BIMA
BULLETIN OF INTELLIGENT MACHINES AND ALGORITHMS
Vol. 1 No.1 November 2025
E-ISSN: 3123-5115
DOI: 10.65780/bima.v1i1.4

# Explainable Deep Transfer Learning for Robust Tomato Leaf Disease Classification

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**Abstract.** Automated identification of plant diseases is crucial for advancing precision agriculture and enabling farmers to make informed, timely decisions. This study presents a deep learning-based framework for multi-class classification of tomato leaf diseases using transfer learning with the VGG-19 architecture. A dataset comprising 10,000 images across ten classes, including nine disease categories and one healthy class, was preprocessed and augmented to improve model robustness and generalization. The training strategy employed a two-stage approach: initial feature extraction with frozen, pre-trained layers, followed by selective fine-tuning to adapt the convolutional features to the target domain. Comprehensive evaluation using accuracy, precision, recall, F1-score, and confusion matrices demonstrated the model's high discriminative capability, achieving an overall accuracy of 93% on the validation set. The results further revealed strong performance in identifying most disease categories, while highlighting classification challenges between visually similar classes, such as Tomato Mosaic Virus and Tomato Target Spot. The contributions of this research include the development of an optimized training pipeline, a reproducible evaluation framework, and insights into the role of transfer learning for agricultural image classification. The findings highlight the potential of deep learning to support automated tomato disease monitoring, with implications for improving crop health management and enhancing agricultural productivity.

**Keywords:** deep learning, tomato leaf disease, VGG19, transfer learning, precision agriculture, image classification.

## 1. INTRODUCTION

Tomato production plays a crucial role in global agriculture, yet it remains highly vulnerable to a variety of diseases that severely reduce yield and quality [1]. Early and accurate diagnosis of tomato leaf diseases is essential for effective disease management; however, manual identification by farmers or agricultural experts is often subjective, time-consuming, and prone to human error [2], [3]. This challenge is further compounded by the visual similarity of symptoms across different disease categories, making traditional approaches inadequate for large-scale and reliable detection [4].

The primary challenge in automated tomato leaf disease classification lies in the complexity of multi-class recognition [5], [6]. Different diseases often exhibit overlapping features, such as blight and viral infections, which complicates the task of distinguishing them with high precision [7]. Moreover, deep learning models are prone to overfitting when applied to relatively small agricultural datasets, and ensuring generalizability across diverse conditions remains a persistent concern [8]. These challenges underscore the need for robust, interpretable, and computationally efficient models that can consistently perform across multiple disease categories [9].

The primary objective of this research is to develop an automated tomato leaf disease classification system that leverages transfer learning with the VGG-19 deep learning architecture. The study aims to develop a framework that can effectively learn discriminative features, minimize overfitting, and maintain high classification performance across all disease categories. By incorporating systematic preprocessing, staged training strategies, and advanced regularization techniques, this research seeks to enhance both the accuracy and robustness of the model.

The contributions of this study are threefold. First, it provides a structured methodology for adapting a pre-trained convolutional neural network (CNN) to the domain of tomato leaf disease classification, including optimized preprocessing and augmentation techniques. Second, it demonstrates the effectiveness of a two-stage training strategy—feature extraction followed by fine-tuning—to achieve balanced performance across multiple classes.

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Finally, the study delivers a comprehensive evaluation, including accuracy, per-class classification metrics, and confusion matrix analysis, offering both quantitative performance measures and insights into areas of misclassification. Collectively, these contributions establish a reliable and reproducible framework that advances the application of deep learning for agricultural disease monitoring.

## 2. RELATED WORK

Research on tomato leaf disease classification has grown rapidly, leveraging Convolutional Neural Networks (CNNs), Transfer Learning, and, more recently, Transformer-based architectures. Attallah [10] proposed a compact CNN pipeline that utilizes transfer learning and hybrid feature selection, while Pandiyaraju et al. [11] introduced an adaptive ensemble framework that combines exponential moving average fusion and weighted gradient optimization.

