

A Review of Machine Learning Approaches for Tomato Plant Disease Classification

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Abstract

Tomatoes represent one of the most extensively cultivated and economically significant crops globally. Nevertheless, their productivity is frequently undermined by a range of plant diseases, which, if not promptly detected or effectively managed, can result in substantial yield reductions and economic repercussions. Traditional methods for disease identification are often labor-intensive, subjective, and reliant on expert knowledge, making them inefficient for large-scale agricultural operations. In recent years, machine learning (ML) has emerged as a promising avenue for automating and improving the accuracy of disease detection and classification. This review offers a comprehensive analysis of both conventional ML techniques and advanced deep learning (DL) methodologies specifically applied to the classification of tomato plant diseases. It examines the underlying methodologies of each approach, highlights commonly utilized datasets and evaluation metrics, and discusses the practical limitations associated with their implementation. Key challenges, such as data availability, model robustness, and the deployment of these solutions in real-world agricultural settings, are also addressed.

1. Introduction

Tomato crops are integral to global agriculture, making significant contributions to the economy and food supply across various regions [1]. As a versatile and nutrient-dense vegetable, tomatoes are cultivated extensively, particularly in areas characterized by favorable climatic conditions. However, these plants are highly vulnerable to a multitude of diseases caused by fungi, bacteria, and viruses. Such diseases can substantially diminish both the yield and quality of the crop, resulting in economic losses for farmers and disruptions in food supply chains. Timely and accurate disease detection is crucial for effective management; however, traditional identification methods predominantly rely on manual visual inspections conducted by agricultural experts [2]. These approaches are often labor-intensive, susceptible to human error, and challenging to scale.

ML has emerged as a transformative technology within agriculture, providing a data-driven methodology to automate disease detection processes. By analyzing patterns in images and environmental data, ML models can accurately classify various disease types. These systems not only enhance diagnostic precision but also facilitate real-time and large-scale monitoring, rendering them invaluable tools in the realm of precision agriculture. The purpose of this review is to deliver a comprehensive overview of the ML techniques employed in tomato plant disease classification. The paper commences with a discussion of the most prevalent tomato diseases and the fundamental principles of ML in agricultural contexts. It subsequently explores both traditional and modern

classification approaches, compares their performance, and highlights challenges associated with dataset quality, model generalization, and the deployment of these models in real-world settings.

2. Background and Fundamentals

Sustainable tomato production is crucial for ensuring food security and supporting global agricultural economies. Tomatoes are not only consumed fresh but also serve as key raw materials for various processed products, including sauces, pastes, and juices. Given their economic and nutritional significance, the health of tomato crops has a direct impact on both local and international markets. However, tomato plants are often affected by a wide range of diseases, particularly in the humid and warm climates where they are commonly grown. Accurate diagnosis and timely intervention are critical for maintaining yield and quality. Recent advancements in artificial intelligence, especially in ML, have led researchers and practitioners to explore intelligent systems capable of automatically detecting and classifying plant diseases with high accuracy. Understanding the nature of tomato diseases and the role of ML in agricultural diagnostics is essential to appreciating the potential of current solutions.

Table 1 Common tomato diseases and key visual features

Disease	Causal Agent	Visual / ML Features
Early Blight	<i>Alternaria solani</i>	Brown concentric spots; yellow halos
Late Blight	<i>Phytophthora infestans</i>	Dark, water-soaked lesions; mold on undersides
Leaf Mold	<i>Cladosporium fulvum</i>	Olive-green patches; curled edges
Septoria Leaf Spot	<i>Septoria lycopersici</i>	Small circular spots with dark borders
Mosaic Virus	Tomato mosaic virus	Mottled leaf color; deformation
Yellow Leaf Curl Virus	TYLCV	Upward leaf curl; yellowing veins

2.1 Tomato Plant Diseases

Tomato plants are susceptible to a variety of diseases, each characterized by unique symptoms and impacts on crop health. These diseases can be broadly categorized into fungal, bacterial, and viral infections. Among the most notable fungal diseases is early blight, caused by *Alternaria solani* [3]. This condition primarily affects the lower, older leaves and is characterized by concentric brown or black spots surrounded by a yellow halo [4]. As the infection progresses, affected leaves dry out and fall off, weakening the plant and diminishing its photosynthetic capacity. Late blight, caused by *Phytophthora infestans* [5], is even more destructive, producing large, irregular, water-soaked lesions on leaves, stems, and fruits. These lesions necrotize rapidly and can be covered with a white fungal growth under moist conditions. It leads to potential crop failure within days if weather conditions are favorable. Another significant disease is leaf mold, caused by the fungus *Passalora fulva* [6], which thrives in greenhouse environments. It manifests as pale yellow spots on the upper leaf surfaces and olive-green mold growth underneath, ultimately weakening the plant and making it more susceptible to other infections. Bacterial spot, caused by *Xanthomonas* species [7], leads to water-soaked lesions on leaves, stems, and fruit. These lesions can enlarge, darken, and develop a yellow halo. This results in leaf drops and considerable damage to fruit.

In addition to fungal and bacterial pathogens, tomato crops are affected by several viruses, including the Tomato Mosaic Virus (ToMV) [8], which causes mottling, leaf distortion, reduced fruit size, and stunted growth. ToMV is highly contagious and spreads easily through contaminated tools or plant debris. Another damaging condition is Septoria leaf spot, caused by *Septoria lycopersici* [9], which forms small, circular lesions with dark brown margins and gray centers on the lower leaves. As this disease progresses, the affected leaves turn yellow and drop off, diminishing plant vigor and yield. These diseases not only jeopardize the health and productivity of tomato crops but also impose significant economic burdens on farmers due to increased pesticide use, yield losses, and reduced marketability of infected fruits. Therefore, early and accurate detection of these diseases is essential. However, manual inspection by trained agronomists is often time-consuming, costly, and impractical for large-scale operations, highlighting the need for automated, ML-driven solutions to enhance disease management in modern agriculture.

