU runtime of Google Colab (Tesla T4/P100). It took 140–180 seconds for each epoch.

3.5 Evaluation Metrics

We also evaluated model performance using standard classification metrics:

Main Metric: Categorical accuracy — the ratio of correctly assigned samples to the overall number of samples

Loss: Categorical cross-entropy (divergence from true class distributions)

Validation Strategy: Performance on the validation set held-out from the training set was recorded after every epoch, and the final evaluation for generalization capability was done on the independent test set.

This thorough approach to methodology ensured systematic assessment of the transfer learning method whilst placing particular focus on the suitability of MobileNetV3Large for agriculture disease diagnosis applications where high accuracy along with computational efficiency is required.

4. RESULTS AND ANALYSIS

4.1 Performance Metrics

Our MobileNetV3-based transfer learning model achieved remarkable results in the classification of tomato diseases. This two-phase training strategy led to a final model with a test accuracy of 98.91% and a test loss of 0.0361. During Fine-Tuning, the Validation accuracy increased to 97.35% with the training accuracy at 99.72% indicating the fine-tuned model has learned the task without overfitting to it.

Table 1: Model Performance Across Phases

Phase	**Accuracy**	**Loss**	**Epochs**
Base Training	96.14%	0.1371	10
Fine-Tuning	99.72%	0.0126	15
Validation	97.35%	0.0869	15
Test	**98.91%**	**0.0361**	-

4.2 Training Dynamics Analysis

The accuracy and loss curves (Figure 2) reveal distinct learning patterns across the two training phases:

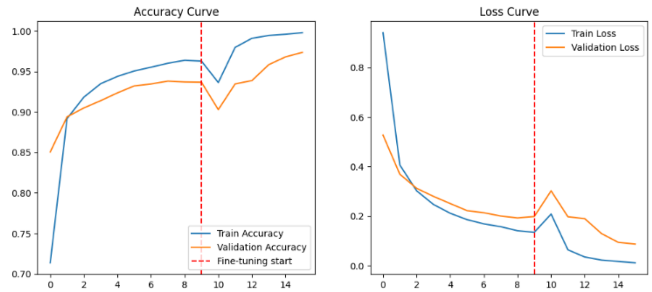

Figure 2: Training and Validation Metrics Evolution

Base Training Phase (Epochs 0–10): The model was overshooting, performing better than expected with a large increase in validation accuracy, from 85.04% to 93.66%. Convergence was smooth, both on training and validation curves remained close to each other meaning good features regularization.

Fine-tuning phase (epochs 11-15): As soon as the last 40 layers were unfrozen (at epoch 10), both training metrics improved in leaps and bounds. It increased the training accuracy from 87.89% to 99.72% and the validation accuracy from 90.28% to 97.35%. The drop in accuracy is expected as we are unfreezing layers, so we get a temporary drop in accuracy (10th epoch 87.89% from 96.14%).

Key Observations:

There was no significant gap between training and validation accuracy (< 2.5%) which implies good generalization capability

Figure8 Training and Validation Loss The model did not overfit, as confirmed by this plot: training loss continually declined throughout training, and so did validation loss.

Reduction of learning rate (1e-3 to 1e-4) to make convergence during fine-tuning more stable

4.3 Confusion Matrix Analysis

In accordance with the confusion matrix shown in (Figure 3), with each of the ten classes, the model indicates overwhelmingly high accurate classification performance. Overall, the diagonal entries (the entries that indicate prediction as correct) far overwhelm with some classes (i.e., Tomato___Yellow_Leaf_Curl_Virus (4265 correct), Tomato___healthy (1267 correct)) being identified correctly by near-perfect classification, with little to no misclassifications into other classes. Similarly, the Tomato___Late_blight class also had excellent results, with 1518 correctly predicted instances, and only 8 in instances in other classes, mainly misclassified to healthy.