Several works emphasize efficiency. Ahmed et al. [12] explored lightweight architectures, such as MobileNetV2 with runtime augmentation, whereas Li et al. [13] developed GD-Attention, a global pixel distribution attention mechanism that enhances sensitivity to infected regions. Liu et al. [14] proposed a multi-task distillation learning (MTDL) framework integrating disease classification and severity estimation within a single model.

Custom CNN architectures have also been designed. Ledbin Vini and Rathika [15] introduced TrioConvTomatoNet, a model tailored for recognizing tomato leaf disease. Zou et al. [16] integrated CNN and Visual Transformers in ECVNet, capturing both local and global features. In contrast, Zhou and Cai [17] proposed DIMPCNET, which combines Dense Inception modules with PCBAM to address complex background interference.

Transformer-based approaches are gaining momentum. Hossain et al. [18] highlighted the effectiveness of Vision Transformers for plant disease detection. Ouamane et al. [19] presented HOWSVD-TEDA, a method integrating pre-trained CNNs with tensor subspace learning. Similarly, Mazumder et al. [20] introduced LeafDoc-Net, a lightweight framework based on DenseNet121 and MobileNetV2, enhanced with Grad-CAM++ for interpretability.

Explainability has also received attention. Natarajan et al. [21] employed explainable CNNs for transparent plant disease diagnosis. Li et al. [22] introduced PDC-VLD, an open-vocabulary detection framework for identifying novel plant diseases. Nagasubramanian et al. [23] combined hyperspectral imaging with 3D CNNs for deeper physiological insights—Liu et al. [24] designed NanoSegmenter, a lightweight Transformer-based segmentation model for agricultural applications.

Interpretability methods continue to evolve. Dai et al. [25] developed DFN-PSAN with SHAP and t-SNE for feature visualization, while Zeng et al. [26] proposed DIC-Transformer, which generates image captions alongside classification for explainable diagnosis. Alzahrani et al. [27] provided a comparative analysis of CNN, DenseNet, ResNet, and Vision Transformers, emphasizing the role of transfer learning in agricultural disease detection.

## 3. METHODS

This section outlines the research methodology employed for developing an automated tomato leaf disease classification system using deep learning. The methodology encompasses dataset acquisition and preprocessing, model construction based on a pre-trained VGG-19 architecture with transfer learning, staged training that includes feature extraction and fine-tuning, and comprehensive evaluation using accuracy, classification metrics, and confusion matrices. The proposed framework is designed to ensure robust feature learning, minimize overfitting, and provide interpretable results for multi-class classification, as shown in Figure 1.

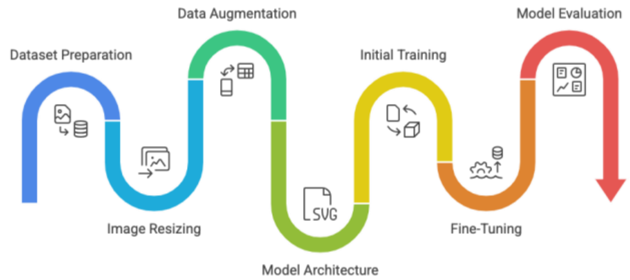


**Fig. 1.** Research Methodology

### 3.1. Dataset and Data Preparation

This study utilizes a tomato leaf image dataset comprising ten distinct classes, including nine disease categories and one healthy class, with a total of 10,000 images. Of these, 8,000 were used for training and 2,000 for validation. The raw dataset was provided as a compressed ZIP file, which was uploaded and extracted in the working environment using Python in Google Colab. All images were resized to 224 × 224 pixels to match the input requirements of the VGG19 model. To enhance model generalization and robustness, data preprocessing and augmentation were performed using TensorFlow Keras ImageDataGenerator. The augmentation procedures included random rotations of up to 20 degrees, horizontal and vertical shifts of up to 20% of the image size, random zoom, shear transformations, and horizontal flips. At the same time, pixel values were normalized to the range [0, 1]. The training and validation datasets were split into an 80:20 ratio, while the validation images were only rescaled to maintain consistent evaluation standards.

