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Review

Machine Learning and Deep Learning for Crop Disease Diagnosis: Performance Analysis and Review

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Abstract: Crop diseases pose a significant threat to global food security, with both economic and environmental consequences. Early and accurate detection is essential for timely intervention and sustainable farming. This paper presents a review of machine learning (ML) and deep learning (DL) techniques for crop disease diagnosis, focusing on Support Vector Machines (SVMs), Random Forest (RF), k-Nearest Neighbors (KNNs), and deep models like VGG16, ResNet50, and DenseNet121. The review method includes an in-depth analysis of algorithm performance using key metrics such as accuracy, precision, recall, and F1 score across various datasets. We also highlight the data imbalances in commonly used datasets, particularly PlantVillage, and discuss the challenges posed by these imbalances. The research highlights critical insights regarding ML and DL models in crop disease detection. A primary challenge identified is the imbalance in the PlantVillage dataset, with a high number of healthy images and a strong bias toward certain disease categories like fungi, leaving other categories like mites and molds underrepresented. This imbalance complicates model generalization, indicating a need for preprocessing steps to enhance performance. This study also shows that combining Vision Transformers (ViTs) with Green Chromatic Coordinates and hybridizing these with SVM achieves high classification accuracy, emphasizing the value of advanced feature extraction techniques in improving model efficacy. In terms of comparative performance, DL architectures like ResNet50, VGG16, and convolutional neural network demonstrated robust accuracy (95–99%) across diverse datasets, underscoring their effectiveness in managing complex image data. Additionally, traditional ML models exhibited varied strengths; for instance, SVM performed better on balanced datasets, while RF excelled with imbalanced data. Preprocessing methods like K-means clustering, Fuzzy C-Means, and PCA, along with ensemble approaches, further improved model accuracy. Lastly, the study underscores that high-quality, well-labeled datasets, stakeholder involvement, and comprehensive evaluation metrics such as F1 score and precision are crucial for optimizing ML and DL models, making them more effective for real-world applications in sustainable agriculture.

Keywords: machine learning; deep learning; crop disease; crop disease diagnosis; sustainable agriculture

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1. Introduction

Sustainable agriculture has gained critical importance due to increasing food demand and the depletion of environmental resources [1–3]. Sustainable agriculture refers to the practice of farming that meets current food and fiber needs without compromising the ability of future generations to meet theirs. This concept includes maintaining healthy ecosystems, minimizing environmental impact, and promoting biodiversity while ensuring food security. A recent study by [4] offers insight into the potential challenges facing sustainable agriculture in coastal areas. The authors develop a framework to assess the impacts of sea level rise (SLR) on nitrate loading in coastal agricultural watersheds, specifically focusing on the Tar-Pamlico River Basin in North Carolina. The study found that as sea levels rise, agricultural runoff increases nitrate levels in water bodies, exacerbating water quality issues. This impact is most severe during periods of low plant uptake and increased water flows, as observed in winter and spring. This study highlights the intricate connection between climate change, agricultural practices, and water management, suggesting the need for more robust adaptive strategies to protect water resources while ensuring agricultural productivity in coastal regions [4].

The impacts of climate change, compounded by human-induced factors such as dams and reservoirs, are substantial for agricultural systems. Changes in rainfall patterns, temperature, and sea level rise affect water availability and quality, influencing crop production. For instance, the study on the Tar-Pamlico River Basin by [3] demonstrates how climate change leads to increased hydroclimatic extremes, which, in combination with human activities like dam construction, can exacerbate the variability of water flows. This variability affects both irrigation and the delivery of essential nutrients, potentially reducing crop yields. Dams and reservoirs also alter natural river flows, leading to sedimentation and disrupted ecosystems, further compounding the pressures of climate change on agriculture. Therefore, managing these factors is critical to sustaining agricultural productivity in affected regions.

The integration of ML methods into agricultural practices presents a promising solution to these challenges, providing data-driven insights and optimizing resource management [4]. Traditional crop disease diagnosis, which relies on human expertise, is time-intensive and can yield inconsistent results. For example, in apple leaf disease detection, traditional visual inspection often results in low efficiency and insufficient accuracy. Studies have shown that this approach can lead to misdiagnosis because of its reliance on the subjective judgment of human experts, particularly when diseases present similar symptoms [5]. Another major limitation is that traditional methods are labor-intensive and slow. Given the vast amount of crops that need to be inspected in large-scale agricultural operations, relying solely on human expertise can be impractical and costly [6].

ML and deep learning (DL) techniques offer an alternative, transforming disease detection and diagnosis by equipping farmers with rapid, reliable, and environmentally friendly tools to manage crop diseases effectively [7,8]. Automated crop disease diagnosis is vital for improving agricultural productivity, especially with the increasing global population. Challenges such as climate change, emerging pathogens, and declining arable land demand sophisticated solutions for crop disease detection and management. ML- and DL-based systems address these challenges by improving diagnostic precision and speed, which are critical for efficient disease management and boosting agricultural yields. Traditional methods, often based on visual assessment, are subjective and prone to human error, particularly in regions where expert availability is limited [8]. Automating the diagnostic process enhances accuracy, effectiveness, and reliability in identifying crop diseases.

The application of ML and DL techniques offers several benefits, including higher crop yields, better disease management, improved food security, and reduced chemical use. These technologies support precision agriculture, agricultural research, crop insurance, farm management, and environmental monitoring. By reforming crop disease diagnostics, ML and DL contribute to achieving the United Nations' Sustainable Development Goals (SDGs), particularly SDG 2 (Zero Hunger) and SDG 13 (Climate Action), fostering sustainable agriculture and enhancing global food systems.

Evaluating the performance of ML and DL algorithms in diagnosing crop diseases is essential. Performance analysis helps identify effective and sustainable approaches to managing crop diseases [9]. This paper presents a review of several ML and DL algorithms frequently used in sustainable agriculture, including Support Vector Machines (SVMs), RF, k-Nearest Neighbor (KNN), and DL models such as VGG16, ResNet50, and

DenseNet121. The performance of these models is systematically assessed through various metrics, including accuracy, precision, recall, and F1 score.

Research Aim and Objectives

This paper aims to provide a thorough review and analysis of the effectiveness of advanced ML and DL techniques in sustainable agriculture, focusing on the classification and diagnosis of crop diseases that pose a serious threat to agricultural productivity. The findings from this performance analysis offer valuable insights for researchers, practitioners, and policymakers in sustainable agriculture. By understanding the strengths and limitations of different ML algorithms, stakeholders can make informed decisions about adopting ML techniques. This review also aims to advance the field by identifying research gaps and proposing future avenues for improving the effectiveness and applicability of ML in sustainable agriculture.

The objectives of the review are as follows:

1. To provide a comprehensive review of state-of-the-art ML and DL techniques applied in crop disease diagnosis within sustainable agriculture. This includes summarizing the most relevant ML and DL algorithms, such as SVM, RF, KNN, and advanced DL models like VGG16, ResNet50, and DenseNet121.
2. To evaluate the performance of these ML and DL techniques through a systematic assessment using performance metrics such as accuracy, precision, recall, and F1 score. This performance evaluation aims to identify which models are most effective in various agricultural contexts, thereby offering guidance to practitioners and researchers on selecting suitable algorithms for specific agricultural applications.
3. To analyze the challenges posed by agricultural datasets, including issues like image distribution imbalances, and their significant impact on the performance of ML and DL models in crop disease diagnosis. This objective aims to identify the limitations of current models and provide insights for improving future dataset handling.
4. To identify the strengths and weaknesses of different ML models in sustainable agriculture, emphasizing how these models can contribute to achieving higher crop yields, improved food security, and more efficient disease management while also addressing the environmental and resource constraints of sustainable agriculture.
5. To propose future research directions aimed at enhancing the application of ML techniques in sustainable agriculture, with a specific focus on overcoming current limitations, such as dataset imbalances, and improving model robustness for better real-world implementation.

This review paper distinguishes itself from the existing literature by providing a comprehensive performance evaluation of ML and DL techniques for crop disease diagnosis, using critical metrics such as accuracy, precision, recall, and F1 score. Unlike previous reviews that primarily offer a broad overview of techniques, this paper delivers a detailed quantitative comparison of the effectiveness of both ML and DL algorithms, providing valuable insights into their suitability for various agricultural scenarios. Most existing studies focus either on ML-based or DL-based techniques, often analyzing just one or two algorithms in isolation. In contrast, this paper undertakes a comprehensive performance analysis, covering a wide range of techniques by evaluating four classical ML algorithms (K-NN, SVM, and RF) alongside five state-of-the-art DL algorithms. This holistic approach ensures a more thorough understanding of how different techniques perform across diverse agricultural applications. Furthermore, this paper analyzes dataset challenges, particularly image distribution imbalances, and their significant impact on model performance, highlighting current limitations and identifying critical areas for future research, such as developing strategies to handle imbalanced datasets and improve model robustness. The contributions of this paper are as follows:

1. A comprehensive review of four ML and five DL techniques for crop disease diagnosis.
2. Performance evaluation of various algorithms using metrics such as accuracy, precision, recall, and F1 score.

3. Identification of challenges in datasets, including image distribution imbalances and their impact on model performance.
4. Analysis of the strengths and weaknesses of different ML models in sustainable agriculture.
5. Proposals for future research directions to enhance the application of ML in agriculture.

The remainder of this paper is structured as follows. Section 2 provides a summary of relevant related studies, while Section 3 presents an analysis of a dataset related to crop disease and outlines the fundamental workflow for both ML and DL algorithms. This paper analyzes the performance of diverse DL and classical ML algorithms in Section 4, with Section 5 providing the paper's conclusion.

2. Methodology

This review includes papers published between 2021 and 2024. A few studies that were published before 2019 are also covered. Specifically, the review focused on papers that developed crop disease diagnosis on classification and detection using ML and DL algorithms. The following databases for scientific literature were queried to find relevant articles: Google Scholar and ScienceDirect. The following search terms were used for queries: ML, DL, crop, crop disease diagnosis, crop disease classification, crop disease detection, classification techniques used in crop disease diagnosis, transfer learning, and fine-tuning. Furthermore, the union of the outlined search terms was used with a set of terms relating to DL crop disease classification, including VGG16, DenseNet121, ResNet50, SVM, KNN, and K-means, to mention but a few. The following inclusion criteria were used in this review: crop disease detection and classification techniques, DL, and ML. Ph.D. theses, M.Sc. theses, and case study papers were excluded from this study. Figure 1 shows the preferred reporting items for the systematic review and meta-analysis (PRISMA) diagram used for this survey.

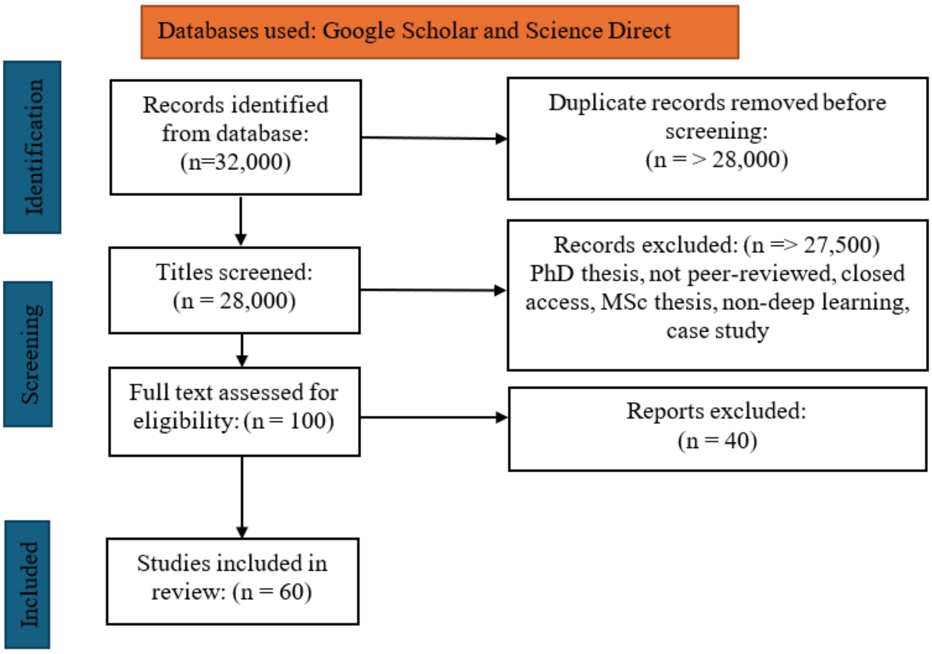

Figure 1. Preferred reporting items for systematic reviews and meta-analysis (PRISMA) diagram for this study.

