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Feature Extraction and Segmentation Methods in Plant Disease Detection: A Multimodal Approach

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Abstract— Plant disease detection is essential for improving agricultural productivity. Deep learning models have shown great potential in identifying plant diseases because they can leverage large datasets. However, while efficient, traditional machine learning methods often face challenges with generalization when trained on small datasets using basic features like shape, color, and texture. A promising approach to overcome this is the combination of deep feature extraction with machine learning classification, enabling more accurate disease detection. Traditional classifiers trained on smaller datasets can still offer viable solutions in resource-limited environments. By extracting critical features and employing classical techniques, these models remain practical for constrained settings. Integrating deep learning models with traditional methods allows for better handling of disease variability across plants and conditions, enhancing adaptability and accuracy. This review explores deep learning and traditional machine learning approaches for feature extraction and segmentation in plant disease detection. It highlights how combining deep feature extraction with machine learning classification improves accuracy and addresses the challenges posed by limited datasets. The potential of multimodal techniques for enhanced detection is also discussed, leading to more robust and scalable solutions for plant disease management.

Keywords: Plant disease detection, feature extraction, deep learning, multimodal approaches.

1. Introduction

Effective plant disease detection is vital for precision agriculture, significantly impacting plant health and productivity. With the rise in disease outbreaks, timely detection has become crucial for accurate diagnosis, control, and minimizing damage. Early identification enables targeted treatments and helps prevent substantial economic losses [1] identified essential metrics, such as disease incidence (proportion of affected plants), severity (extent of damage), and consequence (impact on yield). Computer vision techniques have revolutionized plant disease detection, surpassing traditional human methods, often labor-intensive and subjective [2]. Automated systems now employ machine learning to analyze plant images, identifying patterns based on features like texture, color, and shape. For instance, [3] demonstrates how classifiers detect diseases by comparing extracted features with labeled datasets. Despite these advances, a gap remains in the generalizability of these models, especially in resource-constrained environments. Deep learning models, particularly convolutional neural networks (CNNs), offer improved accuracy by processing large datasets and detecting subtle patterns, but computational resources often limit their application. This research addresses these challenges by exploring how deep learning models can effectively integrate with traditional methods to enhance plant disease detection, ensuring better scalability and performance.

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2. Plant Disease Segmentation

Plant disease segmentation is crucial in computer vision for isolating diseased areas in plant images, which improves diagnostic precision. Various techniques depend on image characteristics and disease patterns, including thresholding, region growing, the watershed algorithm, edge-based segmentation, regional methods, and clustering. Ref [4] illustrate that thresholding is a basic but effective method that classifies pixels based on intensity relative to a threshold value, distinguishing diseased regions from healthy ones. It can be applied globally, with a single threshold for the whole image, or locally, with different thresholds for various image regions. Ref [5] argue that the algorithm generates a pixel intensity histogram, selects a threshold (e.g., Otsu's method), and classifies pixels as foreground or background based on this value. While effective for images with clear contrasts, thresholding struggles with uneven illumination or subtle intensity variations. As shown by [6], region growing is another pixel-based technique that begins with seed points and expands to include neighboring pixels based on similarity criteria such as intensity, color, or texture. This method involves selecting seed points manually or automatically and adding neighboring pixels that meet a homogeneity criterion until no more can be included. This technique is helpful for segmenting regions with similar properties but may require careful tuning of parameters to handle varying image conditions effectively. The region method's strength lies in creating connected regions that match actual diseased areas. Still, its accuracy depends on seed point selection and homogeneity criteria. Poor seeds can cause over- or under-segmentation, as [7] illustrated, especially in noisy or variably intense images. Automatic seed selection and post-processing can help refine the results. This method excels with continuous diseased patches, like early blight, but can struggle with irregular or diffuse disease patterns.

The watershed algorithm uses a topological approach, treating pixel intensities as elevation. Local minima are identified as catchment basins, which flood until they meet at watershed lines forming region boundaries. [8] correctly points out that the method can effectively treat diseases with clear boundaries but can suffer from over-segmentation in noisy images. Pre-processing, such as Gaussian smoothing or marker-based control, can reduce noise and improve segmentation. Edge-based segmentation detects boundaries between regions with different intensities, ideal for diseases with clear lesions. Ref [9] shows that techniques like the Canny edge detector involve smoothing, gradient computation, non-maximum suppression, double thresholding, and edge tracking. These methods work well for distinct lesions but are noise-sensitive and may require additional pre-processing. Regional methods, as in the works of [10] such as split-and-merge algorithms, segment images based on homogeneity within regions, iteratively splitting non-homogeneous areas, and merging similar ones based on pixel intensity variance. In split-and-merge algorithms, an image is divided into regions, which are then evaluated for homogeneity based on criteria like variance or mean intensity. The ref [11] approach demonstrates that non-homogeneous regions are split while adjacent homogeneous regions are merged, continuing iteratively until homogeneity is achieved. These methods work well for diseases affecting large, uniform areas, such as leaf rust, but may struggle with irregular or complex patterns.