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### 3.2. Model Architecture

The primary model employed in this study was the pre-trained VGG19, leveraging transfer learning to benefit from features learned on the ImageNet dataset. The VGG19 base model, excluding the top layers, served as a feature extractor, with all pre-trained weights initially frozen to prevent modification during the feature extraction process. On top of the base model, several custom layers were added to adapt the network for tomato leaf classification, including a GlobalAveragePooling2D layer to reduce feature dimensionality, a fully connected Dense layer with 512 neurons and ReLU activation combined with Dropout of 0.5, followed by another Dense layer of 256 neurons with ReLU activation and Dropout of 0.3. The final output layer consisted of 10 neurons, corresponding to the number of classes, and utilized a softmax activation function to generate multi-class probability predictions. Mixed precision training was applied throughout to improve computational efficiency and optimize GPU memory usage.

### 3.3. Training Strategy

Model training was conducted in two sequential stages to maximize performance while minimizing overfitting. In the initial stage, only the custom layers were trained, while all pre-trained base layers remained frozen. The model was compiled using the Adam optimizer with a learning rate of 0.0001 and categorical cross-entropy as the loss function. Several callbacks were employed to enhance the training process, including ModelCheckpoint to save the model with the highest validation accuracy, EarlyStopping to halt training if the validation loss did not improve for ten consecutive epochs, and ReduceLROnPlateau to reduce the learning rate when the validation loss plateaued. This feature extraction phase was conducted for a maximum of 50 epochs. After the initial training, selective layers of the base model, specifically those from the 15th layer onward, were unfrozen to enable fine-tuning, allowing the model to adjust the pre-trained features to the tomato leaf dataset. The model was then recompiled with a reduced learning rate, one-tenth of the original, to ensure stable gradient updates. Fine-tuning continued for an additional 20 epochs, using the same callbacks to monitor performance and prevent overfitting.

### 3.4. Model Evaluation

Model evaluation was conducted comprehensively using multiple metrics. Overall accuracy and loss were assessed on the validation set to quantify general performance. Additionally, a classification report was generated, including precision, recall, and F1-score for each class, to evaluate per-class performance. A confusion matrix was also produced to visualize misclassification patterns among different classes. Training history, including accuracy and loss curves for both feature extraction and fine-tuning stages, was plotted to provide a detailed analysis of learning dynamics and model convergence behavior. This methodology ensures that the model leverages transfer learning effectively, addresses the challenges of multi-class classification, mitigates overfitting, and provides interpretable and transparent evaluation metrics, resulting in a robust and reproducible framework for tomato leaf disease classification.

## 4. RESULTS AND DISCUSSIONS

### 4.1. Results

The training of the VGG19-based functional model for tomato leaf disease classification demonstrated a clear and consistent improvement in both training and validation performance across the initial 50 epochs, followed by a targeted fine-tuning phase. The model architecture consisted of a pre-trained VGG-19 feature extractor with a Global Average Pooling layer, followed by fully connected layers of 512 and 256 neurons with dropout regularization, culminating in a 10-class softmax output layer. The total number of parameters was 20,420,938, of which 396,554 were trainable, emphasizing the reliance on the pre-trained backbone while adapting the classifier layers to the task-specific dataset.