Performance Measures

Various performance metrics are commonly employed in the literature to assess the efficacy of ML models, including the F1 score, accuracy, sensitivity, and precision. These four metrics are contingent upon the counts of true positives (TPs), true negatives (TNs), false positives (FPs), and false negatives (FNs). The calculations for these metrics can be derived from Equations (1)–(4).

Accuracy is termed to be the ratio of correctly classified samples to the total number of samples in the dataset.

$$Accuracy = \frac{TN + TP}{TN + TP + FP + FN} \tag{1}$$

Precision indicates the proportion of the predicted positive instances that are actually positive, signifying that higher precision results in fewer false positives.

$$Precision = \frac{TP}{TP + FP} \tag{2}$$

Recall measures the classifier's ability to identify all positive instances, with higher recall implying fewer false negatives. Conversely, lower recall suggests a higher number of false negatives, so improving recall may lead to a decrease in precision.

$$Recall = \frac{TP}{TP + FN} \tag{3}$$

$F1$ score is calculated by dividing the product of recall and precision with the sum of recall and precision.

$$F1 - Score = 2 \times \frac{Recall \times Precision}{Recall + Precisio} \tag{4}$$

3. Related Work

This section presents a review of related studies.

3.1. SVM-Based Solutions for Crop Disease Diagnosis

Different studies have been conducted on crop disease diagnosis. The authors of [10] developed an approach for detecting guava leaf diseases using SVM. This was accomplished by utilizing a dataset of 70 images, which underwent preprocessing and segmentation employing K-means clustering. Feature extraction was conducted using a gray-level co-occurrence matrix, which captures the frequency of different combinations of intensity levels occurring together in an image. Subsequently, these extracted features were employed to train an SVM classifier, achieving an accuracy of 98.17%. The authors of [7] devised an automated system for leaf extraction and disease classification employing SVM. Leaf image acquisition was conducted using a Raspberry Pi, which also facilitated image transmission over the internet via an online web-based server. The images were delivered on a host PC where the image features were extracted after being segmented using the watershed and graph cut segmentation model [8]. Otsu's method as applied by [7] played a crucial role in categorizing the difference between the two indices into distinct groups—specifically, background and leaf. Additionally, the gray-level co-occurrence matrix (GLCM) was employed to determine the optimal threshold for identifying the leaf's background, leveraging GLCM's ability to provide insights into gray-level distribution. The dataset was further segmented into four quadrants based on a specific threshold value. The first quadrant was used to compute local entropy, while the second quadrant aided in extracting the entire leaf from the foreground by employing the inverse of the background. Finally, SVM was employed for classification, achieving an impressive accuracy rate of 97%.

The authors of [9] conducted a thorough examination of various ML techniques, including SVM, emphasizing their methodologies, datasets, performance metrics, and practical applications. Furthermore, the review offered a critical evaluation of current models, highlighting their limitations and identifying existing gaps. The authors concluded that although ML-based approaches show significant promise for improving agricultural disease management, there is an immediate necessity for more resilient, scalable, and adaptable solutions to effectively tackle the diverse conditions and complexities associated with agricultural diseases.

3.2. KNN-Based Solutions for Crop Disease Diagnosis

The KNN classifier was employed in [11] to create a method for disease detection and classification that effectively identified and categorized the specified diseases. This accomplishment was facilitated through the application of several image processing techniques, including the K-means clustering algorithm, which organizes similar pixels into a predetermined number of clusters. The extracted clusters were then fed into a KNN classifier, which effectively classified seven diseases on five different species and obtained 96.76% accuracy. This is a result of its simplicity and usefulness for different classification problems, since it does not require any prior knowledge or training as compared to other ML algorithms like SVM.

In a separate investigation, a hybrid model that combined Random Forest (RF) and KNN was developed by [12] for the purpose of identifying plant diseases. This methodology comprised four fundamental stages: initial preprocessing, segmentation through K-means clustering, extraction of texture features utilizing the gray-level co-occurrence matrix (GLCM) algorithm, and ultimately, classification achieved through the ensemble model formed by integrating the two classification techniques, RF and KNN. RF techniques were applied for optimum feature selection, while KNN was used for classification. The performance of this ensemble model was evaluated, and it achieved 97.8%. The model was compared to SVM, and it outperformed SVM by over 3%.

Furthermore, the authors of [13] implemented a DL-based approach for diagnosing crop diseases that employed multimodal mix-up augmentation. This method was capable of simultaneously predicting the type of crop, identifying the presence of diseases, and evaluating the severity of those diseases. The approach utilized a combination of multimodal data, which included crop images alongside environmental factors such as temperature, humidity, and dew points. The study reported an accuracy of 90.37% for the proposed model.

3.3. VGG16 and RESNET50 Applications in Crop Disease Classification

Furthermore, VGG16 was employed in [14] for the classification of diseases affecting rice plants. This model is renowned for its intricate architecture, comprising 16 layers and the application of small convolutional filters arranged in succession to create a profound network. Consequently, it is frequently applied in tasks related to image classification and object detection. Flask, a Python-based microweb framework used for constructing web apps, was utilized in conjunction with VGG16 for disease diagnosis. From a dataset of 4000, VGG16 obtained an accuracy of 90%. In a separate study, the authors in [15] devised a method for detecting crop diseases in grapes and tomatoes utilizing the VGG16 architecture. VGG16 is a pre-trained model used to improve the performance of DL models. The model was evaluated on a dataset with grapes and tomato images, and it achieved a classification accuracy of 98.40% for grapes and 95.71% for tomatoes.

A custom DL-based model designed for the identification and classification of plant leaf diseases was implemented in [16]. This implementation utilized a modified red deer optimization algorithm (MRDOA) as an effective feature selection method, which led to the identification of optimized and significant features while reducing the size of the MRDOA. Furthermore, a DL convolutional neural network (DLCNN) classifier was employed to improve classification accuracy, effectively categorizing various plant diseases into separate groups. Utilizing ResNet50, the model extracted diverse features from plant leaf images, encompassing color, texture properties, and segmentation. The performance evaluation of the proposed PDICNet model yielded an impressive accuracy of 99.73%.

A different study presented a DL-based model for the identification of plant leaf diseases utilizing ResNet50 and InceptionResNet, as detailed in [17]. The researchers modified the final two layers of the pre-trained architecture by substituting them with newly designed layers. Subsequently, they trained these layers on an augmented dataset of palm leaves, resulting in a remarkable classification accuracy of 100%. This outcome underscores the enhanced performance of the model in comparison to earlier DL approaches.

3.4. DenseNet Architecture Applications for Crop Disease Detection

The authors of [18] implemented the DenseNet121 architecture to enhance the detection of diseases in tomato leaves, focusing on the application of novelty detection techniques to identify previously unrecognized diseases while addressing the gradient vanishing issue that often affects DL models. This architecture is designed to facilitate early diagnosis and reduce potential crop losses by delivering precise and reliable disease detection for tomato plants. The model demonstrated an impressive accuracy of 98.3%, indicating its effectiveness in differentiating among various types of leaf diseases in tomatoes, thereby establishing its dependability. Additional performance metrics included a precision of 98%, a recall of 99%, and an F1 score of 99%.

In a separate investigation, the authors of [19] implemented a feature combination strategy utilizing the DenseNet169 architecture for the detection and classification of citrus diseases. The primary objective of the study was to improve the classification of crop diseases by employing a DL approach (DenseNet169) across two experimental scenarios: one utilizing original features and the other incorporating a combination of features. This methodology was applied to classify four distinct categories using the LDI dataset, which comprised 3000 images representing both healthy and unhealthy specimens. The DenseNet169 model attained an impressive accuracy of 96%, surpassing the 91.3% accuracy achieved by the model that relied solely on original features. This significant difference underscores the substantial positive influence of the feature combination approach on the model's capacity to identify and classify diseases in citrus plants.

Additionally, a comparative evaluation of various pre-trained CNN models, including DenseNet121, VGG16, InceptionV4, and ResNet50, was conducted in [20]. Using the PlantVillage dataset for training purposes, DenseNet121 demonstrated superior performance, attaining a remarkable accuracy of 99.81%. This model, specifically designed for image classification, is distinguished by its use of dense layers that incorporate tightly connected structures. In this architectural framework, each layer conveys its produced feature maps to the layer below while simultaneously receiving new inputs from the layers situated above it. Additionally, concatenation occurs between consecutive layers, allowing the subsequent layer to integrate knowledge from all prior layers. Additionally, DenseNet121 architecture is distinguished by its compact and streamlined structure, wherein the feature maps from earlier layers are directly connected to later layers. This arrangement facilitates improved gradient propagation and allows for the integration of a wider variety of features. The summary of the reviewed articles is shown in Table 1.

As shown in the review, most of the studies focused on either ML-based or DL-based techniques, and very few focused on both ML-based and DL-based techniques. Additionally, while many studies have focused on just one or two DL or ML algorithms, this research undertakes a comprehensive performance analysis of classical ML- and DL-based crop detection techniques. The analysis covers four ML algorithms and five DL algorithms. Moreover, most of the studies did not include a comprehensive discussion, nor did they include a comparative performance analysis. This study encompasses an extensive performance analysis of crop detection techniques based on KNN, SVM, RF, and DL. Furthermore, it conducts a comparative performance evaluation between ML-based and DL-based approaches. The different analysis will help us access the potential of ML- and DL-based techniques in effectively tackling crops in diseases. It will also help us identify improved, effective, and sustainable solutions to crop disease diagnosis.

Table 1. Summary of related studies.

Citation	Algorithm Used	Dataset Used (Total Images)	Classification Accuracy	Predicted Property	Country
[10]	SVM	Private (70)	76%	Disease type (8 diseases)	India
[7]	SVM	Private (20)	97%	Disease type (5 classes)	Saudi Arabia
[8]	SVM	Private (3000)	Dice index: 0.95	Disease type (2 diseases, 2 crops)	Netherlands
[11]	KNN	Ankras and Reddit-Plant leaf (237)	96.76%	Disease type (5 diseases, 1 crop)	India
[12]	RF, KNN	Private (1000)	97.8%.	Disease type (3 diseases)	India
[13]		Korea AI challenge (4675)	90.37%	Disease type (6 crop, 5 diseases)	Korea
[14]	VGG16	Kaggle (4500)	90%	Disease type (4 diseases, 1 crop)	India
[15]	VGG16	PlantVillage (54,303)	98.40% (Grapes), 95.71% (Tomatoes)	Disease type 14 diseases, 2 crops)	India
[16]	PDICNet model	PlantVillage (20,798) Rice Dataset (1600)	99.73%	Disease type (38 classes)	India
[17]	Inception ResNet50	Date Palm dataset (2631)	99.62%	Disease type (3 classes)	Egypt
[18]	DenseNet121	Tomato Dataset (3000)	98.3%	Disease type (10 classes)	India
[19]	DenseNet169	LDI dataset (3000)	96%	Disease type (4 diseases, 1 crop)	Indonesia
[20]	DenseNet121	PlantVillage (54,305)	99.81%	Disease type (38 diseases)	India

4. Performance Analysis

This section begins by outlining the general workflow for ML- and DL-based approaches. It is followed by an evaluation of some datasets. Finally, a performance analysis of various ML and DL techniques is presented.