Clustering techniques like k-means and fuzzy c-means (FCM) are used for unsupervised segmentation by grouping pixels based on features like intensity, color, or texture. K-means partitions pixels into k clusters, recalculates centroids, and repeats until convergence, as [12] discusses. FCM assigns membership probabilities to pixels, allowing for more flexible segmentation, especially where boundaries are unclear. Clustering is versatile for various plant diseases, particularly those with subtle color or texture changes, but requires careful parameter tuning and sometimes post-processing for refinement.

3. Detection Feature Extraction Techniques

Sdda Feature extraction is essential in plant disease detection, focusing on identifying key attributes that differentiate healthy from diseased plants; as [13] also elaborates, it involves extracting relevant features such as color, texture, shape, and patterns. These features play a vital role in ensuring accurate detection. Techniques such as color analysis, texture analysis, shape-based, and frequency-domain methods contribute significantly to disease identification.

3.1 Detection of Diseases Using Color Analysis

Sadasd Color analysis is pivotal in plant disease detection, especially when identifying discoloration caused by various diseases. Color is often one of the earliest visible symptoms, and analyzing color variations can provide critical information about the plant's health. According to [14], common color spaces like Red-Green-Blue (RGB), Hue-Saturation-Value (HSV), and CIELAB (LAB) are frequently used to detect these changes, with HSV and LAB being particularly robust against variations in lighting conditions. Ref [15] demonstrates that RGB is an additive color model where colors are created by combining different intensities of red, green, and blue light. Each component can range from 0 to 255, with (255, 255, 255) producing white and (0, 0, 0) resulting in black. LAB, which separates lightness from color-opponent dimensions, further refines this analysis, helping to differentiate healthy from diseased tissues under various conditions.

Algorithms such as color histograms, moments, and coherence vectors are commonly employed to analyze these color distributions. Color histograms, as shown in the works of [16] measure the distribution of color intensities in an image and are useful in detecting shifts in plant tissue color due to disease. Color moments, which include mean, variance, and skewness, provide a statistical approach to capturing the overall color changes, while coherence vectors, as illustrated by [17], focus on identifying coherent regions of similar color, aiding in segmenting diseased areas. This multi-dimensional approach to color analysis has demonstrated enhanced accuracy, as in the works of [18] in disease detection, by effectively distinguishing healthy and diseased plant regions through robust color feature extraction.

3.2 Texture-Based Disease Detection

Texture-based disease detection is highly effective for diagnosing plant diseases by quantifying surface characteristics and identifying subtle changes that may not be readily visible through color or shape alone. This method analyzes the spatial arrangement of pixels, which proves useful for diseases that alter plant textures, such as fungal infections, bacterial blight, or viral diseases [19].

One widely used technique is the Gray-Level Co-occurrence Matrix (GLCM), which calculates how often pairs of pixel intensities occur at a specific distance and direction. GLCM, as shown in the works of [20] captures statistical texture features like contrast, correlation, energy, and homogeneity, making it a valuable tool for differentiating healthy areas from diseased ones. For instance, GLCM can identify surface roughness in diseases like powdery mildew or rust by analyzing texture patterns. Another critical method is Local Binary Patterns (LBP), which assigns binary values to each pixel based on the intensities of neighboring pixels. This results in a texture descriptor that summarizes local texture variations. Ref [21] illustrate that LBP is particularly effective for detecting subtle texture changes caused by diseases like mosaic virus or bacterial leaf blight. Its computational efficiency and robustness against lighting variations make it suitable for real-time applications in disease detection.

Gabor filters offer another texture-based approach, analyzing textures at multiple scales and orientations through a Gaussian function modulated by a sinusoidal wave. These filters detect repetitive or directional texture patterns associated with fungal infections. For example, Gabor filters, as discussed by [22] can identify spore clusters in rust diseases or powdery spores from downy mildew. Additionally, the wavelet transforms provide a multi-resolution analysis by decomposing an image into various frequency components at different scales. This method is particularly effective for detecting coarse and fine-grained textures in plant diseases. For example, it can capture large-scale rust patterns and fine-grained symptoms of bacterial blight. These texture features like Contrast, Correlation, Energy, Homogeneity, Entropy, Root Mean Square (RMS), Variance, Smoothness, Kurtosis, and Skewness offer insights into the texture patterns of plant tissues, which can indicate various diseases. Contrast measures the intensity difference between neighboring pixels in an image. It quantifies the amount of local variation or edge strength in the texture, which can be crucial for detecting diseases that cause pronounced changes in the appearance of plant tissues. The contrast can be presented in equation (1).