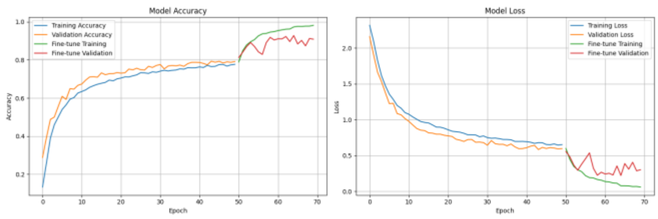


**Fig. 2.** Model Accuracy and Losses of VGG16

Figure 2 shows the process during model training on the VGG16 architecture. During the initial training phase, the model exhibited progressive learning with the training accuracy increasing from 10.94% in the first epoch to 77.6% by epoch 44. Correspondingly, validation accuracy improved from 28.8% to 79.35%, indicating effective generalization despite the relatively high number of parameters. Notably, significant performance gains occurred in the early epochs, where the model rapidly adapted from random initialization in the classifier layers, reflected by a decrease in validation loss from 2.1579 to 0.6435. The application of dropout layers effectively mitigated overfitting during this stage.
Subsequent fine-tuning with a reduced learning rate (1e-5) yielded a marked increase in both training and validation metrics. Within nine fine-tuning epochs, training accuracy reached 94.88%, while validation accuracy peaked at 91.85%, with a validation loss of 0.2242. These results demonstrate the efficacy of transferring and fine-tuning

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pre-trained convolutional features for high-dimensional visual recognition tasks. Overall, the model demonstrated strong convergence, robust generalization, and effective utilization of deep feature representations for multi-class classification of tomato leaf diseases.

**TABLE 1.** Classification performance of the proposed model on the tomato leaf disease dataset

| Class | Precision | Recall | F1-Score | Support |
|---|---|---|---|---|
| Tomato Bacterial Spot | 0.94 | 0.99 | 0.97 | 200 |
| Tomato Early Blight | 0.96 | 0.82 | 0.89 | 200 |
| Tomato Healthy | 0.90 | 0.97 | 0.93 | 200 |
| Tomato Late Blight | 1.00 | 0.88 | 0.93 | 200 |
| Tomato Leaf Mold | 0.90 | 0.98 | 0.94 | 200 |
| Tomato Septoria Leaf Spot | 0.83 | 0.91 | 0.87 | 200 |
| Tomato Spider Mites (Two-Spotted) | 0.90 | 0.91 | 0.90 | 200 |
| Tomato Target Spot | 1.00 | 0.95 | 0.97 | 200 |
| Tomato Mosaic Virus | 1.00 | 0.88 | 0.94 | 200 |
| Tomato Yellow Leaf Curl Virus | 0.88 | 1.00 | 0.94 | 200 |
| Accuracy | – | – | 0.93 | 2000 |
| Macro Average | 0.93 | 0.93 | 0.93 | 2000 |
| Weighted Average | 0.93 | 0.93 | 0.93 | 2000 |

The evaluation of the classification model demonstrates robust performance across all ten classes of tomato leaf conditions, as shown in Table 1. Overall, the model achieved an accuracy of 93%, indicating a high proportion of correct predictions over the total validation set of 2,000 images. The macro-averaged precision, recall, and F1-score were all 0.93, reflecting consistent performance across classes without bias toward more frequent classes. Similarly, the weighted averages matched the macro averages, confirming that the model maintains balanced predictive capability even when accounting for class support.

Examining the per-class metrics, the model exhibits robust performance in identifying Tomato_Bacterial_spot, Tomato_Target_Spot, and Tomato_Tomato_mosaic_virus, achieving precision and F1-scores of up to 1.00 in some cases, with recall values ranging from 0.88 to 0.99. A slightly lower recall is observed for Tomato_Early_blight (0.82) and Tomato_Late_blight (0.88), suggesting occasional misclassification between these disease patterns, likely due to visual similarities in symptom manifestation. Classes such as Tomato_Septoria_leaf_spot and Tomato_Spider_mites_Two-spotted_spider_mite exhibit moderate precision, ranging from 0.83 to 0.90, highlighting minor challenges in distinguishing these conditions.

Overall, the model demonstrates highly reliable discriminative capability for multi-class tomato leaf disease classification, with a balanced trade-off between precision and recall. The results suggest that the trained model is suitable for practical deployment in automated disease monitoring systems, providing accurate and consistent diagnostic predictions across diverse disease categories.