4.1. General Flow Process of Machine Learning and Deep Learning Systems

ML and DL projects follow structured workflows, outlined in Figures 2 and 3 [21]. These workflows comprise distinct phases, including data acquisition, preprocessing, feature/instance selection, parameter optimization, and model building/testing. Specifically, ML workflows involve data acquisition, preprocessing, feature selection, instance selection, parameter optimization, and model building (encompassing training, splitting, testing, and validation). In contrast, DL workflows consist of data acquisition, preprocessing, splitting, hyperparameter tuning, transfer learning, model training/testing, and deployment. The subsequent section provides a detailed explanation of each phase in the ML and DL workflows.

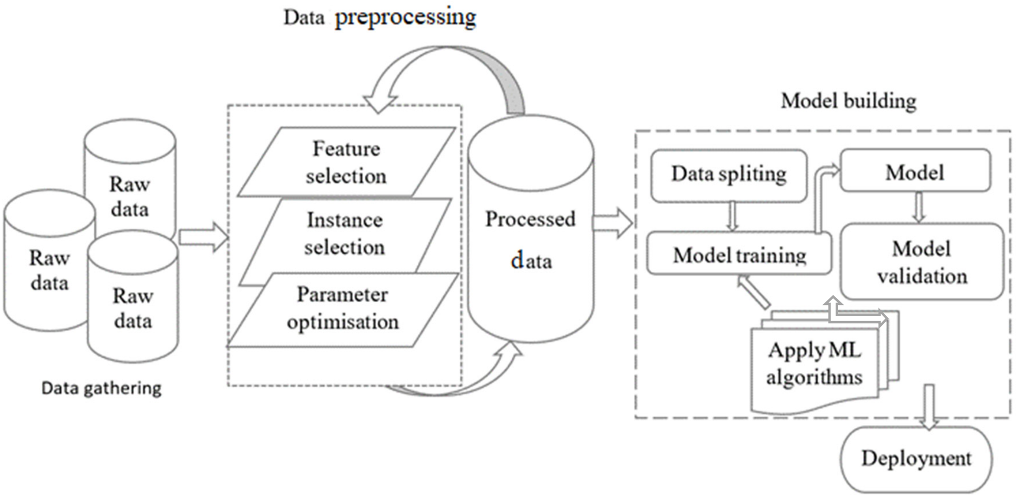

Figure 2. General workflow of an ML-based crop detection technique.

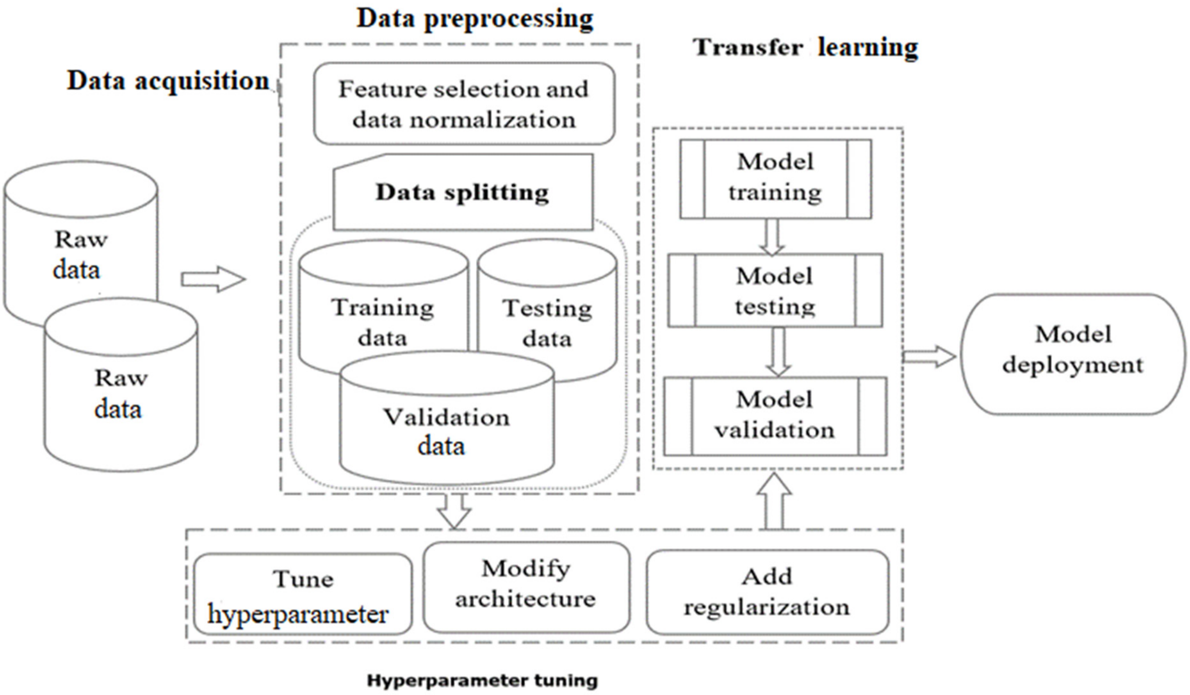

Figure 3. General workflow of a DL-based crop detection technique.

4.1.1. Data Acquisition and Preprocessing

Data acquisition in both ML and DL involves gathering data from diverse sources such as private or public datasets. Whether for ML or DL, these datasets can include text, images, videos, and sensor data, tailored to the problem being addressed. Common data sources like remote sensing technologies—using satellite and drone imagery—provide vast amounts of data, especially for agriculture or environmental monitoring. For ML, obtaining private datasets manually often results in smaller sets, which can hinder model accuracy. DL, on the other hand, generally requires significantly larger datasets to train its models effectively due to the complexity of the neural networks involved. Both methods follow similar steps for data collection, but DL requires far more data to achieve robust performance, particularly in tasks such as image or speech recognition.

Despite the shared approach, key differences exist between ML and DL in the treatment and handling of data. While both involve processes such as data extraction, validation, and quality assurance, DL places a stronger emphasis on large-scale data integration and often involves more complex preprocessing steps due to the intricate structure of deep networks. DL models can automatically learn features from raw data, reducing the need for manual feature extraction, which is a critical step in ML. Furthermore, storage and management of data are also more intensive in DL, given the sheer volume of data required to train deep networks, highlighting the need for more scalable and efficient data handling mechanisms compared to traditional ML methods.

Data preprocessing is essential for both ML and DL algorithms, as it enhances the quality and structure of the data before feeding them into models. Common preprocessing steps in both ML and DL include noise removal, feature selection, feature extraction, and segmentation, with the primary goal of improving model performance. In ML, preprocessing focuses on manual feature extraction and selection to highlight key patterns and relationships, which models rely on for accurate predictions. This step is crucial since ML models cannot autonomously detect features from raw data. Additionally, data are typically split into training, validation, and testing sets, ensuring that models are evaluated effectively on unseen data while avoiding bias from ordered data or improper sampling.

In DL, data preprocessing shares similarities with ML but differs in some significant aspects. While both approaches involve dataset partitioning, DL focuses more on data augmentation, where techniques like rotating, flipping, or scaling images increase dataset size and variability, thus improving generalization. Unlike ML, DL models have the advantage of automatically extracting features during training, reducing the need for manual intervention in feature selection. Additionally, DL models often require adjustments to input data size to align with model requirements, such as resizing images to match the input dimensions of CNNs. Data preprocessing in DL, therefore, aims to prepare large, varied datasets that enhance the model's ability to learn complex patterns autonomously, with less emphasis on manual feature engineering.

4.1.2. Feature Selection

The objectives of feature selection, as highlighted by [16], are to identify and retain a subset of relevant features from a larger pool of available features while discarding irrelevant or noisy data. This process aims to streamline future analysis tasks by focusing only on the most informative and discriminative features. The authors of [22] emphasize that feature selection contributes to enhancing classification outcomes by identifying and prioritizing essential characteristics that contribute to reducing computational complexity. Models trained on a reduced feature set tend to exhibit greater robustness and reproducibility compared to those trained on a larger feature set. This underscores the importance of feature selection in optimizing the performance and efficiency of ML algorithms.

Feature selection in crop disease detection and classification is crucial for building accurate and efficient models. Different features can be used to train ML and DL algorithms, including image-based features, texture features, shape descriptors, local binary patterns (LBPs), and segmentation features, to mention a few. Image-based features include color histograms, which analyze the distribution of colors in images to capture color-based information about the diseased regions. Texture-based feature selection techniques are used to extract features related to texture patterns, which can be indicative of specific diseases. Shape descriptors are used to extract features related to the shape of lesions or affected areas. LBPs are effective for texture analysis and can be used to differentiate between healthy and diseased regions. Segmentation techniques are used for identifying and isolating regions of interest within the images, and superpixel-based segmentation involves grouping of pixels into perceptually meaningful clusters, which can serve as features.

4.1.3. Hyperparameter Tuning

Hyperparameter tuning/optimization is an iterative process of finding the best set of hyperparameters for an ML model to achieve optimal performance. It is also referred to as configurations that are not learned from the data but rather need to be set prior to training. This process involves defining and selecting hyperparameter search space, choosing a search strategy (Bayesian optimization, genetic algorithm, random, and grid search), evaluating matric definition, data splitting for validation, performing hyperparameter search and selecting the best, evaluating on the test set, final modeling, deployment, and monitoring.

4.1.4. Transfer Learning

Transfer learning utilizes pre-existing knowledge and applies it to the specific problem at hand. This entails utilizing pre-trained models for image classification/detection on a large dataset, which are subsequently adjusted to fit the specific dataset being examined. The frequently preferred approach is replacing the last layers of the pre-trained network to customize it for a distinct classification objective. During the training process, only the recently added layers are set to be trainable, while the remaining layers are frozen. This training procedure is often accompanied by fine-tuning, particularly when dealing with a small training dataset that lacks sufficient samples for training a DL model from the ground up.

4.1.5. Instance Selection and Parameter Optimization

Instance selection, which is also referred to as instance-based learning, is termed as an ML technique used to re-size image sizes of a dataset while preserving its important characteristics. This is achieved by selecting a subset of instances from the original dataset to be used for model training aimed at improving the model's performance or reducing computational cost. This methodology is employed to reduce computational complexity, improve model generalization, reduce noise, and handle imbalanced datasets. The authors of [23] employed instance segmentation for their strawberry images in designing a higher-capacity model that was more robust and generalizable. Random sampling, stratified sampling, distance-based selection, cluster-based selection, greedy algorithms, model-based selection, and active learning are techniques involved in instance selection.

Parameter optimization, known as hyperparameter tuning, is among the important steps in the ML pipeline, which involves finding the best set of hyperparameters for a given model and dataset. A hyperparameter is a setting or configuration that is not learned from the data but rather set prior to training; hence, they are known to govern the behavior of the learning algorithm. The steps involved in parameter optimization are hyperparameter definition, selection of a hyperparameter search space, choosing a search strategy (grid, random, Bayesian optimization, genetic algorithms), evaluation matric definition, split data for validation, performance of a hyperparameter search, selection of the best Bayesian hyperparameter, test dataset evaluation, final model training, and deployment and monitoring. Parameter optimization is also known to be an iterative process.