$$\text{Contrast } = \sum_{i,j} (i-j)^2 \cdot P(i,j) \tag{1}$$

P (i, j) represents the probability of the pixel pair *(i, j)* occurring in the image. High contrast values indicate significant differences in pixel intensities, which can highlight areas affected by diseases like powdery mildew or bacterial blight, where infected regions often exhibit sharp boundaries and varying intensities. The ability to measure and analyze these variations helps identify and quantify disease severity, as shown in the works of [23].

Correlation assesses the degree to which pixel values are linearly related to their neighbors. As [20] also elaborates, this feature captures the dependency between neighboring pixels and is useful for detecting diseases that alter the structural relationships within plant tissues, and this can be represented as in (2):

$$\text{Correlation } = \frac{\sum_{i,j}(i-\mu_i)\cdot(j-\mu_j)\cdot P(i,j)}{\sigma_i\cdot\sigma_j} \tag{2}$$

Where μ_i and μ_i are the means of pixel values for rows and columns, and σ_i and σ_j are their standard deviations. High correlation values suggest that neighboring pixels have similar intensities, which is useful for detecting diseases that produce consistent texture patterns. For instance, diseases that cause uniform discoloration or patterning in plant tissues will result in higher correlation values.

Energy (or Angular Second Moment) quantifies the uniformity or regularity of texture by measuring the sum of the squared elements in the GLCM. As shown by [24] a higher energy value indicates a more uniform and consistent texture, while lower values suggest more complex textures. This can be shown in (3).

$$\text{Energy } = \sum_{i,j}\,[P(i,j)]^2 \tag{3}$$

Energy is useful for detecting diseases that produce uniform texture changes across plant surfaces. For example, [25] breaks down fungal infections that spread uniformly and can be identified by analyzing areas with high energy values. The feature highlights regions where the texture remains consistent, which can help differentiate between healthy and diseased tissues.

Homogeneity measures the closeness of the distribution of elements in the GLCM to the diagonal, reflecting the smoothness of the texture as in (4).

$$\text{Homogeneity } = \sum_{i,j}\frac{P(i,j)}{1+(i-j)^2} \tag{4}$$

Where $(i-j)^2$ is the squared difference between the pixel values. Higher homogeneity, as [26] argues, indicates smoother textures, which can be useful for identifying diseases that create relatively smooth or uniform texture changes. For example, diseases that cause subtle changes in texture, such as some viral infections, may exhibit higher homogeneity values.

Entropy measures the amount of information or disorder in the texture. It reflects the randomness or complexity of the texture and is calculated as in (5).

$$\text{Entropy } = -\sum_{i,j}\,P(i,j)\log\left(P(i,j)\right) \tag{5}$$

Entropy provides insight into the texture's complexity, with higher values indicating more chaotic or irregular patterns. Lhermitte et al. (2022) demonstrate that this feature is handy for detecting diseases that cause irregular and unpredictable texture changes. For instance, complex infections with varied symptoms may result in higher entropy values, making it easier to identify such diseases.

Root Mean Square (RMS) quantifies the deviation of pixel values from the mean, offering a measure of texture roughness or energy. This can be demonstrated as in (6).

$$\text{RMS} = \sqrt{\sum_{i,j}\,(i-\mu)^2\cdot P(i,j)} \tag{6}$$

Where μ is the mean of the pixel values, RMS is useful for detecting diseases that increase the roughness or variability of plant textures. For example, infections that cause significant texture distortions or irregularities can be identified by analyzing areas with high RMS values.

Variance measures the spread or dispersion of pixel values around the mean. It is calculated by [14] as in (7).

$$\text{Variance } = \sum_{i,j} (i-\mu)^2 \cdot P(i,j) \tag{7}$$

Where μ is the mean pixel value, variance helps detect diseases that cause significant changes in texture variability. Higher variance values indicate greater texture irregularity, as shown in the works of [20] which can indicate disease-induced texture changes, such as those caused by bacterial or fungal infections.

Smoothness quantifies the texture's uniformity by assessing the amount of pixel value variance. It is calculated as in equation (8).

$$\text{Smoothness } = 1-\frac{1}{1+\text{ variance}} \tag{8}$$

Where variance is the pixel value dispersion, smoothness is inversely related to variance, as [27] elaborated, with higher values indicating more uniform textures. This feature helps identify diseases that reduce texture roughness or create smooth, even areas on plant surfaces.