2.2 Machine Learning in Agriculture

ML has emerged as a transformative tool in agriculture, particularly for plant disease detection and classification. ML algorithms can analyze vast amounts of agricultural data, including images, sensor readings, and environmental variables, to uncover patterns difficult for human observers to detect. In the context of tomato

plant disease classification, ML offers the potential to automate the diagnostic process, making it faster, cost-effective, and more consistent than traditional methods [10]. The typical ML pipeline for disease classification begins with data collection. Image data are often gathered from field conditions or public datasets, such as PlantVillage, capturing a range of disease symptoms under various lighting and environmental conditions. However, raw data usually require preprocessing to prepare them for training. Common preprocessing techniques include resizing images to a uniform scale, enhancing contrast, removing noise, and augmenting the dataset through techniques such as flipping, rotating, or cropping images to artificially expand the training data and improve model generalization [11].

Following preprocessing, the next step is feature extraction. In traditional ML approaches, features are manually engineered based on domain knowledge. For example, researchers might extract features based on color (e.g., RGB or HSV histograms) [12], texture (e.g., using Local Binary Patterns or the Gray Level Co-occurrence Matrix) [13], or shape (e.g., edge descriptors or contour features) [14]. These features quantify the visual differences between healthy and diseased leaves, enabling the model to learn distinguishing patterns of various diseases. In contrast, modern DL approaches, particularly Convolutional Neural Networks (CNNs), automate feature extraction, learning abstract representations directly from raw pixels, often achieving superior accuracy and scalability compared to traditional models [15]. Once features are extracted, they are input into the model training phase, where algorithms learn to map these features to disease labels. Traditional classifiers such as Support Vector Machines (SVM), Decision Trees, k-Nearest Neighbors (k-NN), Random Forests, and Artificial Neural Networks (ANNs) have been widely utilized in early research. Each algorithm offers distinct advantages; for instance, SVMs perform well in high-dimensional spaces and are effective on small- to medium-sized datasets [16], while Random Forests are robust against overfitting and provide interpretable results [17]. k-NN, being a non-parametric method, is simple to implement but can be computationally intensive on large datasets [18].

After training, models are evaluated using performance metrics to assess their effectiveness. Common metrics include accuracy, precision, recall, and the F1-score, which provide detailed insights into model performance, particularly in imbalanced datasets [19]. Confusion matrices are often used to visualize the number of instances correctly or incorrectly classified in each category, revealing potential weaknesses in the model's ability to differentiate between specific diseases [20]. In summary, the integration of ML into agriculture, especially in disease classification, has facilitated the development of powerful automated tools that can significantly assist farmers, agronomists, and researchers. These systems are increasingly robust and accessible, with the potential to transform agricultural disease monitoring and management, ultimately improving crop health and contributing to more resilient food systems.

3. Conventional Machine Learning Methods

Conventional ML methods have been foundational in developing automated plant disease classification systems, particularly prior to the rise of DL. These methods rely on meticulously designed pipelines where meaningful features are extracted from input data to train classification models. The performance of such models is largely contingent upon the quality of the features and the choice of algorithm. In the context of tomato plant disease classification, conventional ML has demonstrated considerable success, especially in scenarios with limited data and computational resources.

3.1 Feature Engineering Techniques

Feature engineering involves identifying, extracting, and selecting relevant features from raw input data. In tomato disease classification, this process typically entails analyzing images of tomato leaves to identify patterns and traits that differentiate healthy plants from diseased ones. The three most commonly employed feature types are color, texture, and shape [21]. Color features are particularly significant, as many plant diseases induce discoloration of the leaf surface. Color histograms in Figure 1 represent the distribution of color values in the RGB color space [22]. This situation helps distinguish between symptoms such as chlorosis, necrosis, and dark spots caused by various pathogens [22].

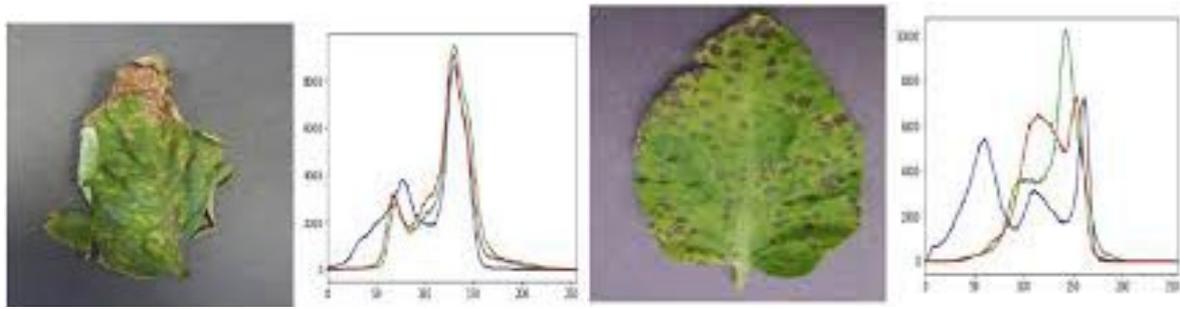


Fig. 1 Example of color histogram feature extraction from tomato leaf images

Texture features provide critical information about the surface quality of leaves, which can often be altered due to fungal or bacterial infections. Techniques such as the Gray Level Co-occurrence Matrix (GLCM) quantify texture based on the spatial relationship of pixel intensities [23]. GLCM features such as contrast, correlation, energy, and homogeneity effectively represent disease-induced variations in texture [23]. Another widely used texture descriptor is the Local Binary Pattern (LBP), which encodes local texture by comparing each pixel to its neighbors, capturing fine-grained details useful for identifying subtle symptoms [24]. Both are illustrated in Figure 2 using leaf images to highlight their effectiveness in texture analysis.