4.1.6. Model Building, Training, and Validation

Model building in both ML and DL involves selecting the appropriate algorithm, preparing data, and iterating through different configurations to create an optimal model. For ML, this includes data preparation, feature engineering, model selection, hyperparameter tuning, and iterative refinement. After selecting the best model, retraining using both training and validation data ensures better generalization. In DL, the process is similar but places a stronger emphasis on adjusting model architectures, like neural networks, to optimize the learning process. For both ML and DL, hyperparameter tuning, regularization, and model evaluation help in refining the model to achieve better performance. However, DL typically involves deeper layers and requires more computational resources during model building compared to ML.

Model training, validation, and testing serve critical roles in evaluating the generalization ability of models in both ML and DL. For ML, data are split into training and validation sets to monitor performance and compute evaluation metrics such as accuracy and F1 score. Hyperparameter tuning plays a key role in both ML and DL, allowing adjustments for improving performance. DL training follows a similar iterative process but typically involves more complex architectures and optimization techniques. Model validation, whether through train–test splits or cross-validation, is crucial for both ML and DL, ensuring the models generalize well on unseen data. Finally, model testing provides the final assessment of new data, highlighting how well both ML and DL models perform in real-world scenarios.

4.1.7. Model Deployment

Deploying an ML model involves integrating it into real-world applications, such as web apps, APIs, mobile apps, or existing software, to make it accessible and usable. This process encompasses several key steps, including model serialization, API creation, endpoint setup, data processing, error handling, security measures, authentication, model initialization, testing, monitoring, and ongoing maintenance, ultimately enabling the model to be efficiently loaded and utilized in various environments.

4.2. Datasets Analysis

This section includes a detailed analysis of the PlantVillage dataset, which was chosen for this study due to its reliability and suitability for general comparisons. Most of the models examined in this research were trained on the PlantVillage dataset to ensure consistency and fairness in comparison. This choice allows for a standardized benchmark across the different studies evaluated.

Plant datasets are often made up of images or other data relating to diverse plant species. These datasets are developed to aid in the advancement of research and development in sectors such as agriculture, botany, plant pathology, and computer vision. Plant datasets can be used for tasks such as plant recognition, disease detection, growth monitoring, and classification of plant species.

The applications of plant datasets are diverse because researchers and data scientists can use these datasets to train ML and DL models for plant disease identification, plant species classification, or anomaly detection. By analyzing the images and associated data, valuable insights can be gained to improve crop management, develop targeted pest control strategies, and enhance overall agricultural practices.

4.2.1. PlantVillage Dataset

The PlantVillage dataset is a widely recognized public resource utilized in the fields of agriculture and crop disease identification. It comprises images depicting a range of crops afflicted by different diseases. Over the years, multiple iterations of the PlantVillage dataset have been developed, each featuring distinct attributes and improvements. The initial version of the dataset was established by the PlantVillage initiative, spearheaded by Dr. David Hughes at Penn State University. It features images of both diseased and healthy plants from a variety of crops, documented under diverse conditions and environments. It encompasses a range of crops, such as tomatoes, potatoes, and grapes, each exhibiting distinct specific diseases.

An initial iteration of PlantVillage, released in 2016, included numerous images depicting both damaged and healthy plants, thereby offering a broad spectrum of samples. This dataset underwent enhancements in 2017, resulting in an updated version characterized by superior data quality, including higher-resolution images and enhanced labeling accuracy. The year 2018 saw the introduction of another version of the PlantVillage dataset, which incorporated additional classes and advancements in data curation practices. In 2019, a further refined iteration of the dataset was developed, featuring even more diverse samples and enhanced data preprocessing techniques. In 2020, an updated iteration of the PlantVillage dataset was released, reflecting some of the most recent enhancements in data collection and curation methodologies.

The PlantVillage dataset, which is publicly accessible, contains over 54,303 annotated images depicting both healthy and diseased leaves of various crops. These images were gathered under controlled environmental conditions. This extensive collection was assembled by researchers at Penn State University and features photographs of 14 distinct crop species, including apple, blueberry, cherry, grape, orange, peach, pepper, potato, raspberry, soybean, squash, strawberry, and tomato. The dataset encompasses examples of seventeen major diseases, which include four bacterial infections, two fungal diseases, two viral infections, and one condition caused by mites. Furthermore, among the 12 crop species represented, there are images of healthy leaves that show no visible signs of disease.

The PlantVillage dataset, as noted by the authors in [24], encompasses more than 38 distinct diseases and conditions. The images within this dataset were sourced from various origins and meticulously annotated by specialists in plant pathology. Each image is categorized by the specific plant species, the nature of the disease or condition affecting the leaf, and a severity score that reflects the extent of the damage. The PlantVillage dataset can be downloaded from its official website at [24].

The authors of [24] evaluated the quality of the PlantVillage dataset, which was trained utilizing the AlexNet model and achieved a classification accuracy of 99.35%. Furthermore, they emphasized the importance of expanding the training data to improve accuracy. It was noted that obtaining new images from diverse perspectives is essential. A summary of the PlantVillage dataset is provided in Table 2.

Table 2. Summary of the PlantVillage dataset.

Name of Crop	Number of Images	Type and Number of Diseases				Percent (%)
		Fungi	**Bacteria/Mold**	**Virus/Mite**	**Healthy**	
Apple	2536	Fungi—Scab (504), Fungi—Black_rot (496), Fungi—Ceader_apple_rust (220)	Bacteria (0) Mold (0)	Virus (0) Mite (0)	1316	4.67%
Blue_berry	1202	Fungi (0)	Bacteria (0) Mold (0)	Virus (0) Mite (0)	1202	2.21%
Cherry	1526	Fungi—Powdery_mildew (842)	Bacteria (0) Mold (0)	Virus (0) Mite (0)	684	2.81%
Corn	308	Fungi—Cercospora_leaf_spot (410), Fungi—Common_Rust (953), Fungi—Northen_leaf_blight (788)	Bacteria (0) Mold (0)	Virus (0) Mite (0)	929	5.67%
Grape	3251	Fungi—Black_rot (944) Fungi-Esca_black_measels (1107) Fungi—Leaf_blight (861)	Bacteria (0) Mold (0)	Virus (0) Mite (0)	339	5.98%
Orange	4405	Haunglongbird (4405)	Bacteria (0) Mold (0)	Virus (0) Mite (0)		8.11%
Peach	2126	Fungi (0)	Bacterial—Bacterial_spot (1838)	Virus (0) Mite (0)	288	3.91%
Pepper-bell	198	Fungi (0)	Bacterial—Bacterial_spot (797)	Virus (0) Mite (0)	1183	3.64%%
Potato	1721	Fungi (0)	Bacterial—Early_blight (800) Bacterial—Late_blight (800)	Virus (0) Mite (0)	121	3.16%
Rasberry	297	Fungi (0)	Bacteria (0) Mold (0)	Virus (0) Mite (0)	297	0.54%
Soybean	4072	Fungi (0)	Bacteria (0) Mold (0)	Virus (0) Mite (0)	4072	7.49%
Squash	1468	Fungus—Powdery_mildew (1468)	Bacteria (0) Mold (0)	Virus (0) Mite (0)		2.70%
Strawberry	1251	Fungi (0)	Bacteria (0) Mold (0)	Mite-Leaf_scorch (887) Virus (0)	364	2.30%
Tomato	14,529	Fungi—Septoria_leaf-spot (1417), Fungi—Leaf_mold (761), Fungi—Target_spot (1123)	Bacterial-Bacterial_spot (1702) Bacterial—Early_blight (800) Bacterial—Late_blight (1527)	Spider_mite (1341) Virus-Tomato_mosaic_virus (299) Virus-Yellow_leaf_curl (4286)	1273	26.75%
Total	54,303	Fungi = 16,299	Bacterial = 8264	Mite = 2228 Virus = 4585	12,068	

Key: The figures in brackets represent the number of images.

The PlantVillage dataset, as illustrated in Table 1, encompasses a variety of crops, such as apple, blueberry, corn, cherry, grape, orange, peach, pepper (bell), potato, raspberry, soybean, strawberry, squash, and tomato. The distribution of infected and uninfected images within the dataset is depicted in Figures 4 and 5. The data indicate that tomato has the largest quantity of images, with soybean and orange ranking just after it. Furthermore, the dataset exhibits a significantly higher quantity of healthy images in comparison to unhealthy ones, suggesting an imbalance that undermines the potential for developing a classifier with robust generalization capabilities. Notably, raspberry has the fewest diseased images, while cherry is characterized by the lowest count of healthy images. This imbalance indicates that the dataset is inadequate for constructing a DL model. Nevertheless, crops that are adequately represented within the dataset can be utilized to create a classifier. For instance, tomatoes present a viable option for developing an effective classifier. The ratio of healthy to diseased images for other crops can be enhanced through the application of data augmentation techniques. Furthermore, efforts should be made to increase the number of images for crops with limited representation, such as cherry and raspberry. Additionally, incorporating widely cultivated crops like rice and wheat into the dataset could further enrich its diversity.

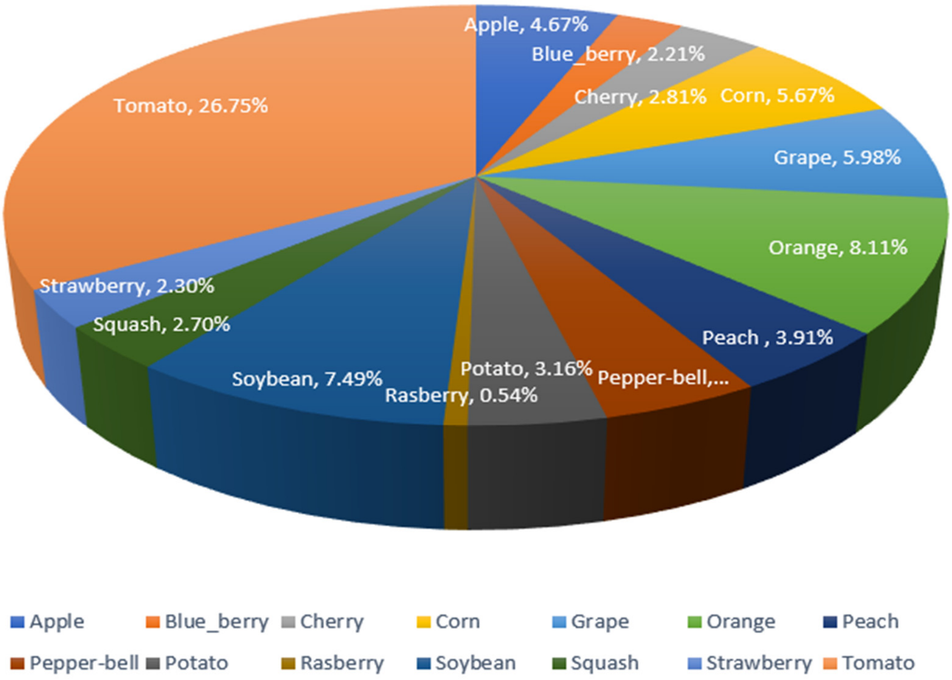

Figure 4. Crop distribution in the PlantVillage dataset.