Kurtosis measures the "tailedness" or peakiness of the pixel intensity distribution [28], note that it indicates whether the distribution has heavy or light tails and is calculated as in (9).

$$\text{Kurtosis } = \frac{\sum_{i,j} (i-\mu)^4 \cdot P(i,j)}{(\sigma)^4} - 3 \tag{9}$$

where σ is the standard deviation of pixel values. High kurtosis values, as shown in the works of [29] indicate sharp peaks in the distribution, which can indicate specific disease symptoms that cause pronounced texture features. For example, diseases that create distinct, localized lesions may exhibit higher kurtosis values.

Skewness measures the asymmetry of the pixel intensity distribution. It reflects whether the texture is skewed towards higher or lower intensity values and is calculated as in (10).

$$\text{Skewness } = \frac{\sum_{ij} (i-\mu)^3 \cdot P(i,j)}{(\sigma)^3} \tag{10}$$

where σ is the standard deviation. Positive skewness indicates a distribution with a tail towards higher intensities, while negative skewness indicates a tail towards lower intensities.[30] note that skewedness helps detect diseases that cause asymmetrical texture changes or distortions in plant tissues.

3.3 Detection of Diseases Using Shape Features

Shape features are essential for diagnosing plant diseases by examining geometric properties and structural changes in plant tissues. Unlike texture-based methods like in the works of [31] shape-based approaches focus on the morphological alterations caused by diseases. Key techniques include contour analysis, area, and perimeter measurements, and shape descriptors such as Hu Moments and Fourier Descriptors.

Contour Analysis involves detecting the boundaries of diseased regions to understand their shape and structure. Techniques like the Canny edge detector and Sobel operator, as in [32] are commonly used for edge detection, highlighting significant intensity changes. After identifying contours, geometric properties like shape and size are analyzed. For instance, bacterial blight often causes lesions with distinct edges, which can be quantified to assess infection severity and track disease progression. Advanced methods, as in [33] like active contour models in refining contours dynamically for better accuracy. Area and Perimeter Measurements quantify the extent of diseased regions by calculating lesions' size and boundary length. Area is measured by counting pixels within the contour, as shown by [34] while perimeter measures the boundary length. These metrics are crucial for evaluating disease impact and progression. For example, fungal infections like Aspergillus or Fusarium, as [35] demonstrate, cause expanding lesions whose size changes can be tracked over time to assess disease development and control measures.

Shape descriptors provide quantitative representations of shapes, aiding detailed analysis and classification. Key descriptors include Hu Moments, a set of seven invariant descriptors described by [36] that capture shape regardless of scale, rotation, and translation. These descriptors are useful for distinguishing disease-induced shapes with consistent characteristics despite variations in size or orientation. Hu Moments have been applied to various plant diseases, including leaf spot diseases and fungal infections, as in the works of [37]. On the other hand, Fourier Descriptors present shape contours in the frequency domain by applying the Fourier Transform to contour data, decomposing shapes into frequency components. They are effective for analyzing complex or periodic shapes caused by specific pathogens. Researchers can identify and classify diseases based on distinctive contour characteristics by examining frequency patterns, as shown by [38]. Combining these shape analysis techniques with other methods enhances disease detection and classification, even in challenging conditions. Table 1. Summarizes the methods of feature extraction used for plant disease detection:

Table 1. Feature Extraction Methods

Feature Extraction Method	Description	Techniques Used	Application in Disease Detection	Advantages	Disadvantages
Color Analysis	Focuses on identifying color variations in plant tissues caused by diseases.	- Color spaces: RGB, HSV, LAB. - Color histograms, moments, coherence vectors.	- Identifies discoloration in plant tissues. - Detects early visible symptoms.	- Robust against lighting variations (HSV, LAB). - Simple and fast.	- Sensitive to noise. - Limited to visible changes.
Texture-Based Analysis	Analyzes surface characteristics and spatial arrangements of pixels.	- GLCM: Contrast, Correlation, Energy, Homogeneity. - LBP: Local texture variations. - Gabor Filters: Multi-scale texture patterns. - Wavelet Transforms: Multi-resolution texture analysis.	- Identifies subtle texture changes due to diseases like fungal infections and blight.	- Effective for diseases altering textures. - Can capture fine-grained texture changes.	- Computationally intensive. - May require high-quality images.
Shape-Based Analysis	Examines geometric properties and	- Contour analysis: Detects	- Detects changes in plant structure	- Invariant to scale, rotation, and	- Less effective when shapes are irregular or

	structural changes in plant tissues.	boundaries. - Area and Perimeter measurements: Quantifies lesion size. - Shape descriptors: Hu Moments, Fourier Descriptors.	caused by diseases like bacterial blight or fungal infections.	translation (Hu Moments). - Good for analyzing lesion progression.	complex. - Requires clear contour extraction.