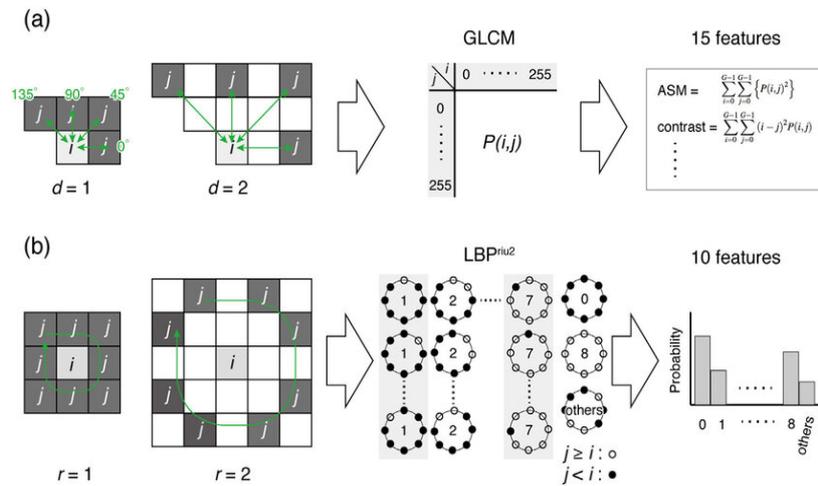


Fig. 2 Visual illustration of LBP and GLCM texture feature extraction from leaf images

While less frequently utilized, shape features can also help distinguish diseases that cause physical deformation of leaves or irregular lesion patterns. Features such as area, perimeter, circularity, and aspect ratio can provide additional cues when combined with color and texture data [25]. The effectiveness of these handcrafted features hinges on their ability to represent disease-specific patterns present in the image data.

3.2 Classical Algorithms

Once features are extracted, they are employed to train ML models that classify the input into predefined disease categories. Several classical algorithms have been utilized in tomato disease classification tasks, each with its strengths and limitations. SVMs are among the most popular classifiers in agricultural image analysis. They are particularly effective in high-dimensional feature spaces and are renowned for their ability to create optimal decision boundaries between classes using kernel functions [26]. SVMs have demonstrated strong performance in disease classification tasks, especially with relatively small and clean datasets.

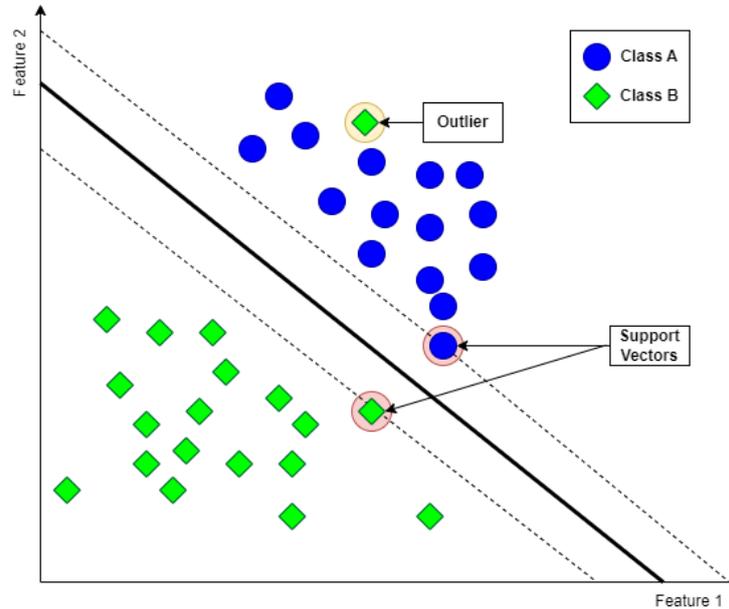


Fig. 3 Schematic diagram of an SVM separating feature classes

Figure 3 illustrates the classification process in an SVM, which categorizes data into two classes, designated as Class A and Class B, within a two-dimensional feature space. The solid black lines, referred to as hyperplanes, serve as the decision boundaries that separate the two classes. The primary objective of the SVM is to identify a hyperplane that maximizes the distance to the nearest data points from each class, known as support vectors (highlighted by red circles). This maximization creates a margin, the space between the dashed lines, which the SVM seeks to widen as much as possible. A larger margin enhances the model's ability to accurately classify new data points. Additionally, the diagram indicates outliers (highlighted by yellow diamonds), which are data points that have been incorrectly classified. In SVM, these outliers may be permissible within the framework of "soft margins," allowing for wider and more generalized margins while still striving for accurate classification. This flexibility is crucial for handling real-world data that may not always conform to ideal conditions.

The k-NN algorithm is a non-parametric classifier that predicts the label of a new sample based on the majority label among its 'k' closest neighbors in the feature space [27]. While k-NN is straightforward to implement and interpret, it can be computationally expensive for large datasets and is sensitive to irrelevant features and noise. Decision Trees and Random Forests are widely employed due to their interpretability and robustness. Decision Trees split data based on feature thresholds, forming an easily understandable tree-like model. However, single trees are prone to overfitting [28]. Random Forests mitigate this limitation by combining multiple decision trees through ensemble learning, which generally results in better generalization and accuracy [29]. Figure 4 illustrates a Decision Tree flowchart and Random Forest Architecture.

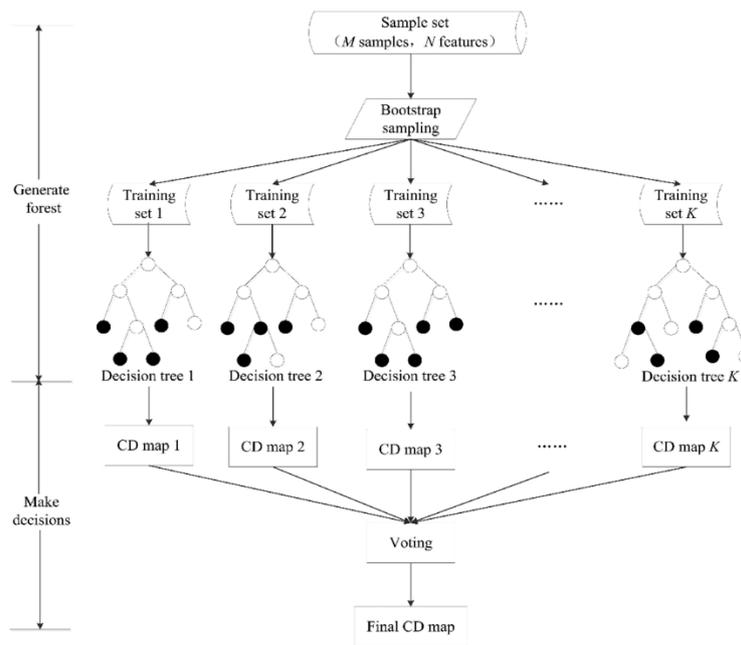


Fig. 4 Random forest architecture

Naïve Bayes classifiers, based on Bayes' Theorem and assuming feature independence, are computationally efficient and perform well in many practical applications, particularly with high-dimensional data [30]. However, their assumptions may not hold true for real-world image data, potentially limiting their accuracy in more complex tasks. ANNs have also been employed in traditional ML settings. Although simpler than DL models, ANNs can capture non-linear relationships in the data and perform effectively when provided with sufficient training samples and well-engineered features [31]. They have been particularly useful in earlier studies before the widespread adoption of CNNs.