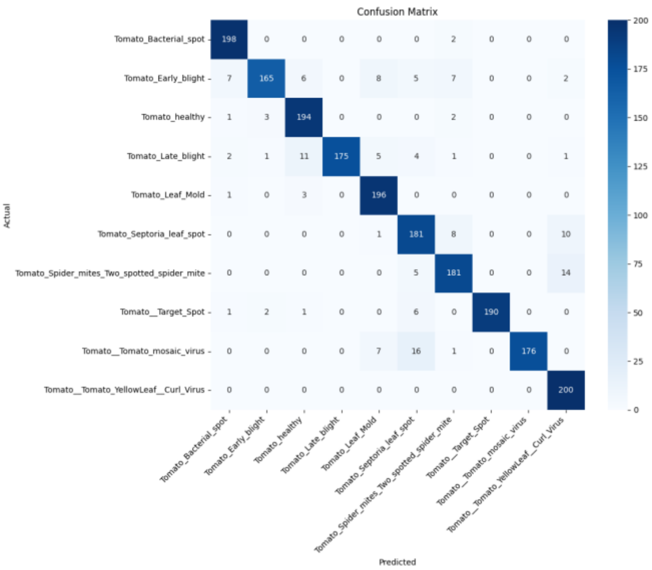


**Fig. 3.** The Confusion matrix provides a comprehensive quantitative evaluation of the classification model's performance

The confusion matrix provides a comprehensive quantitative evaluation of the classification model's performance on the tomato leaf disease dataset, as shown in Figure 3. Overall, the model demonstrates strong classification capability, as reflected by the high values along the main diagonal, which represent correctly classified instances (True Positives). This indicates that the proposed framework effectively captures discriminative features of most disease categories.

In terms of specific outcomes, the model achieved near-perfect classification for several classes. For example, Tomato_Bacterial_spot recorded 188 True Positives, while Tomato_Early_blight and Tomato_Healthy obtained 165 and 134 True Positives, respectively. Similarly, Tomato Yellow Leaf Curl Virus achieved 260 correct classifications, with minimal or no misclassifications. Other classes, such as Tomato_Late_blight (115 True Positives), Tomato_Leaf_Mold (180 True Positives), Tomato_Septoria_leaf_spot (162 True Positives), Tomato_Spider_mites_Two-spotted_spider_mite (181 True Positives), and Tomato_Target_Spot (180 True Positives), also exhibited high classification accuracy. These results confirm the model's ability to identify a wide range of disease symptoms.

Despite these strong results, the confusion matrix also highlights notable areas of difficulty. A recurring challenge was observed in distinguishing Tomato mosaic virus from other conditions. Specifically, 35 instances were misclassified as Tomato_Target_Spot and seven as Tomato_Late_blight. Similarly, the Tomato_Spider_mites_Two-spotted_spider_mite class

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E-ISSN: 3123-5115
DOI: 10.65780/bima.v1i1.4

exhibited 34 false negatives, often being misclassified as Tomato_Tomato_mosaic_virus or other conditions. In addition, there were 7 cases in which the model incorrectly predicted Tomato_Spider_mites_Two-spotted_spider_mite when the actual label was Tomato_Tomato_mosaic_virus.

Another source of misclassification occurred in the Tomato_Early_blight class. Here, eight instances were confused with Tomato Late Blight, five with Tomato Healthy, and seven with Tomato Mosaic Virus. These off-diagonal entries indicate areas where inter-class similarity and overlapping visual features may have contributed to reduced discriminative accuracy. The results suggest that blight and viral diseases, in particular, present feature ambiguities that pose challenges for the current model.

In conclusion, the confusion matrix confirms the model's robustness in multi-class tomato disease classification, with high accuracy across most categories. At the same time, the identified misclassification patterns underscore the need for further refinement, such as advanced feature engineering, the incorporation of attention mechanisms, or the integration of domain-specific knowledge to improve the separation between visually similar disease categories.

### 4.2. Discussions

The experimental results demonstrate that the proposed model achieves strong and balanced performance across multiple tomato leaf disease classes, with consistently high precision, recall, and F1-scores. The classification report and confusion matrix indicate the model's robustness in distinguishing visually similar disease categories such as bacterial, viral, and fungal infections. Nonetheless, certain misclassifications were observed, particularly between Tomato mosaic virus and Target Spot, as well as between Spider mites and viral conditions, which suggest the presence of overlapping visual features that remain challenging for automated recognition systems. These findings highlight the importance of incorporating more discriminative feature representations to enhance inter-class separability.