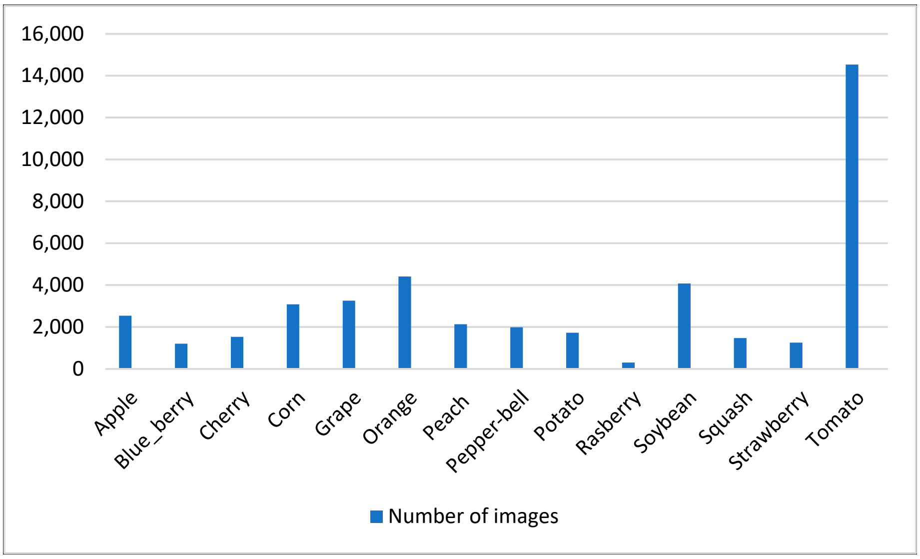

Figure 5. Distribution of healthy and unhealthy samples in the PlantVillage dataset.

Figure 6 depicts an examination of crop diseases using data derived from the PlantVillage dataset. The figure indicates that most images within the dataset are categorized as fungi and bacteria. Notably, the quantity of fungi images far exceeds that of bacteria images, and it is also considerably greater than the counts of virus, mite, and mold images. This observation highlights the uneven distribution of the dataset. Additionally, it is worth noting that the images representing mites and molds are the least prevalent. It is imperative for researchers to thoroughly evaluate this information before utilizing the dataset. The images of mold and mites may be excluded from the dataset before they are employed to train a DL model. Additionally, data augmentation techniques can be applied to increase the number of images representing mold and mites. Furthermore, reducing the number of images of fungi and bacteria can facilitate a more balanced distribution of images across all categories. Implementing these strategies may enhance the efficacy of crop detection methodologies.

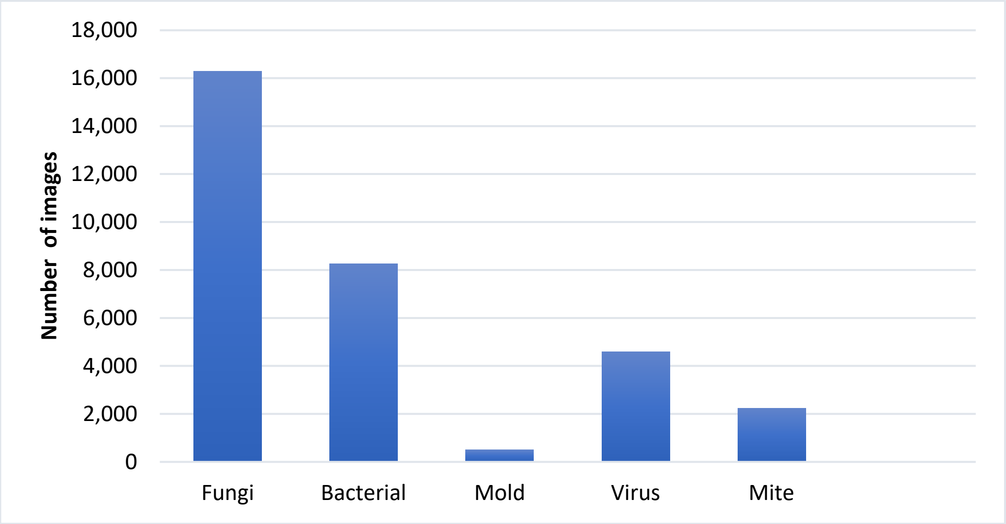

Figure 6. Statistics of crop diseases in PlantVillage dataset.

4.2.2. Other Datasets

Aside from PlantVillage, the AI Challenger dataset [25] provides a diverse range of images for plant disease detection, annotated with multiple disease types. This dataset covers different crops and environmental conditions, offering a valuable resource for training models that require high variability in input data. It is especially useful for multi-label classification tasks, enabling researchers to fine-tune their models for different plant species and disease types. The IP102 dataset [26] focuses on insect pest detection, containing over 75,000 images across 102 species of insects. This dataset is highly valuable for developing models that address pest-related crop diseases. Cassava Leaf Disease [26] is another dataset available on Kaggle, aimed at identifying diseases in cassava plants. It consists of around 21,000 labeled images and provides an opportunity to work with real-world agricultural problems, especially in regions where cassava is a staple crop. Moreover, the authors of [27] collected some datasets from Bangladesh. The dataset consists of nine classes of rice diseases, with each class consisting of 100 images. These datasets contribute to advancing AI-driven agricultural solutions.

4.3. Performance Analysis of ML-Based Crop Disease Techniques

Figure 7 shows the summary of studies that developed ML-based techniques for crop detection diagnosis. Most of the studies featured in this analysis used the PlantVillage dataset. As shown in the figure, many ML algorithms have been used to develop improved techniques for crop disease diagnosis, including SVM, KNN, RF, ELM, Artificial Neural Network (ANN), CNN, Decision Tree (DT), and RNN, among others. Most of the research used SVM, KNN, CNN, and RF in disease identification and classification since they can be used in numerous combinations and tailored to individual crops and diseases. Furthermore, the method of choosing is influenced by aspects such as the type and quality of data available, computational resources, and the unique requirements of the situation at hand. This section examines the performance of studies that employed SVM, KNN, RF, and other ML methods. The three algorithms were chosen because they are the most often utilized ML algorithms in the literature. In addition, to ensure fairness, we present the performance analysis of research that used the same dataset.

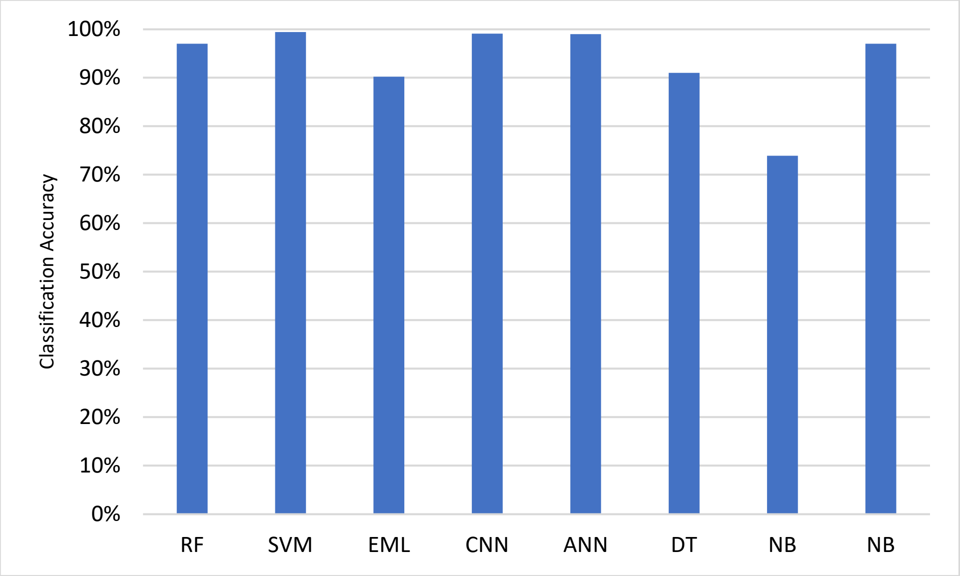

Figure 7. Classification accuracy of other ML algorithms from different authors.

4.3.1. Performance Analysis of SVM-Based Crop Detection Techniques

The SVM classifier is the most popular model used in the literature. SVM can be utilized for binary and multivariate classification, particularly when there are several predictions. This is reinforced by its well-known capability for dealing with many categorical and continuous data elements. SVM can be used to classify entities into specific groups. It can also be used to classify instances that are not supported by data. Figure 8 depicts SVM performance from a few studies that employed it and were able to achieve outstanding results.

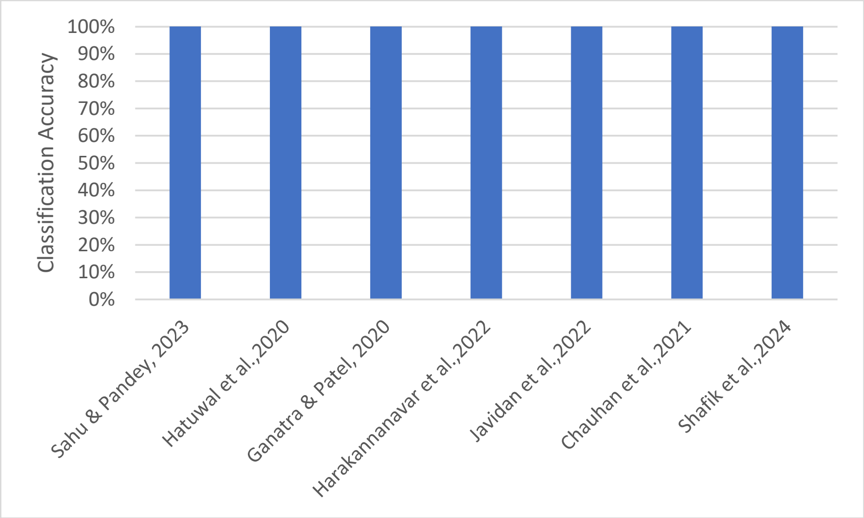

Figure 8. Classification accuracies of SVM-based crop detection techniques. Data sourced from [28–33].

As shown in Figure 8 and Table 3, all the compared techniques produced satisfactory results, with classification accuracy ranging from 67% to 98%. They also achieved an F1 score ranging from 66% to 97%. Also, some techniques achieved a classification accuracy and F1 score of above 97% and 76% [28,29], respectively. This shows that the proposed SVM models correctly classified 91% of the diseases in the dataset used for training. This also shows that the SVM models correctly predicted 98% of the samples across the dataset. This is quite remarkable, as SVM proves to be an algorithm that can be used to develop an effective crop disease diagnosis system.

Table 3. Performance of SVM-based crop detection techniques.

Citations	Algorithm Used	Accuracy	F1 Score	Recall	Precision	Number of Crops Used	Number of Diseases
[28]	SVM + RF	98.9%	97.8%	-	-	14	39
[29]	SVM	78.61%	77%	77%	78%	5	16
[30]	SVM	67.27%	66.02%	66.97%	66.99%	-	38
[31]	SVM	89%	91.5%	97.8%	96.7%%	1	6
[22]	SVM	98.97%	-	-	-	1	4
[32]	SVM	93.4%	91.3%	92.8%	93.4%	14	21
[33]	SVM	76.16%	-	-	-	1	4

The comparative performance analysis of the SVM-based crop detection algorithms reveals significant variations in accuracy, F1 score, recall, and precision. Notably, algorithm [28] achieves exceptional performance with 98.9% accuracy and 97.8% F1 score, utilizing 14 crops and 39 diseases. This suggests that larger, diverse datasets can substantially enhance algorithm performance. In contrast, algorithms [30,31] demonstrate lower accuracy and F1 scores, potentially due to fewer crops and diseases (16 and 38, respectively). An experiment that was carried out by [32], exhibited a performance accuracy of 93.4% on 15 crops and 38 diseases. This was achieved by introducing two plant disease detection models of early fusion as well as lead voting ensemble integration with nine pretrained CNN. Interestingly, single-crop algorithms [22] show competitive performance, indicating effective feature extraction and classification. Additionally, the authors of [33] achieved a low accuracy of 76.16% by implementation of a RF for classification.