3.3 Evaluation Metrics

Evaluating the performance of ML models is crucial for developing reliable disease classification systems. Various metrics are employed to assess model performance, especially in multi-class classification tasks such as identifying different types of tomato diseases.

Accuracy is the most commonly reported metric, referring to the proportion of correctly classified samples over the total number of samples [32]. While useful, accuracy can be misleading when the dataset is imbalanced, meaning some disease classes are significantly more common than others. To provide a more nuanced view of model performance, precision and recall are often reported. Precision measures the proportion of true positive predictions among all positive predictions made by the model, indicating how many of the predicted disease labels are accurate [33]. Recall, conversely, measures the proportion of actual disease instances correctly identified by the model, demonstrating how well the model captures relevant cases [34].

The F1-score combines both precision and recall into a single metric using the harmonic mean. It offers a balanced measure, especially useful when addressing uneven class distributions [35]. This metric is particularly important in agricultural applications, where false positives (e.g., misidentifying a healthy leaf as diseased) and false negatives (e.g., failing to detect a real infection) can significantly impact treatment decisions. A confusion matrix in Figure 5 visually represents classification performance, displaying true labels versus predicted labels across all classes. This tool enables researchers to pinpoint specific classes where misclassification is most likely to occur, thereby enhancing their overall understanding of model performance [20].

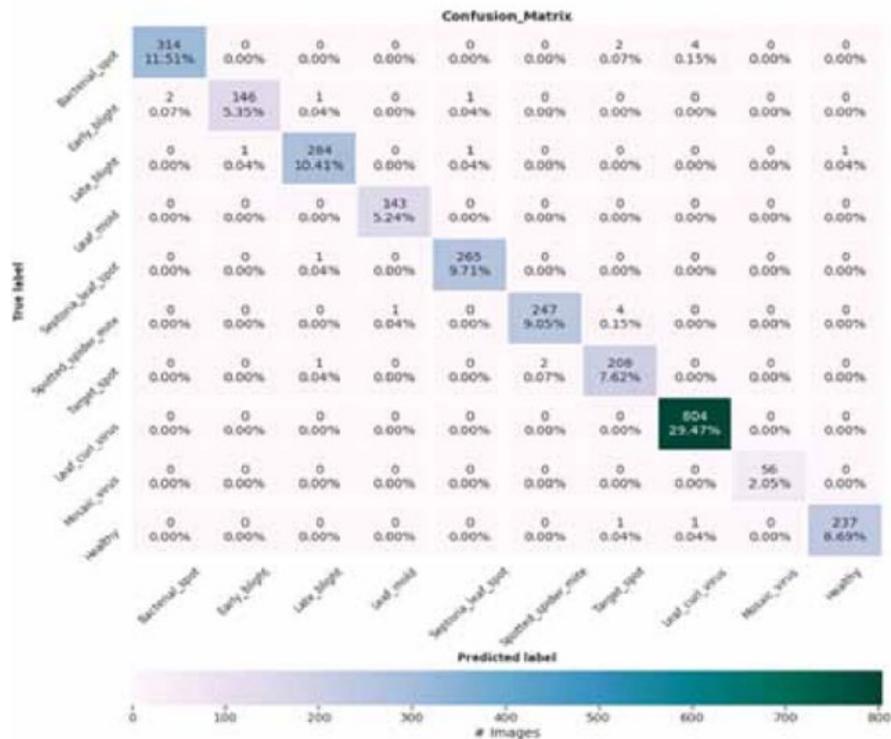


Fig. 5 Confusion matrix showing classification results for multiple tomato diseases

4. State-of-the-Art Deep Learning Approaches

With the increasing availability of computational resources and large-scale annotated datasets, DL has emerged as a dominant paradigm in plant disease classification. Unlike conventional ML techniques that rely on manual feature extraction, DL models can automatically learn relevant features from raw data, significantly improving accuracy and scalability. CNNs, in particular, have revolutionized image-based disease classification tasks. Additionally, hybrid architectures and ensemble models have been developed to enhance robustness and generalization. This section discusses the leading DL architectures applied to tomato plant disease classification, explores advanced hybrid models, and compares their performance to traditional ML methods.

4.1 Convolutional Neural Networks (CNNs)

CNNs are a class of DL models specifically designed for image analysis. They excel at learning hierarchical representations of visual data through stacked convolutional, pooling, and fully connected layers. In the domain of tomato disease classification, CNNs have consistently outperformed traditional algorithms due to their ability to extract complex features directly from leaf images.

Several pre-trained CNN architectures have been adapted for tomato disease diagnosis through transfer learning. AlexNet [36], one of the earliest deep CNNs, has been widely used for image classification tasks due to its relatively simple architecture and strong performance on moderate-sized datasets. VGGNet, recognized for its deep and uniform layer structure (typically employing 16 or 19 layers), has been utilized in numerous agricultural studies due to its ability to capture fine-grained image details [37]. More recently, ResNet (Residual Network) has gained preference due to its introduction of residual connections, which facilitate the training of much deeper networks without degradation issues [38]. Variants such as ResNet-50 and ResNet-101 have demonstrated superior classification accuracy on complex datasets related to plant diseases.