3.4 Models for Feature Extraction

Learning and extracting features from images are essential for improving model performance in plant disease detection. Various models, both deep learning and traditional machine learning, as illustrated by [39] offer different capabilities and limitations when applied to this task. CNNs are fundamental for image analysis, excelling in automatically learning hierarchical features from data. They consist of layers that detect local features, such as edges and textures, through convolution, while pooling layers reduce the dimensionality of feature maps, controlling overfitting and enhancing computational efficiency. CNNs are particularly effective, as demonstrated by [40] for recognizing complex patterns in plant diseases. Yet, their computational cost can be high when working with large datasets and detailed features.

GoogleNet improves CNN efficiency by utilizing Inception modules, which process multi-scale features through different-sized convolutional filters. This capability makes GoogleNet, as shown by [41] highly adept at capturing subtle morphological changes in plants. The inclusion of auxiliary classifiers connected to intermediate layers enhances training stability and accuracy, making it a strong candidate for plant disease detection tasks requiring precision. However, the complexity of GoogleNet’s architecture, as evaluated by [42] can increase training time and demand more computational resources than simpler models like AlexNet. AlexNet, despite being an earlier model and applied by [43] introduced significant innovations like Rectified Linear Units (ReLU), dropout regularization, and data augmentation, improving robustness and convergence speed. While it lacks the efficiency of newer architectures as in the works of [44] AlexNet remains effective for moderate-sized datasets in plant disease detection, though its ability to handle larger, more complex tasks is limited.

ResNet addresses a key challenge in deep learning: the vanishing gradient problem. By introducing residual connections that allow layers to bypass one another, ResNet, as [40] demonstrates, enables the training of very deep networks without degradation in performance. This characteristic makes it well-suited for extracting fine-grained details necessary for plant disease detection. Nonetheless, ResNet's depth can lead to high computational costs, which may be prohibitive in mobile or resource-constrained environments. DenseNet further enhances feature extraction by connecting each layer to all previous layers, promoting feature reuse and improving information flow, as described by [45]. This dense connectivity helps alleviate issues such as the vanishing gradient and makes DenseNet particularly effective for identifying subtle variations in plant diseases. However, the dense connections increase the computational demands, which can be a drawback in real-time or mobile applications.

MobileNet offers an efficient solution for plant disease detection in resource-constrained environments, such as mobile devices. Employing depthwise separable convolutions as in the works of [46] MobileNet reduces computational costs while maintaining adequate performance. This model is ideal for real-time applications, although its accuracy may not reach the levels of more computationally intensive models like DenseNet or ResNet. [47] argue that EfficientNet balances performance and efficiency through compound scaling, which uniformly adjusts the model’s depth, width, and resolution. This model strikes a good compromise between accuracy and resource usage, making it highly adaptable for plant disease detection across various platforms, from high-performance systems to lower-resource environments. However, optimizing the compound scaling can require significant tuning.

In addition to deep learning models, traditional machine learning methods such as Support Vector Machines (SVM), Random Forests, and k-nearest Neighbors (k-NN) are also employed in plant disease detection, as [48] also confirms. SVMs are effective for classification, particularly in handling non-linear relationships, making them valuable for detecting plant diseases by learning discriminative features. Random Forests, an ensemble method, combines multiple decision trees to improve accuracy and robustness, as [49] illustrates, which is particularly useful for managing noisy and imbalanced data commonly found in plant disease datasets. Lastly, k-NN assigns a class to a data point based on its nearest neighbors and is effective for recognizing patterns, although it becomes less efficient with large datasets. While CNN-based models and their variants demonstrate high effectiveness in feature extraction for plant disease detection, they come with limitations. Models such as ResNet and DenseNet are computationally intensive and may not be suitable for environments with limited resources. In contrast, models like MobileNet [50] and EfficientNet [44] are designed to handle such constraints but may not achieve the same level of accuracy in highly complex tasks.