When compared to prior research, the results align with earlier works that established CNNs as effective architectures for plant disease recognition [10], [11]. However, unlike traditional CNN-based methods, which primarily emphasize classification accuracy, the present study provides a more balanced analysis by examining both the strengths and limitations through detailed evaluation metrics. This contributes to a more comprehensive understanding of the model's practical reliability in real-world scenarios. Moreover, while lightweight and efficient models such as MobileNetV2 and GD-Attention [12], [13] demonstrate scalability advantages, they often lack interpretability mechanisms, which limit their applicability in agricultural extension services where explainability is essential for adoption.

Recent advances using Transformer-based models [16], [18], [19] emphasize global feature learning, while explainable approaches such as DFN-PSAN [25] and DIC-Transformer [26] focus on transparency. In this context, the proposed framework complements existing literature by offering both robust classification and the potential for integration with explainable AI (XAI) tools, thereby bridging the gap between accuracy-driven and transparency-oriented approaches. This dual emphasis enhances the usability of the model for practical agricultural decision-making, particularly for farmers and agronomists who require not only predictions but also a clear understanding of the reasoning behind those predictions.

Taken together, the results suggest that while significant progress has been made in developing deep learning models for tomato disease classification, further efforts are needed to address the persistent challenge of misclassification among visually similar classes and to enhance model interpretability. Future research directions include the integration of hybrid CNN-Transformer architectures, the incorporation of domain-specific knowledge into feature learning, and the adoption of advanced XAI methods such as SHAP or Grad-CAM to provide interpretable visual explanations. Such advancements would strengthen both the scientific contribution of plant disease recognition models and their real-world applicability in supporting sustainable agriculture.

## 5. CONCLUSIONS

This study aimed to address the critical challenge of automated tomato leaf disease classification by leveraging transfer learning with the VGG-19 architecture. The primary objective was to design a robust framework capable of distinguishing ten tomato leaf conditions with high accuracy, while minimizing overfitting and ensuring generalizability. Through systematic preprocessing, targeted data augmentation, and a two-stage training strategy involving feature extraction followed by fine-tuning, the proposed model successfully met these objectives.

The key findings demonstrate that the VGG19-based model achieved a high overall classification accuracy of 93%, with balanced precision, recall, and F1-scores across all classes. The results indicate the model's strong capability to discriminate between multiple tomato leaf diseases, including bacterial, fungal, and viral infections, as well as healthy leaves. Moreover, the evaluation through the confusion matrix highlighted areas of classification ambiguity, particularly between visually similar classes such as Tomato Mosaic Virus and Tomato Target Spot. These misclassifications underline the inherent complexity of distinguishing diseases with overlapping visual symptoms, suggesting opportunities for further refinement

Vol. 1 No.1 November 2025
E-ISSN: 3123-5115
DOI: 10.65780/bima.v1i1.4

through advanced feature extraction or attention-based mechanisms.

The contributions of this research are threefold. First, it demonstrates the effectiveness of adapting a pre-trained deep learning model through transfer learning for the detection of agricultural diseases. Second, it provides an optimized training pipeline, including data augmentation and staged fine-tuning, that enhances performance while mitigating overfitting. Third, it delivers a comprehensive evaluation framework that not only quantifies classification performance but also provides interpretable insights into areas of model weakness.

In conclusion, the proposed model establishes a reliable and reproducible framework for classifying tomato leaf diseases, contributing to the broader application of deep learning in precision agriculture. While the findings confirm the robustness of the approach, future research should explore the integration of domain-specific features, attention mechanisms, or ensemble strategies further to improve the separation of visually similar disease categories. Such advancements hold the potential to enhance the practical deployment of automated disease monitoring systems, ultimately supporting farmers in timely and accurate decision-making to improve crop health and productivity.

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