The analysis highlights several key insights. Firstly, dataset size and diversity play a crucial role in algorithm performance. Algorithms utilizing more crops and diseases tend to perform better. Secondly, optimization techniques and feature extraction methods significantly impact performance. The superior performance of the algorithm proposed in [28] may be attributed to its optimized feature selection and classification strategy. The authors developed a precision agriculture solution that uses SVM, RF, and Fuzzy C-Means. Fuzzy C-Means was used for image segmentation. The results suggest that SVM-based algorithms can achieve high accuracy in crop disease detection, especially when combined with robust feature extraction, image segmentation, and classification techniques. Hybrid SVM models can produce better performance when trained on a large-scale dataset. Therefore, SVM models should be trained on a dataset with a sizable number of images and features to attain good results. A nature-inspired optimization technique can be used for feature selection. The SVM model developed by [30] produced low classification accuracy. This could be due to the model being trained on a dataset with numerous images and classes. This is an indication that SVM models are not suitable for the classification of large-scale datasets. The training complexity of SVM highly depends on the size of the training dataset.

Future research should focus on exploring ensemble methods, transfer learning, and DL architectures to further improve performance. Additionally, investigating the impact of data augmentation, class imbalance, and hyperparameter tuning on SVM-based crop disease detection algorithms would provide valuable insights.

4.3.2. Performance Analysis of KNN-Based Crop Detection Techniques

The KNN classifier is now being utilized for crop disease diagnosis, with its predictions relying only on the quality and amount of data being utilized. As illustrated in Figure 8, all the compared techniques generated good results, as evidenced by the categorization performance accuracy range of 64% to 100%. This implies that the suggested KNN models successfully identified between 64 and 100% of the samples across the dataset. This is quite novel, as KNN demonstrates that it can be utilized to create an effective crop disease diagnosis system even though the models were trained on small, medium-sized or imbalanced datasets.

The comparative performance analysis of the KNN-based crop detection algorithms reveals varying degrees of success in accuracy, F1 score, recall, and precision. As shown in Figure 9 and Table 4, the algorithm developed by the authors of [34] achieves perfect accuracy (100%) with a single crop and six diseases, while the algorithm in [10] demonstrates similarly impressive results (97.3% accuracy, 95.2% F1 score) under the same conditions. The authors of [34] employed K-means clustering as an image processing technique for segmentation, since it can group pixels based on their intensity similarities, making it a unique characteristic that is optimal for segmentation. Additionally, K-means clustering has the capability of uncovering hidden patterns, creating meaningful clusters as well as providing valuable insights from data without the need for labeled information. Its simplicity, scalability, and interpretability make it a valuable tool in various domains. Furthermore, expert knowledge was also incorporated into the technique developed by [34], which can assist farmers in identifying crop ailments, making the appropriate decision, and selecting the right treatment for the disease on time, resulting in better crop yield. The authors of [10] used K-means clustering to partition the data space into Voronoi cells. The ability to identify image boundaries by contour tracing was particularly beneficial, as was the extraction of informative features via GLCM.

Notably, the algorithms developed in [32,35] achieve exceptional performance with a single crop, suggesting effective feature extraction and classification strategies. The KNN algorithm in [36] achieved a classification accuracy of 91%. Algorithm [37], utilizing 14 crops and 39 diseases, demonstrates a respectable accuracy (94.1%) but a lower F1 score (77.22%), potentially indicating class imbalance issues. The modest F1 score of the algorithm developed in [37] highlights the challenges of scaling KNN-based approaches. ML was used for classification by the authors in [38] who achieved a classification accuracy of 84.94%. The KNN algorithms may have performed poorly due to several factors: the training dataset had limited images, which restricted model learning, and many images contained unnecessary noise and backgrounds, complicating accurate segmentation. Additionally, variations in environmental conditions like lighting, moisture, and the capturing device introduced inconsistencies that made it hard to find similar images. The dataset also suffered from imbalanced and non-uniform samples, while differences in symptom characteristics across geographic locations further added complexity. These combined challenges likely impeded effective model training and performance.

Key observations include the significant impact of dataset size and diversity on performance, the potential for single-crop algorithms to achieve high accuracy with optimized feature extraction, and the challenges posed by class imbalance and noise in larger datasets. Future research should explore ensemble methods, distance metric optimization, and handling high-dimensional data to enhance KNN-based crop disease detection. Additionally, investigating the effects of data preprocessing, feature selection, and hyperparameter tuning on KNN performance would provide valuable insights.

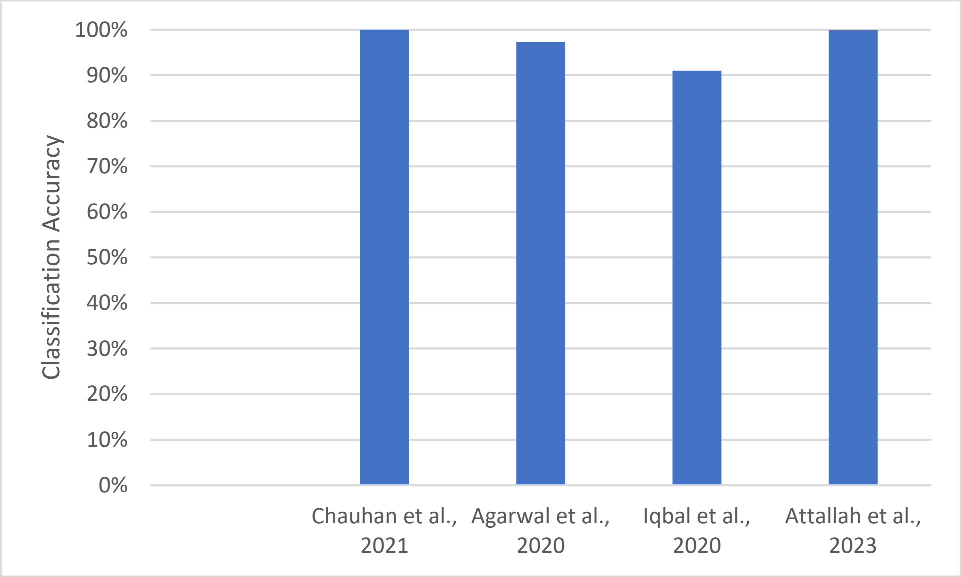

Figure 9. Classification accuracies of KNN-based crop detection techniques. Data sourced from [32,34,36,37].

Table 4. Performance of KNN-based crop detection techniques.

Citation	Algorithm Used	Accuracy	F1 Score	Recall	Precision	Number of Crops Used	Number of Diseases
[32]	KNN	100%	-	-	-	1	6
[34]	KNN	97.3%	95.2%	97.5%	97.8%	1	6
[36]	KNN	91%	77.2%	-	-	1	10
[37]	KNN	99.92%	77.22%	-	-	14	39

4.3.3. Performance Analysis of RF-Based Crop Detection Techniques

The RF algorithm is a popular supervised ML that employs a combination of multiple decision trees, with each tree trained using different subsets of the entire dataset, reducing overfitting and improving classifier accuracy. It is also an ensemble learning method that is used for both classification and regression tasks in ML. As shown in Figure 9 and Table 5, the RF-based technique developed by the authors in [39] produced a modest precision and F1-score of 92.85% and 92.84%, respectively. They used an RF classifier for automatic crop leaf disease detection. The RF-based technique generates numerous decision trees and combines them to provide more precise predictions. Furthermore, RF effectively manages missing values in data, thereby enhancing its ability to maintain a high level of accuracy. This can be achieved by using Global Feature Descriptors (GFDs), a mathematical representation that captures the overall characteristics of an entire or specific image and summarizes the content. One of the most popular GFD techniques is the HSV. The HSV approach relies on the development of masks using color information. Additionally, it utilizes the color intensity and brightness of the HSV color system. HSV is considered the most straightforward technique for image segmentation, as it can effectively isolate the region of interest from the images. Applying a threshold to the HSV image produces masks for a healthy and diseased potato leaf image in the RGB color space. Some studies also used GLCM for texture feature extraction. The authors in [39] extracted deep features from CNN and then fed the deep features into RF for classification.

Table 5. Performance of RF-based crop detection techniques.

Citation	Algorithm Used	Accuracy	F1 Score	Recall	Precision	Number of Crops Used	Number of Diseases
[39]	RF	92.85%	92.84%	92.84%	92.85%	1	8
[40]	RF	84.94%	-	-	-	1	4
[32]	RF	80.68%	85.5%	85.7%	85%	1	3
[41]	RF	96.1%	92.1%	88.6%	95.9%	14	38
[42]	RF + CNN	77	77	77	81	1	7

The comparative performance analysis of the RF-based crop detection algorithms reveals varying degrees of success in accuracy, F1 score, recall, and precision. Algorithm [39] demonstrates a precision of 92.85% with a single crop and eight diseases. In contrast, the algorithm proposed by the authors of [40] shows relatively lower accuracy (84.94%) with a single crop and four diseases.

Algorithm [41] stands out, achieving 96.1% accuracy, 92.1% F1 score, 88.6% recall, and 95.9% precision using 14 crops and 38 diseases. This suggests that RF implementation of the authors in [41] effectively handles larger, more diverse datasets. The algorithm developed by the authors of [32] demonstrates modest accuracy (80.68%) and balanced recall and precision (85.7% and 85%, respectively) with a single crop and three diseases. The RF model developed by [32] was trained on gray images and not RGB images. This could also affect the performance of the models. This shows that the quality of images used to train ML models is very important. Moreover, the algorithm developed by the authors in [42] produced a relatively low accuracy of 77%. They developed a hybrid model for potato leaf disease classification using RF and CNN.

Key observations include the significant impact of dataset size and diversity on performance, the potential for RF-based algorithms to achieve high accuracy with optimized feature extraction, and the challenges posed by class imbalance and noise in larger datasets. Future research should explore ensemble methods, hyperparameter tuning, and handling high-dimensional data to further enhance RF-based crop disease detection.

4.3.4. Performance Analysis of Other ML Algorithms on PlantVillage Dataset

Apart from SVM, KNN, and RF, previous studies have employed various other ML algorithms, including ELM, ANN, Naïve Bayes (NB) algorithm, and DT. ANN, resembling a biological system, models the processing of information through interconnected processing elements forming a network structure. This characteristic enables ANN to extract patterns from complex data due to its intrinsic understanding. DT is recognized for its robustness and success in classification and detection, making it widely applied in areas such as medical diagnosis, speech recognition, and character recognition. The Extreme Learning Machine (ELM) model, introduced by [41], represents a straightforward form of feed-forward neural networks. Furthermore, the authors specifically devised a Single-Hidden Layer Feed-Forward Neural Network (SLFN) for diagnosing crop diseases. The technique has the capacity to randomly choose hidden nodes and analytically determine the output weights of the SLFNs. SLFNs tend to provide good generalization performance at commendable learning speed because inputted weights are randomly assigned, and hidden layer biases can be learned in distinct observation.

Figure 10 shows the comparison between different ML techniques that were trained on the PlantVillage dataset. As shown in Figure 11 and Table 6, the compared ML algorithms achieved classification accuracies ranging from 80.42% to 99.7%. The ANN-based model developed by [43] produced a classification accuracy and F1 score of 98.22% and 93.55%, respectively. The authors of [31] developed a model for plant disease diagnosis using a combination of SVM, GLCM, CNN, and K-means algorithms. GLCM was used to convert the images into a new color space. K-means clustering is used to segment the infected region in the image. KNN was used to extract the textual features of the segmented region. The extracted features are then used to train the CNN algorithm, which achieved a commendable classification accuracy of 99.6%. The results show that combining the use of image processing techniques with CNN and ML algorithms can improve their performance. The results also show that using image segmentation techniques (such as K-means algorithm) and feature selection techniques (such as PCA) can improve the performance of ML- and DL-based crop detection models.