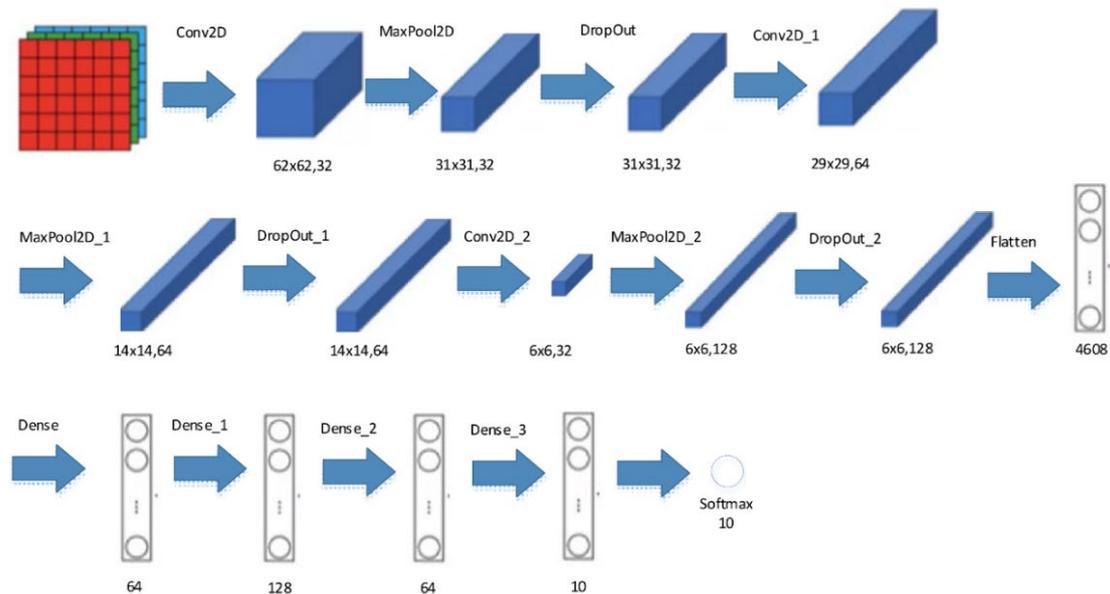


Fig. 6 CNN architecture overview with alexnet, vggnet, and resnet on tomato leaf images

Figure 6 illustrates the architecture of a CNN used for tomato leaf classification. The convolution and pooling layers extract crucial features, while the dropout layer mitigates overfitting. The features are then smoothed and processed through dense layers, culminating in a Softmax layer that classifies the leaves as healthy or diseased. These models are typically fine-tuned on tomato leaf datasets using transfer learning, allowing them to leverage pre-learned weights from large datasets like ImageNet and adapt them to specific agricultural tasks with limited training data. This fine-tuning significantly reduces training time and enhances convergence, particularly when only a small number of labeled tomato disease images are available.

4.2 Hybrid and Ensemble Models

To improve classification performance and address the limitations of individual models, researchers have explored hybrid and ensemble approaches. Hybrid models combine different types of neural networks or incorporate additional components to enrich feature representation and capture temporal dynamics. For instance, some studies have proposed integrating CNNs with Recurrent Neural Networks (RNNs), particularly Long Short-Term Memory (LSTM) networks, to capture both spatial and sequential patterns [39]. While CNNs effectively extract spatial features, RNNs are adept at learning dependencies in sequences, such as the progressive changes in disease symptoms over time.

In addition to hybrid models, ensemble techniques have been widely adopted. These models aggregate the predictions of multiple CNNs, either of the same type with different initializations or of different architectures (e.g., VGG + ResNet), to form a more robust classification decision [40]. This voting or averaging strategy helps reduce model variance and improve reliability, particularly in datasets with noise or variable values. Attention mechanisms have also been integrated into CNNs, enabling the model to focus on the most informative regions of the image. These networks dynamically weigh different parts of the input image, often enhancing performance when disease symptoms are subtle or localized.

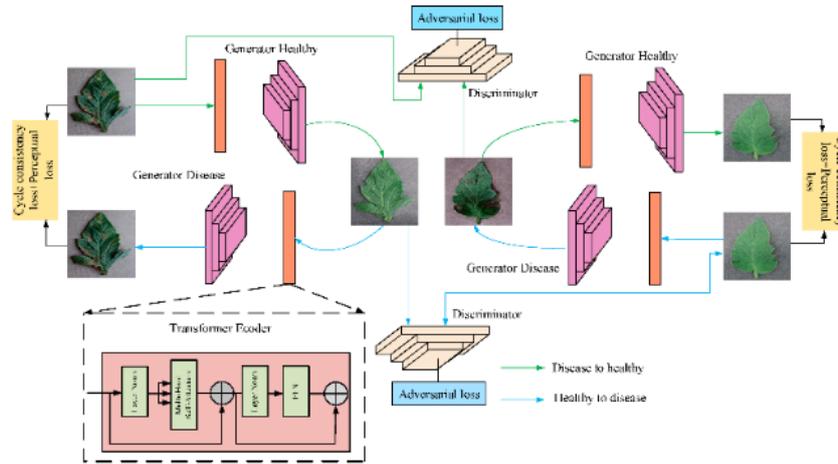


Fig. 7 CNN-based architectures for tomato leaf disease detection

Figure 7 illustrates the workflow of CNN architectures, including AlexNet, VGGNet, and ResNet, applied to the detection of tomato leaf diseases. The process begins with input leaf images, which may represent either healthy or diseased samples. These images are processed through successive convolutional and pooling layers that extract hierarchical features such as texture, color, and shape. The extracted features undergo further processing by deeper network layers to distinguish between disease categories with high accuracy. The figure also includes adversarial loss and discriminator components, which enhance robustness and prevent overfitting, thereby improving the model's generalization across varying image conditions.

These advanced models are particularly valuable in field applications, where disease symptoms may vary due to factors such as lighting, occlusion, or overlapping symptoms. Hybrid and ensemble approaches mitigate the risk of misclassification by combining multiple perspectives or learning paths.