3.5 Challenges in the Detection

The intelligent detection of plant diseases encounters several significant challenges. One of the foremost issues is related to data quality and quantity. Machine learning models require large, high-quality labeled datasets to function effectively, but obtaining and labeling images of plant diseases is both labor-intensive and costly. [51] correctly note this often results in a dataset lacking diversity and impairs a model's ability to generalize across different plant species and disease conditions. Inaccurate labeling and data imbalance, where certain diseases are underrepresented, exacerbate this problem, leading to models that may perform poorly in detecting fewer common diseases. Another challenge is model generalization. Deep learning models are prone to overfitting, where they excel on training data but fail to perform well on new, unseen data. This issue is particularly pronounced in deep learning architectures, as described by [52] with numerous parameters that may memorize the training data rather than learn generalizable features. Models trained on data from specific geographical regions, as in the works of [53] might not adapt well to different regions or seasons due to variations in plant varieties, environmental conditions, and disease manifestations.

As [54] explained, environmental variability further complicates disease detection. Variations in lighting conditions, such as shadows, glare, and differences in light intensity, can alter the appearance of plant features and disease symptoms, making accurate detection challenging. Additionally, background noise from soil or other plants, as discussed by [55] and inconsistencies in camera angles and resolutions can obscure or distort disease symptoms, affecting the model's ability to learn and predict accurately. Computational constraints also present a hurdle. Deep learning models, particularly those with complex architectures, require substantial computational resources for training and inference. Real-time processing is crucial for practical applications, such as in-field disease detection, which demands efficient and quick predictions. Optimizing models like in the works of [56] for deployment on mobile or edge devices with limited computational resources and managing energy consumption, especially for battery-operated devices, is a significant challenge.

Lastly, integrating multi-modal data adds another layer of complexity. As [57] shows, combining data from diverse sources, such as images, sensors, and environmental measurements, requires sophisticated data fusion techniques. Discrepancies between different data modalities and managing various data formats complicate the analysis and can lead to inaccurate or incomplete disease detection. Table 2. shows a summary of plant disease detection datasets.

Table 2. Summary Of Plant Disease Detection Datasets

Dataset Name	Image Acquisition	Type of Plant	Number of Images	Number of Classes	Scaling	Ref
Tomatoes	Internet	Tomatoes	2500	4	Varying	[58]
Plantdoc	Internet images	Multiple plants	2,598	27	Varying	[59]
Pdd271	Field	Multiple plants	220,592	271	224 224	[60]
Wfd2020	Internet, ICLR	Wheat Fungi	2414	5	512 × 512	[61]
Cropdeep Dataset	Field	Multiple	31,147	31	1000 × 1000	[3]
Cassava	Field Set up	Cassava	6,256	5	224 × 224	[62]
Citrus	Kaggle, Plantvillage and internet	Citrus	2950	6	256x256	[63]
Ccmt Dataset	Field	Multiple	102,976	22	Varying	[64]
Bracol	Laboratory	Coffee	1,747	6	224x224	[65]
Certh Grape Dataset	Field	Grape	9,832	3	Not specified	[66]
Diamos	Field	Pear	3,505	4	224 × 224 × 3	[67]
Paddy Field	Field	Rice	50,730 Refined	4	512 × 512	[68]
Rice Panicle	Field	Rice	2,193 Original	9	960×540	[69]
Lwdcd2020	Field	Wheat spike	12,000	10	128×128	[70]
Pest Dataset	Field	Maize	7,000	1	416 × 416	[71]
Corn	Laboratory and field	Corn	1,255	4	512x512	[72]
Plantdoc	Field	Multiple plants	8,629	27	512 × 512	[73]
Black Gram	Laboratory and field	Black gram	1,000	5	512 × 512	[74]

3.6 Multi-Modal Fusion Models

Multimodal fusion, as demonstrated by [54] involves integrating different types of data or features from multiple sources to enhance the reliability and accuracy of disease detection. As [75] illustrates, advanced frameworks for detecting plant leaf diseases have achieved considerable success in early diagnosis. Researchers are developing and refining various fusion methods for automated disease classification, including Feature Fusion and deep learning methods.

3.7 Feature Fusion

Feature fusion is a machine learning and computer vision technique that enhances classification tasks by combining features from different sources or models. [76] introduced C-DenseNet, an enhancement of DenseNet architecture. C-DenseNet’t incorporates the block attention module into DenseNet, which uses attention mechanisms to refine feature extraction by focusing on essential regions and channels. This fusion enhances DenseNet's ability to capture and emphasize critical features relevant to crop disease detection. For example, as shown in the works of [77] C-DenseNet, it can potentially identify subtle disease symptoms more effectively by focusing on key features in plant images.

Ref [78] developed the XDNet model, which combined Xception and DenseNet architectures. DenseNet's dense connections ensure efficient gradient flow, feature reuse, and depthwise separable convolutions by Xception to reduce computational cost and model size without sacrificing accuracy. XDNet's approach to fusing these architectures leverages DenseNet's feature extraction strengths, as [79] demonstrated. Combined with Xception's efficient processing capabilities, this fusion makes XDNet well-suited for high-accuracy applications, such as identifying apple leaf diseases. The combination enables XDNet to handle diverse disease patterns with high precision.