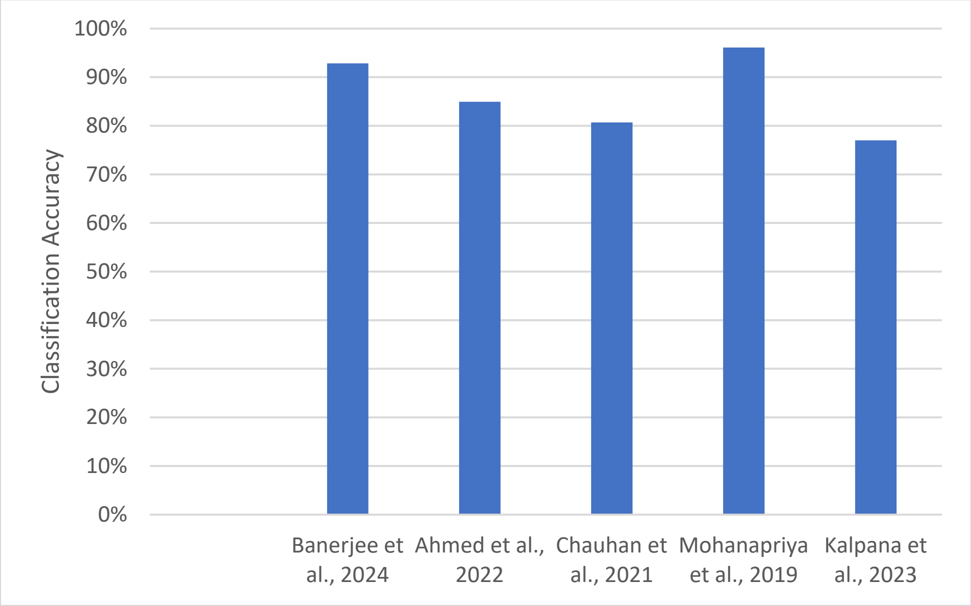

Figure 10. Classification accuracies of RF-based crop detection techniques. Data sourced from [32,39–42].

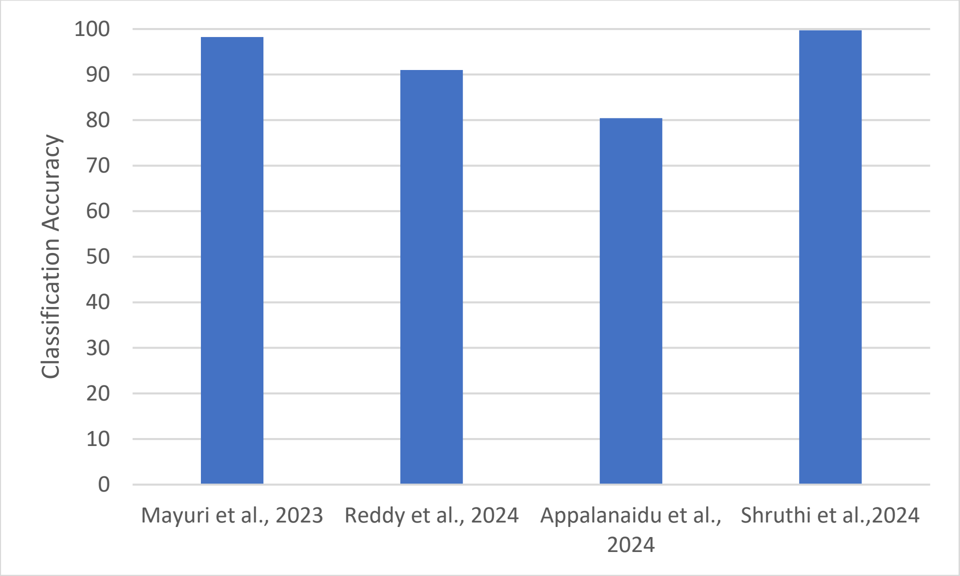

Figure 11. Classification accuracies of other ML-based crop detection techniques. Data sourced from [43–46].

Table 6. Performance of other ML algorithms used with the PlantVillage dataset.

Citation	Algorithm Used	Accuracy	F1 Score	Recall	Precision	Number of Crops Used	Number of Diseases
[43]	ANN	98.22%	-	93.55%	95.77%	14	38
[44]	NB	91%	-	-	-	3	4
[45]	DT	80.42%	-	-	-	8	23
[46]	ELM	99.7%	99.7%	99.6%	99.6%	14	39

The authors in [44] proposed a classification technique for plant diseases using the NB algorithm, achieving a classification accuracy of 91%. Naïve Bayes has been termed to be among the simplest and most efficient classification algorithms in building fast models of ML for fast prediction and high accuracy. It is not only a supervised learning method that can be trained efficiently but also a probabilistic classifier based on an object. Nevertheless, the NB classifier method produces the right grouping solution based on experts' learning. It is beneficial to use Naïve Bayes, since it requires a small amount of training data for variance parameter estimation of the variables required for classification. The authors of [45] designed a plant detection technique using the DT algorithm. The algorithm was trained on over 21,000 images of eight crops and 23 diseases (including healthy plants), and it produced a modest classification accuracy of 80.42%. The authors of [46] designed an improved classification technique for plant leaf disease detection using wavelet kernel ELM and MobileNetV3. The MobileNetV3 was used for feature extraction, while the wavelet kernel ELM model was used for classification. The hybrid model was trained on the PlantVillage dataset and it achieved a remarkable classification accuracy of 99.7%

4.4. Performance Analysis of DL-Based Crop Detection Techniques

Numerous DL-based methods have emerged in the research utilizing various architectures such as CNN, VGG16, ResNet50, DenseNet121, and numerous others. This section provides an evaluation of the performance of these DL-based techniques.

4.4.1. Performance Analysis of CNN-Based Crop Detection Techniques

A CNN is a well-known DL technique that has been extensively utilized in computer vision, including crop disease identification. CNNs are said to be capable of automatically and adaptively learning spatial hierarchies of features from input data, making them ideal for image recognition applications. CNN application, especially in the agricultural field, includes training its model using a dataset by learning to recognize patterns and features in the images from a dataset that distinguishes healthy and unhealthy. Additionally, CNN is also used in classifying new and unseen images by predicting the condition affecting the image based on the learnt patterns and the features. Furthermore, CNN has demonstrated high accuracy in crop disease diagnosis, often surpassing human experts.

Many CNN-based crop disease detection techniques have been developed in the literature. As shown in Figure 12, most of the reviewed CNN-based techniques diagnosed crop diseases with a high classification accuracy of above 92%. The CNN-based method introduced by the authors of [47] achieved a classification accuracy of 98.2%. This approach comprised five layers and was trained using a medium-scale dataset containing 2002 black gram images. Additionally, the authors of [47] highlighted that their proposed method is more time-efficient and has the capacity to promptly detect and identify agricultural diseases in their early stages. This capability is essential for establishing an efficient disease management plan, rendering it a strongly endorsed solution for farmers.

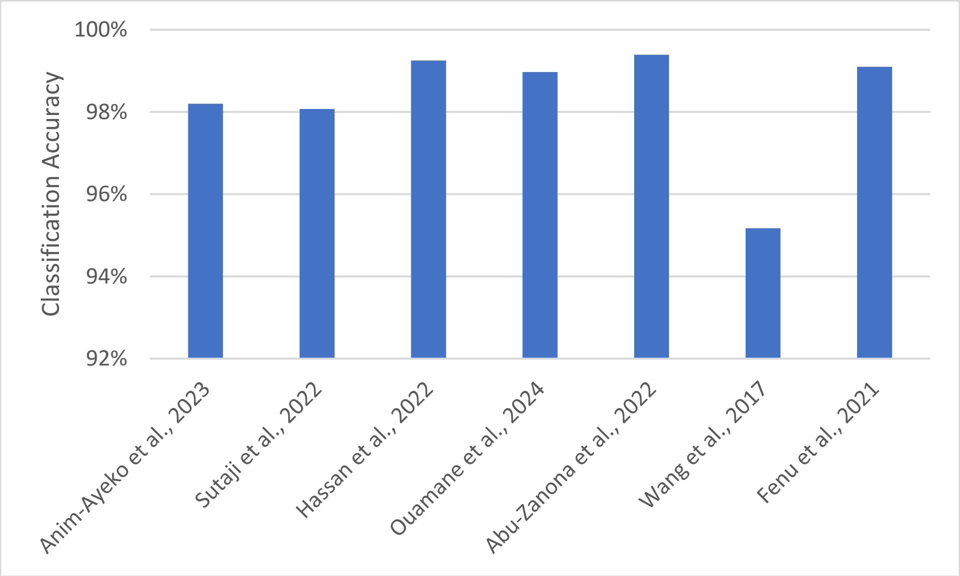

Figure 12. Performance of CNN-based crop detection techniques. Data sourced from [47–53].

The authors of [48] introduced a DL-centric strategy for the automatic classification of plant diseases, employing CNN models. The devised system aims to categorize three distinct types of potato leaf diseases by analyzing their visual symptoms. The model comprises numerous convolutional layers, pooling layers, and fully connected layers. Moreover, transfer learning was employed to enhance a pre-trained CNN model, adapting it particularly for the classification problem at hand. The suggested system exhibited remarkable effectiveness by achieving an overall accuracy of 98.07% on the test dataset, confirming its ability to accurately predict potato leaf diseases.

The authors of [49] developed intelligent image recognition systems based on SVM, transfer learning (MobileNet) algorithm, and CNN approaches, all of which were based on moveable systems that were learned utilizing data from paddy fields and the internet. The MobileNet algorithm contributed to the accuracy of performance through its lightweight design, which allows it to be integrated into frameworks such as Tensor Flow and PyTorch, making it accessible to developers working on large projects.

In a separate study, the authors of [50] developed a CNN model designed to identify the concurrent presence of strawberry leaf spot and leaf blight. Leveraging the feature extraction capabilities of a normalized CNN, the model showcased an innovative approach to detecting multiple classes of fungal infections on a single plant. This achievement was made possible by the model accurately learning the shared characteristics during the training process. For all classes analyzed, the model had an overall accuracy performance of over 98%.

The authors of [51] developed a customized DL model using a specialized architecture called CNN to automatically identify plant diseases. Specifically, the model was designed to categorize potato leaves into three different disorders. The author utilized data augmentation approaches to gather datasets from many sources in order to generate new images based on existing datasets, employing a range of data transformation techniques, integrated and pooled layers, and fully merged layers through feature learning. The model achieved a classification accuracy of 99.39% with an ability to automatically learn features from raw images, thus demonstrating effective detection of three different types of potato leaf disease can be recommended for application. Additionally, [50,51] had remarkable performance accuracy of 98.97% and 99.39% respectively. This was achieved from implementation of 2 different CNN algorithm by each. The summarized performance of the reviewed SNN-based techniques is shown in Table 7 and Figure 12.

Table 7. Performance of CNN-based crop detection techniques.