4.3 Performance Comparison with Classical Methods

DL models consistently outperform traditional ML methods in terms of classification accuracy, robustness, and generalizability. While classical approaches such as SVM and Random Forests can perform adequately on small, curated datasets, their accuracy often declines in complex real-world scenarios [41].

CNNs remain the dominant technique, frequently achieving accuracies exceeding 95% on benchmark datasets such as PlantVillage [42]. Hybrid and ensemble DL approaches enhance this performance further, often reaching above 98%, depending on dataset size, quality, and augmentation strategy [43]. Additionally, DL models exhibit greater scalability, effectively handling multi-class classification and unbalanced datasets. However, these advantages come with high computational demands, reliance on large annotated datasets, and limited interpretability. Despite these challenges, DL remains the preferred choice for tomato disease classification.

Figure 8 illustrates the distribution of DL techniques utilized in this domain. CNNs dominate with usage ranging from 70% to 80%, underscoring their suitability for image-based disease detection. Transfer learning and RNNs are employed less frequently (10-15%), while generative adversarial networks (GANs) and other techniques account for marginal usage (5-10%). This distribution highlights the predominant role of CNNs, with alternative methods contributing only minimally.

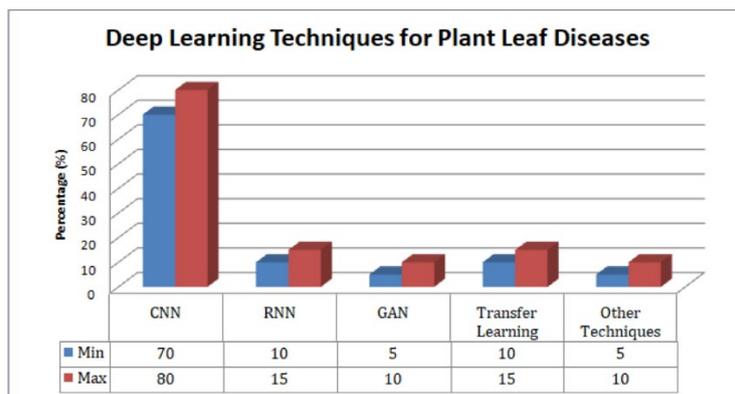


Fig. 8 Classification accuracy of deep learning models on tomato disease dataset

5. Datasets and Tools

The success of ML and DL models in classifying tomato plant diseases heavily relies on the availability of high-quality datasets and suitable tools for preprocessing and annotation. This section explores the most commonly used publicly available datasets and the essential tools and techniques employed to prepare and manage image data for effective model training and evaluation.

5.1 Publicly Available Datasets

The foundation of any image-based classification system is the dataset used for training and validation of the model. In the domain of plant disease detection, the PlantVillage dataset is one of the most widely utilized resources. This open-access dataset includes over 54,000 high-quality, labeled images of healthy and diseased leaves from various crops, including tomatoes. The tomato section of PlantVillage comprises multiple disease classes such as early blight, late blight, leaf mold, Septoria leaf spot, bacterial spot, and others, alongside healthy samples [44]. Images in this dataset are captured under controlled conditions with uniform lighting and plain backgrounds, which facilitates high classification accuracy but may not fully represent field conditions.

In addition to PlantVillage, several tomato-specific datasets have been curated by researchers and institutions, particularly for region-specific agricultural contexts. These datasets are typically smaller but offer more realistic images taken in natural environments with varying lighting, occlusions, and background noise. They are especially useful for training models intended for deployment in real-world farming scenarios. Some datasets are accessible through academic publications, agricultural research centers, or open ML repositories like Kaggle and GitHub. The diversity and realism of these datasets are essential for enhancing the generalizability of models. Figure 9 shows the sample images from PlantVillage.

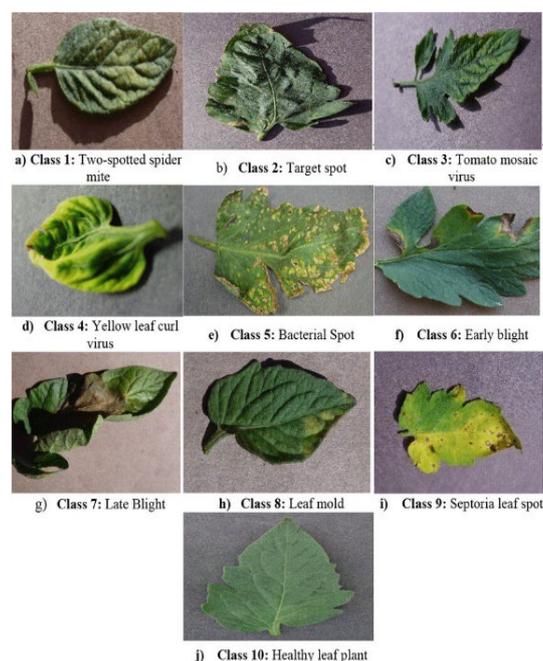


Fig. 9 Sample images from plantvillage dataset

However, a notable limitation in many available datasets is the class imbalance problem, where certain diseases are overrepresented while others are rare. This imbalance can bias the model toward the dominant classes. Researchers often address this by employing data augmentation techniques or implementing resampling strategies during training.

5.2 Image Annotation and Preprocessing Tools

Accurate labeling of images is critical for supervised learning tasks. Tools like LabelImg have become standard for manually annotating regions of interest within images, especially when the objective is not only classification but also localization or segmentation of disease-affected areas [45]. LabelImg allows users to draw bounding boxes and export annotations in formats compatible with popular ML frameworks such as TensorFlow and PyTorch [46].

Beyond labeling, image preprocessing is a key step in preparing data for model training. Libraries such as OpenCV are widely used to perform operations like resizing, noise reduction, background removal, and color normalization. These steps help standardize input data and enhance the quality of feature extraction. Common image augmentation techniques, such as rotation, flipping, scaling, brightness adjustment, and zooming, are applied to artificially expand the dataset and improve model robustness. Augmentation mitigates overfitting and enhances the model's ability to generalize to unseen data.