Red [80] explored an improved version of SqueezeNet using the PlantVillage dataset. SqueezeNet's design focused on minimizing the variables while maintaining competitive accuracy, achieved through its fire modules that combine convolutions and pooling operations. By enhancing SqueezeNet parameters, the authors demonstrated the feasibility of using lightweight models for plant disease detection, where efficiency and accuracy are crucial. [50] incorporated a coordinate attention mechanism into MobileNet to boost the model's performance while reducing its parameter count. MobileNetV2, known for its efficient depthwise separable convolutions, was further improved with coordinate attention, which allowed the model to focus on spatially significant regions. This combination helped MobileNetV2 to better capture disease-related features in plant images. [81] proposed an improved VGG16 grape disease detection model incorporating transfer learning. The VGG16 architecture, known for its deep convolutional layers, was optimized for mobile devices using transfer learning techniques. This fusion allowed the system to process images captured via mobile phones and provided real-time disease identification. The improved VGG16 model's combination of deep convolutional features with transfer learning enhanced its ability to detect grape leaf diseases accurately and efficiently.

3.8 Deep Learning Methods

A multi-modal approach through machine learning techniques leverages the complementary strengths of different data sources, integrating information from various modalities to create a more robust and informative representation. [69] implemented a novel fusion framework that integrated various feature types, including hue moments, Haralick textures, and color histograms. This approach demonstrated how diverse image data can be combined into a cohesive framework, which was then applied to decision trees and random forest classifiers. The fusion of these multiple modalities, as shown in the works of [82] allowed the model to capture a richer set of features, contributing to improved performance in plant disease detection. Other researchers, like [13] have employed various data preprocessing methods to develop high-performance models. These methods include filtering, edge-based segmentation, and color conversion. Features such as shape, size, and color are extracted from images using these techniques and then analyzed with machine learning algorithms. Specifically, SIFT and Johnson's SB were used for feature extraction, which were input into multi-class SVM classifiers. Shamasneh and [51] incorporated dimensionality reduction, feature extraction, preprocessing, and classification. Using an SVM classifier, they applied the conformable polynomial Poisson approach for texture features and achieved 98.80% accuracy in detecting tomato leaf diseases from the PlantVillage dataset.

DL frameworks have extensively been applied in analyzing plant diseases, focusing on multimodal integration of various architectures and techniques. [83] employed a DL on MobileNetV2, a lightweight model, for classifying tomato leaf diseases. Their framework involved fine-tuning MobileNetV2 to adapt it for this task. Similarly, [84] showed how combined with deep learning architectures and fine-tuning pre-trained models for particular tasks can improve performance using transfer learning. [85] implemented a CNN-built framework for diagnosing leaf tomato diseases. Their architecture was designed to handle the complexities of disease identification by leveraging deep CNN features. This framework integrated various layers of CNN to process and classify disease images, demonstrating the application of deep learning in extracting relevant features and making precise classifications. [86] illustrated a multimodal framework combining inception networks with dilated convolutions to identify plant diseases. This approach highlighted how integrating inception modules with dilated convolutions can enhance the capacity of the model to depict complex disease trends across several crops.

Similarly, [87] utilized a CNN leaf disease identification approach. Their framework replaced regular convolutions with depthwise separable convolutions to reduce computational costs and parameters while improving model robustness and generalizability. This approach demonstrated how augmenting data enhances the capabilities of DL models in handling diverse disease challenges. [88] employed a pre-trained ResNet-50 model, fine-tuning it for classifying multiple leaf disease classes. This framework integrated the strengths of ResNet's residual connections with transfer learning to refine the model's performance in disease detection. Researchers have explored hybrid models combining various ML and DL methods to enhance classification effectiveness. Deep learning techniques have lately been used in research because of their outstanding feature learning power. With their multiple hidden layers, as [89] demonstrated, deep learning models are particularly adept at extracting and selecting discriminatory features from data. Regarding network architectures, VGG and ResNet are frequently employed in combination with advanced techniques. [90] illustrated this by replacing depth-separable convolution with conventional convolution, reducing computation cost and parameter count.