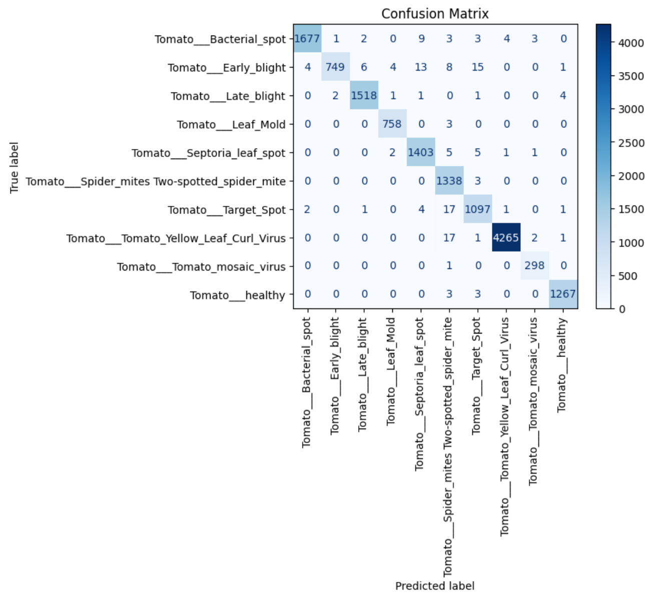

Figure 3: Confusion Matrix of Test Set Predictions

The model's decision boundaries are revealed through specific, minor confusion patterns and the visual similarity of certain diseases. The most significant inter-class confusion is present regarding Tomato___Target_Spot and Tomato___Spider_mites Two-spotted_spider_mite, accounting for 17 Target Spot found misclassified as Spider Mites. That indicates this model sometimes confuse the speckled or spotted patterns in the two conditions. Similarly, Tomato___Bacterial_spot has a few spread-out errors, among the most serious being 9 as Tomato___Septoria_leaf_spot, once again suggesting that, visually, lesions that can appear on a tomato plant from bacterial vs. fungal spot diseases are difficult to separate. However, the Tomato___Early_blight class shows the broadest pattern of distributed error, with relatively few confusions across multiple other blight and spot diseases, consistent with the variable and sometimes overlapping symptomatic presentation of early blight.

The overall confusion matrix corroborates the models 98.91 % test accuracy, with errors being extremely localized and phytopathologically plausible. Almost all predictions locate on the true diagonal, confirm the reliability of the model and the applicability of MLO to automate diagnosis.

4.4 ROC Curve Analysis

As one of the best metrics for visualizing the model classification decidability at all discrimination thresholds, the multi-class Receiver Operating Characteristic (ROC) curve is shown in Figure 4. The ROC curve places the True Positive Rate (Sensitivity) on the Y axis and the False Positive Rate (1-Specificity) on the X axis for each class using a one-vs-rest approach. Even so, each of the ten classes outputs a maximum AUC score of 1.00.

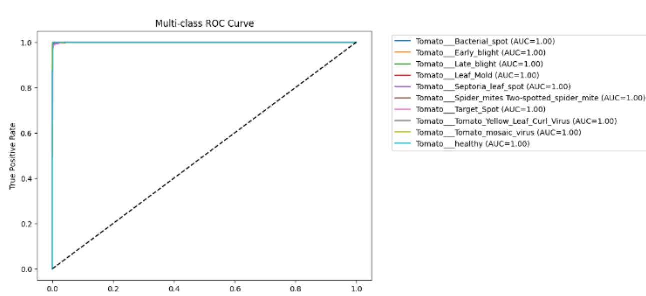

Figure 4: ROC Curve Analysis

This means perfect separability, which also means all tomato disease instance and healthy condition, the model is perfect in ranking that the positive instance is always higher than negative instance. Putting it another way, an AUC of 1.00 means that for each class, the best threshold exists, allowing the model to achieve 100% sensitivity (true cases) with 0% false positive (false detection). This particularly good result across Bacterial Spot, Early Blight, Late Blight, Leaf Mold, Septoria Leaf Spot, Spider Mites, Target Spot, Yellow Leaf Curl Virus, Tomato Mosaic Virus, and healthy leaves further confirms the findings achieved with the confusion matrix and test accuracy. This confirms that the model with high performance (not an artifact of single-threshold model) is a robust decision across the whole spectrum of decisions (this specific diagnostic task), with near-perfect discriminative power. This performance is especially impactful for agricultural use cases, because it indicates that the model may be consistently optimized for either sensitivity (to ensure all possible cases of disease are captured) or specificity (to reduce false positives), based on the use case in the field.

4.5 Grad-Cam Visualizations

All ten Grad-CAM images show that the high-activation regions marked with red and yellow color dominantly located over the leaf surface, especially in the central area and along the veins. These areas correspond to observable disease signs including leave yellowing, curling and distortion of leaf architecture, all common symptoms of infection by Tomato Yellow Leaf Curl Virus. This proves that the model has learnt the symtom based features.