Additionally, some researchers employ advanced preprocessing methods, such as histogram equalization, edge detection, or color space transformations (e.g., converting from RGB to HSV), to emphasize disease-relevant features. The choice of preprocessing methods depends on the specific model architecture and the dataset's characteristics. Together, the availability of robust datasets and powerful preprocessing tools forms the backbone of any effective tomato disease classification system. Ongoing efforts to develop more diverse and realistic datasets, along with improvements in annotation and augmentation methods, continue to drive progress in this field.

6. Challenges and Limitations

Despite the significant progress in applying ML and DL to tomato plant disease classification, several persistent challenges and limitations hinder their full-scale deployment in real-world agricultural environments. These limitations span data availability, model robustness, computational demands, and practical field implementation.

One of the most pressing issues is the imbalance of datasets [47]. In many publicly available datasets, certain diseases are overrepresented while others have very few samples. For example, common diseases such as early blight or bacterial spot often dominate datasets, whereas rare conditions may have only a handful of images. This imbalance can lead to biased models that perform well on frequent classes but fail to correctly classify underrepresented ones. Techniques such as data augmentation, synthetic image generation, and resampling strategies are commonly used to mitigate this issue. However, they do not always replicate the true variability of real symptoms. Another major limitation is overfitting [48], especially in DL models trained on small or homogeneous datasets like PlantVillage. These models often achieve high accuracy on validation sets but fail to generalize to new, unseen images, particularly when tested on field data with noise, variable lighting, occlusion, and different leaf orientations. Overfitting occurs when the model learns to memorize training examples instead of learning general patterns. This problem is exacerbated when models are trained with insufficient regularization or when datasets lack diversity.

The real-time deployment of ML or DL models in agricultural settings remains a significant challenge [49]. Most high-performing models are computationally intensive, requiring substantial memory and processing power. It renders them unsuitable for deployment on low-resource edge devices, such as mobile phones or drones. Furthermore, latency and inference time can become bottlenecks when attempting to detect and respond to plant diseases in real-time. Solutions such as model quantization, pruning, or utilizing lightweight architectures (e.g., MobileNet) are being explored to bridge this gap; however, trade-offs in accuracy often arise. Environmental variability [50] also poses a critical challenge. Field conditions are inherently dynamic, with changes in lighting, background clutter, leaf occlusion, and the presence of non-disease-related artifacts such as dirt or insect bites. Models trained in controlled environments often perform poorly in such settings. To overcome this, robust data collection protocols, domain adaptation techniques, and training on diverse field datasets are needed to ensure models are resilient under varying conditions.

Table 2 List of challenges applying ML and DL to tomato plant disease classification

Challenge	Description	Impact	Possible Mitigation
Dataset Imbalance [47]	Datasets often have significantly more samples of common diseases compared to rare ones, such as the PlantVillage dataset	Models skewed toward majority classes; poor rare-disease recognition	Resampling, augmentation, synthetic data
Overfitting [48]	High-performing DL models trained on homogeneous datasets tend to memorize training examples instead of generalizing to new data	Poor performance on real-world, variable field data	Regularization, cross-domain training, diverse datasets

Challenge	Description	Impact	Possible Mitigation
Computational Demands (Deployment Constraints) [49]	Many models are too heavy for deployment on edge devices like mobile phones or drones	Limits real-time, in-field disease detection and response	Lightweight architectures (e.g., MobileNet variants), compression
Environmental Variability [50]	Field images suffer from challenges such as non-uniform lighting, occlusion, clutter, and insect damage	Models trained under lab or uniform conditions fail in real-world contexts	Domain adaptation; training on diverse, real field data
Lack of Large-Scale Field-Annotated Data [51]	Most datasets are collected under controlled lab conditions, which lack the complexity and variability of real agricultural environments	Model robustness and real-world applicability are compromised	Develop/collect annotated field datasets with stakeholder collaborations

Finally, there is a lack of large-scale, annotated field data [51]. Most existing datasets are collected in controlled settings, which do not reflect the complexity of real agricultural environments. Collecting high-quality field data is labor-intensive, requires expert annotations, and often involves privacy or proprietary concerns from agricultural stakeholders. Without access to diverse, labeled field images, it becomes difficult to train models that are truly applicable in practical farming scenarios. Table 1 lists the challenges of applying ML and DL to tomato plant disease classification, while Figure 10 illustrates examples of challenges in tomato disease detection using ML or DL.

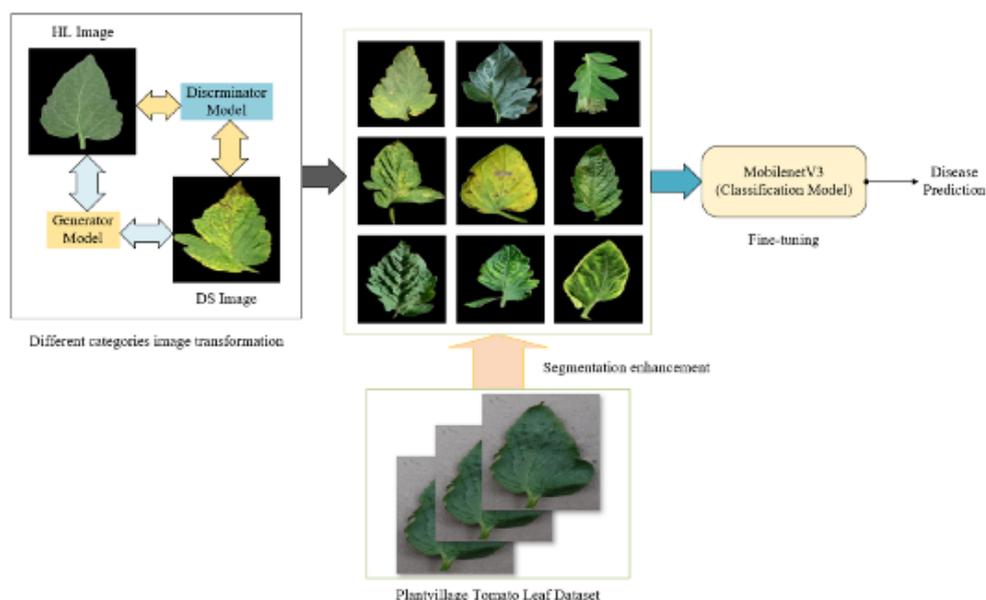


Fig. 10 Challenges in tomato disease detection using ML/DL

In summary, while current ML technologies hold immense promise for improving tomato plant disease management, addressing these challenges is essential to translate academic research into effective, scalable agricultural solutions. Future work should focus on building balanced and realistic datasets, optimizing models for field deployment, and developing adaptive systems that can learn and improve continuously under real-world conditions.