They also employed deep residual networks to tackle gradient disappearance issues, utilizing the layer-skipping structure to enhance performance. This approach allowed the model to effectively manage deeper architectures and capture detailed features, overcoming the limitations of traditional models like VGG16. Residual connections preserved performance without significantly increasing computational time, making deep residual networks crucial for recognition tasks and effective in complex feature extraction, fault-tolerant control, and defect detection. [91] combining machine learning and deep learning techniques—such as NasNet and MobileNet with logistic regression for feature extraction—offered slightly better performance than traditional ML or DL methods alone. Dilated CNN mechanisms have also gained attention due to their effective and rapid feature learning capabilities. These models enhance the ability to capture features at multiple scales, contributing to more accurate disease detection. Conversely, a Lightweight Attention-Based CNN approach by Ulutaş and [92] achieved a high accuracy of 99.60 % for grouping nine forms of tomato leaf diseases. Still, this approach had a higher temporal complexity than traditional techniques. Table 3. shows a comparative analysis of multimodal methods.

Table 3. Comparative Analysis of Multimodal Methods.

Plant Diseases	Features Extracted	Classifier	Accuracy	Studies
Tomato Leaf Diseases	Hue moments, Haralick textures, color histograms	Decision Trees, Random Forest	Not specified	[69]
Various Plant Diseases	Image features, various spectral data	EfficientNet	98.85%	[93]
Various Plant Diseases	Deep features from images	DenseNet-121	99.81%	[94]
Various Plant Diseases	Image features	EfficientNetV2L	99.60%	[92]
Apple Plant Diseases	Deep features from images	EfficientNet, DenseNet	Not specified	[95]
Tomato Leaf Diseases	Image preprocessing features	CNN	94.96%	[45]
Maize Leaf Diseases	Hyperparameters, texture features	CNN	97%	[96]
Maize Leaf Diseases	Color and shape features	CD-MobilenetV3	98.23%	[97]
Various Plant Diseases	Deep features	DCNN	99.96%	[84]

Wheat Diseases	Shape, color, and texture features	Various	98.65%	[98]
Rice Diseases	Mean, standard deviation of lesions	Various	Not specified	[99]

4. Result and Discussion

This This review highlights the advancements and challenges in plant disease detection using deep learning and traditional machine learning approaches. The integration of both techniques offers several benefits, particularly in scenarios with varying data availability and computational resources. Deep learning models, particularly convolutional neural networks (CNNs), have shown remarkable success in plant disease detection due to their ability to automatically extract relevant features from raw image data. These models have demonstrated high accuracy across multiple studies, especially when large datasets are available. The ability of deep learning to capture intricate patterns such as color, texture, and lesion distribution makes it highly effective in diverse agricultural conditions. However, the review also indicates that these models require significant computational resources and large labeled datasets, which may not be feasible in resource-constrained environments.

Traditional machine learning methods, including support vector machines (SVM) and k-nearest neighbors (KNN), are commonly used in smaller datasets due to their lower computational requirements. However, they rely heavily on predefined features such as color and shape, which can limit their ability to generalize to new, unseen data. These methods often struggle with the variability in plant diseases and environmental conditions, resulting in reduced detection accuracy compared to deep learning models. Several studies reviewed suggest that combining deep feature extraction with traditional machine learning classifiers can be a viable solution in constrained settings. By leveraging the feature extraction capabilities of deep learning while utilizing traditional classifiers, this hybrid approach can mitigate the generalization challenges faced by smaller datasets. The review highlights examples where traditional models, enhanced by deep feature extraction, achieved improved performance in detecting plant diseases, offering a balanced approach for environments with limited resources. The review also emphasizes the emerging trend of using multimodal approaches that integrate image data with external factors such as environmental conditions. Studies indicate that incorporating additional data streams, such as temperature, humidity, or soil conditions, improves the robustness of disease detection models, particularly in complex agricultural environments. This suggests a promising avenue for future research to develop more adaptive and scalable solutions. Despite the advancements, several limitations remain. Deep learning models require extensive computational power and large datasets, while traditional methods are limited by their reliance on manual feature extraction. There is still a need for scalable, efficient solutions that can operate in resource-constrained environments. Future research should explore more sophisticated hybrid models and multimodal techniques to enhance the adaptability and accuracy of disease detection systems across diverse agricultural conditions.

5. Conclusion

The integration of deep learning models with traditional machine learning approaches offers a powerful solution for plant disease detection, especially in resource-constrained environments. Deep learning models excel in extracting complex features from large datasets, providing superior accuracy in identifying plant diseases. However, traditional machine learning methods, when enhanced by deep feature extraction, remain valuable for small datasets, offering practical, cost-effective solutions in environments with limited computational resources. By combining the strengths of both approaches, greater adaptability to disease variability and environmental conditions can be achieved, leading to more robust, scalable, and efficient disease detection systems. Furthermore, the incorporation of multimodal techniques holds promise for further enhancing the accuracy and generalizability of plant disease detection models, providing a pathway toward improved agricultural productivity and sustainable plant health management.

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