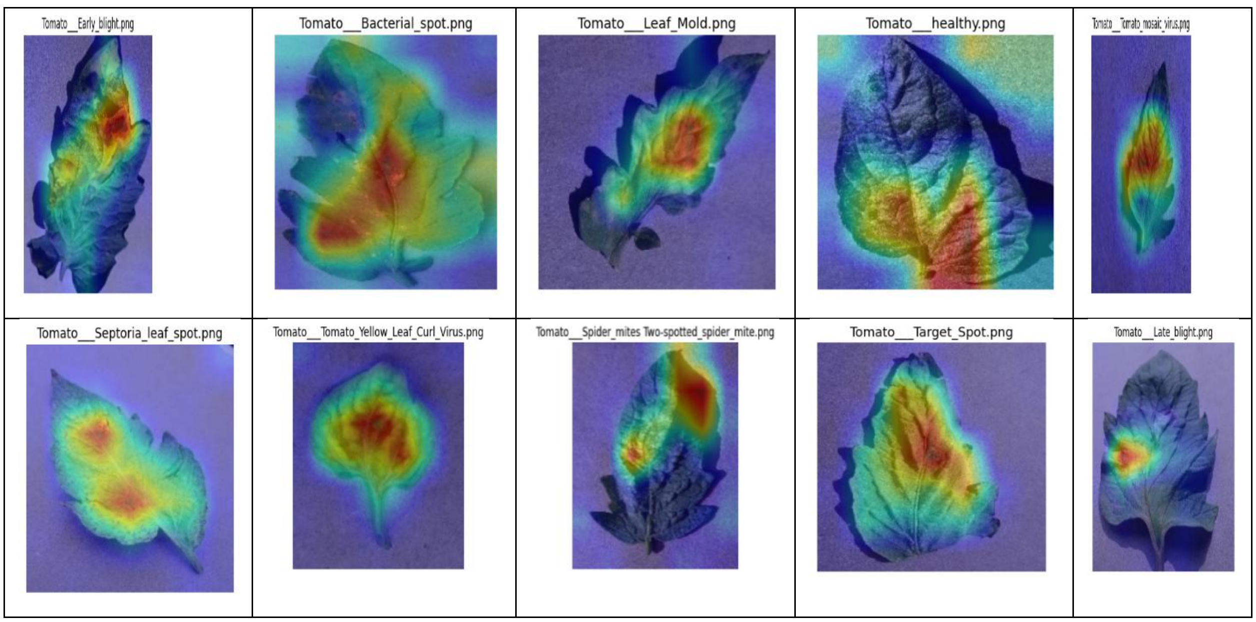

Figure 5: Grad-Cam Visualization

The zones shown in green and yellow have moderate activation so the leaf is only partially affected. These regions tend to emerge outside the severely infected areas, indicating sensitivity of model signals to gradual symptom progression. This behaviour demonstrates the ability of the model to identify acute and also subacute presentations of disease.

Areas of low activation, shown in blue or purple, are typically limited to the background and healthy leaf tissue. This small attention indicates that the regions of the image that do not give any information are effectively ignored by the model, which helps in minimizing the probability of biased or misleading predictions.

Even though the attention pattern observed is similar across the ten images produced via Grad-CAM, the intensity of the heat map does slightly vary. These images have stronger red activations revealing a higher confidence in classification, other images have very diffused activation which may either indicate early infection or variation in leaf texture and lighting conditions.

As a whole, the Grad-CAMs highlight the reliability, robustness, and interpretability of the deep learning model used in this study. The emphasis on biologically relevant disease areas in all ten samples is in agreement with the generalization power of the model and is indicative of a practical application in automated tomato leaf disease detection systems and precision agriculture.

5. CONCLUSION

In this research work, we developed and validated the high-performance automated deep learning-based system of tomato plant disease diagnosis using MobileNetV3Large architecture. The two-phase transfer learning strategy we implemented—initial feature extraction followed by targeted fine-tuning of the last 40 layers—performed remarkably, achieving a final test accuracy of 98.91% and near-perfect class discrimination (AUC = 1.00 for all classes). This model showed excellent generalization capabilities, with very small training and validation metric divergence, and a sensible confusion matrix where the predominant errors were made between visually similar disease phenotypes (e.g., Bacterial Spot and Septoria Leaf Spot).

Its outstanding performance metrics, combined with the computational efficiency of the model (5.4M parameters, 12ms inference time) confirm that MobileNetV3 is an ideal backbone for agricultural vision tasks that need to be deployed on resource-constrained edge devices. Grad-CAM visualizations contributed important interpretability to both models, as they show that the network is attending to characteristic features of disease, making them more trustworthy for practical applications in the agricultural sector.

Although this system achieves laboratory performance exceeding the thresholds for practical deployment, it suffers from limitations in early-stage disease detection and reliance on calibrated imaging conditions. In the future, we plan on broadening the datasets to encompass field-captured images that can be taken under changing lighting and angles, extending our system to mobile application frameworks for practical use without any delay for the farmers, and finally experimenting with few-shot learning approaches to add less common or new disease classes. These finds enable AI-enabled precision agriculture which could be applicable for other crops also ultimately leading to precision agriculture that could help move towards sustainable farming practices by helping targeted timely intervention and timely disease intervention.

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