7. Emerging Trends and Feature Directions

As ML continues to evolve, several emerging trends are poised to address current limitations and enhance the capabilities of tomato plant disease classification systems. These innovations aim to make models more adaptable, transparent, and practical for real-world agricultural applications. Among the most promising developments are few-shot learning, explainable artificial intelligence (XAI), integration with the Internet of Things (IoT), multimodal learning, and the use of GANs for synthetic data generation.

Few-shot learning (FSL) offers a powerful solution to the problem of limited labeled data, particularly for rare diseases. Traditional DL models typically require large amounts of labeled examples to achieve good performance, which can be infeasible in agricultural settings. FSL enables models to generalize from just a handful of examples by leveraging prior knowledge or meta-learning techniques. In the context of tomato disease classification, FSL can facilitate accurate recognition of rare or newly emerging diseases with minimal annotation effort, making it ideal for rapid response scenarios and low-resource environments. XAI is gaining traction as researchers and practitioners seek to understand and trust the decisions made by complex models. Black-box models, particularly deep neural networks, can yield high accuracy but often lack interpretability. XAI techniques, such as saliency maps, Grad-CAM, and SHAP values, help visualize which parts of the input (e.g., specific leaf regions) contribute most to the model's predictions. This transparency is crucial for gaining user trust, enabling agronomists and farmers to validate automated decisions and identify possible model biases or errors.

IoT integration is another transformative trend, combining ML with sensor networks, drones, and mobile devices to facilitate real-time monitoring and decision-making. Tomato plants in smart farms can be continuously observed using IoT devices that collect image data and environmental parameters such as temperature, humidity, and soil moisture. When coupled with ML or DL models, these systems can provide early disease warnings, automated alerts, and treatment recommendations. This integration enhances precision agriculture by enabling data-driven and localized disease management. Multimodal learning is an emerging approach that combines multiple types of data. These include visual imagery, spectral data, weather conditions, and soil measurements to improve classification accuracy. By integrating complementary data sources, models can achieve a more comprehensive understanding of crop health and its environmental context. For instance, combining RGB images with near-infrared or thermal data can enhance the detection of early-stage infections. These infections may not yet be visible to the naked eye. Additionally, multimodal approaches enhance the model's robustness under varying field conditions.

GANs offer an innovative approach to overcoming dataset limitations by generating realistic synthetic images of tomato leaves under various disease conditions. The architecture includes two neural networks, that is a generator and a discriminator. This architecture competes to produce high-quality, believable images.

These synthetic samples can expand real-world datasets, particularly for underrepresented disease classes, improving model accuracy and reducing the need for costly manual data collection. Furthermore, GANs can simulate disease progression or environmental variations, enhancing training diversity.

Table 2 highlights key trends and features designed to address current limitations and strengthen tomato disease classification systems.

Table 2 Trends and features to address current limitations

Trend / Feature	Key Idea	Benefit
Few-Shot Learning (FSL) [52]	Learns from very few labeled examples	Detects rare or new diseases with minimal data
Explainable AI (XAI) [53]	Makes model decisions interpretable (e.g., saliency maps, Grad-CAM, SHAP)	Builds trust, validates predictions, reduces bias
IoT Integration [54]	Links ML or DL with sensors, drones, mobile devices	Enables real-time monitoring and early alerts
Multimodal Learning [55]	Combines multiple data types (images, weather, soil)	Improves accuracy, robustness, and early detection
GANs (Synthetic Data) [56 – 58]	Generates synthetic disease images	Expands datasets, balances classes, simulates conditions

The future of tomato disease classification lies in developing more adaptive, transparent, and context-aware systems. As few-shot learning and GANs address data scarcity, and as IoT and multimodal frameworks provide richer inputs, the next generation of ML or DL models will be more practical and deployable in diverse agricultural settings. Furthermore, XAI will play a vital role in ensuring that these systems are not only accurate but also accountable and trusted by end-users. Continued research in these areas will be essential to creating intelligent, farmer-friendly tools that support sustainable and resilient tomato production.

8. Conclusions

This review has explored the landscape of ML and DL techniques applied to the classification of tomato plant diseases, a critical area of research within smart agriculture. From conventional feature-based methods like SVM and k-NN to more advanced DL architectures such as CNNs and hybrid models, the evolution of computational tools has significantly improved the accuracy and efficiency of disease detection. These methods have demonstrated great potential in identifying a wide range of tomato plant diseases, enabling earlier intervention and supporting better crop management strategies. However, several challenges persist, including dataset imbalance, limited generalization to field conditions, overfitting, and the lack of scalable, real-time deployment systems.

Emerging trends such as FSL, XAI, IoT-based monitoring, multimodal data fusion, and the use of GANs for synthetic data generation are paving the way toward more robust and adaptive agricultural AI systems. These innovations promise to overcome many of the limitations currently faced in deploying ML solutions in real-world farming environments. They also represent a step forward in making precision agriculture more accessible and effective for small-scale and resource-limited farmers.

The future of tomato disease management lies in the integration of intelligent, automated, and interpretable systems that can operate reliably under diverse conditions. Continued interdisciplinary research combining computer vision, plant pathology, data science, and agricultural engineering will be essential to achieve these goals. As agricultural AI systems become more advanced and widespread, they will play a vital role in ensuring food security, minimizing crop losses, and promoting sustainable farming practices on a global scale.

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Conflict of Interest

Authors declare that there is no conflict of interests regarding the publication of the paper.

Author Contribution

The author confirms sole responsibility for the following: study conception and design, data collection, analysis and interpretation of results and manuscript preparation.

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