Citation	Algorithm Used	Accuracy	F1 Score	Recall	Precision	Number of Crops Used	Number of Diseases
[47]	CNN	98.2%	96.3%	95.9%	97.14%	1	5
[48]	CNN	98.07%	-	-	-	1	3
[49]	ResNet9	99.25%	99.33%	99.33%	99.67%	2	6
[50]	DenseNet121	98.97%%	95.9%	93.3%	98.9%	14	38
[51]	CNN	99.39%	-	-	-	2	9
[52]	CNN	95.17%	95.11%	95.17%	95.11%	3	12
[53]	CNN	99.10%	-	-	-	1	4

The results of the compared CNN-based techniques are shown in Table 8 and Figure 13. The comparative performance analysis of the CNN-based crop detection algorithms reveals exceptional accuracy across various datasets. Algorithm [49] achieves the highest accuracy (99.53%) with a single crop and five diseases. Also, the algorithm in [46] demonstrate impressive accuracy (97.66%) with single-crop datasets. Notably, algorithm [47] reports a comprehensive evaluation (92.50% accuracy, 91.89% F1 score, 87.17% recall, 97.14% precision) with a single crop and one disease. In contrast, the algorithm developed by the authors of [52] demonstrates balanced performance (95.17% accuracy, 95.11% F1 score, 95.17% recall, 95.11% precision) using three crops and twelve diseases. The SVM algorithm developed by the authors of [53] achieves high accuracy (98.36%) with a single crop and ten diseases, highlighting the effectiveness of CNN-based approaches in crop disease detection. Also, the authors in [52] respectively affirmed the commendable performance accuracy of CNN while [54] showcased DenseNet121 accuracy of 98.97%.

Table 8. Performance of other DL-based techniques.

Authors	Algorithm Used	Accuracy	F1 Score	Recall	Precision	Number of Crops Used	Number of Diseases
[46]	CNN	97.66%	98.8%	99.5%	99.5%	-	-
[49]	VGG16	99.56%	-	-	-	1	5
[47]	CNN	92.50%	91.89%	87.17%	91.14%	1	1
[52]	CNN	98.07%	95.11%	95.17%	95.11%	3	12
[53]	SVM + CNN	98.36%	-	-	-	1	10
[54]	DenseNet121	98.97%	98.97%	98.97%	99.0%	14	38

Key observations include the exceptional performance of CNN-based algorithms, the benefits of optimized architectures for single-crop datasets, and the challenges posed by larger, more diverse datasets. Future research focused on developing an automated, unbiased should explore transfer learning, data augmentation, and ensemble methods to further enhance CNN-based crop disease detection. The summarized performance of the other DL-based.

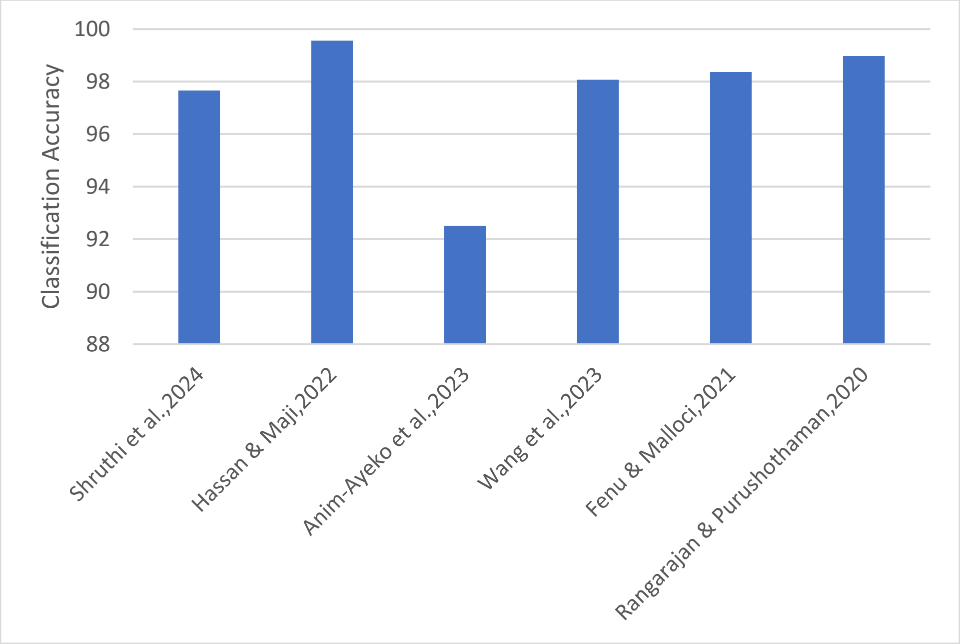

Figure 13. Classification accuracies of other DL-based crop detection techniques. Data sourced from [46,47,49,52–54].

4.4.2. Performance Analysis of VGG16 Crop Detection Techniques

Visual Geometry Group (VGG) is an Oxford University research group identified for its computer visual-related activities, particularly the development of the VGGNet architecture, which is a deep CNN that has been widely used in image classification and object recognition tasks. VGG is usually followed by a number indicating the architecture's specific variant, such as VGG16: a variant with 16 weight layers. Notably, this architecture has been identified to be significant in the field of DL, and it is frequently used for benchmarking and evaluating new models and techniques. This is because of its simplicity and efficacy in producing cutting-edge results, as well as the utilization of small filters. Furthermore, the VGG design comprises many convolutional layers stacked on top of each other that are fully coupled with max-pooling layers as well as fully connected layers, allowing the network to learn complicated features at different levels of abstraction by repeatedly using small filter sizes (3 × 3).

Different crop disease detection techniques have been developed in the literature using VGG16. The authors of [14] developed a web-based application for rice disease classification using VGG16. The application achieved a performance accuracy of 90%. In another study, the authors in [55] proposed a DL-based technique for the detection and classification of four common palm tree diseases using VGG16. The technique achieved a classification accuracy of 99.56%.

The depth of the VGG16 network can be extended by incorporating additional convolutional layers, as it employs small convolution filters across all layers [55]. Conversely, the authors in [56] introduced a DL model designed to automatically diagnose and assess the severity of plant diseases using image data. This initiative drew inspiration from the breakthroughs in DL for image-based recognition of plant diseases. To do this, the researchers trained CNNs with different depths from scratch and adjusted four advanced deep models: VGG16, VGG19, Inception V3, and ResNet50. The VGG models (16 and 19) were particularly remarkable, as they demonstrated substantial enhancements compared to previous architectures. Out of all the models, VGG16 exhibited the most impressive performance, attaining a test dataset accuracy of 90.4%. During training, the deep networks attained accuracies approaching 100%, leading to the early termination of the training process.

The authors of [57] demonstrated the effectiveness of VGG16 in assisting farmers in identifying pear leaf symptoms and offering targeted guidance for pesticide use. Their approach involved designing a multioutput system based on CNN. They evaluated five pre-trained CNN architectures—VGG16, VGG19, ResNet50, InceptionV3, MobileNetV2, and EfficientNetB0—as feature extractors for classifying three diseases and six severity levels. VGG16 gave an accuracy of 64.23% for this particular study due to the small size of the dataset, and thus, there was difficulty in capturing relevant features.

Furthermore, the authors of [58] developed a disease classification in eggplant using a pre-trained VGG16 that used images converted to other color spaces such as hue saturation value, YcbCr, and grayscale for evaluation. VGG16 was also used as a feature extractor from an eighth convolutional layer whereby these features have been used for classifying diseases employing multi-class SVM. This allowed the proposed model, which was implemented by VGG16, to achieve a performance accuracy of 99.4% [59] which was achieved by including features from its various layers that were given to the MSVM to assess classification effectiveness.

The authors of [60] developed a merged neural network that integrated the retrieved features from both VGG16 and AlexNet networks to construct a disease classification model with fully connected layers. The efficacy of the concatenated model was evaluated, yielding a training classification accuracy of 100%, validation accuracy of 97.29%, and testing accuracy of 95.82%. In another study, the authors of [61] presented a VGG16 model to detect plant diseases such that farmers can use it to make timely actions with respect to treatment without further delay. This was achieved by using 19 different classes of crops from the PlantVillage dataset for training and testing. The proposed model comprises thirteen convolutional layers, two batch normalization layers, five max-pooling layers, and three full connection layers. These contributed to the proposed model performance accuracy of 95.2% despite the inputted images having certain illumination conditions and a complex background, since the images were collected from actual leaves from planted crops.

Figure 14 and Table 9 shows the classification accuracies of different VGG16-based crop detection techniques. The comparative performance analysis of the VGG16-based crop detection algorithms reveals impressive accuracy across various datasets. The algorithm achieves the highest accuracy (99.4%) with a single crop and five diseases. Algorithm [58] demonstrates exceptionally balanced performance (98.19% accuracy, 98.12% F1 score, 98.24% recall, 98.33% precision) using two crops and five diseases. Other algorithms [14,62], show similar accuracy (90% and 90.4%, respectively) with a single crop and four diseases. Algorithm [61] achieves 95.2% accuracy with five crops and nineteen diseases, while the VGG16 algorithm in [63] demonstrates 92.5% accuracy using fourteen crops and thirty-eight diseases. These results highlight VGG16's effectiveness in crop disease detection, even with varying dataset sizes and complexities.

Table 9. Performance of VGG16-based crop detection techniques.

Citation	Algorithm Used	Accuracy	F1 Score	Recall	Precision	Number of Crops Used	Number of Diseases
[14]	VGG16	90%	-	-	-	1	4
[62]	VGG16	90.4%	-	-	-	1	4
[56]	VGG16	99.4%	-	-	-	1	5
[58]	VGG16	95.2%	-	-	-	5	19
[60]	VGG16	92.5%	-	-	-	14	38

Key observations include VGG16's robust performance across diverse datasets, the benefits of transfer learning, and the importance of dataset quality. Future research should explore fine-tuning VGG16, data augmentation, and ensemble methods to further enhance crop disease detection accuracy.

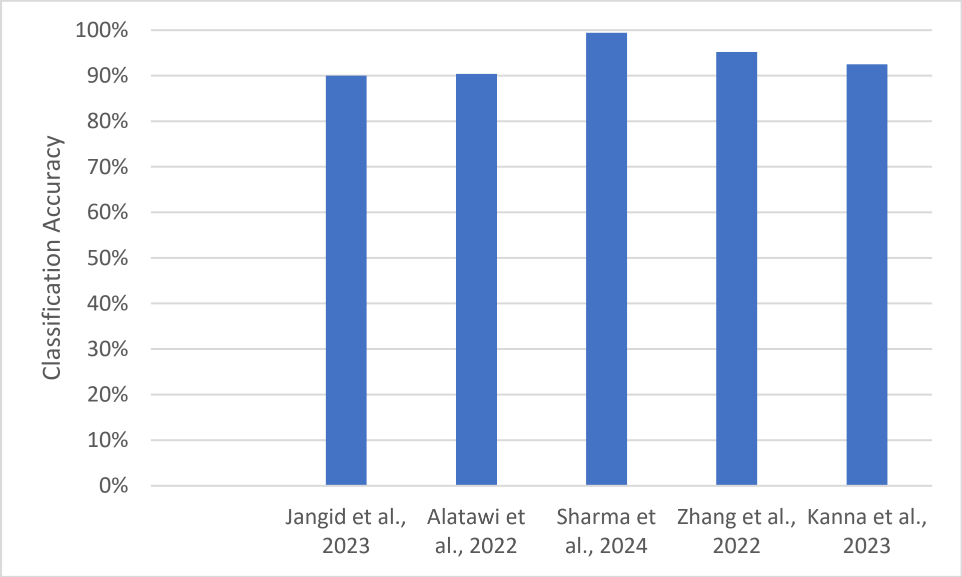

Figure 14. Classification accuracies of VGG16-based crop detection techniques. Data sourced from [14,56,58,60,62].

4.4.3. Performance Analysis of ResNet50 Crop Detection Techniques

Residual Neural Network (ResNet) is a popular DL model architecture that addresses the challenge of vanishing gradients in very deep neural networks, which may hinder their ability to learn effectively. Moreover, ResNet's key innovation is the use of residue learning that involves the introduction of shortcut connections (skip connections) into the network architecture. This feature allows the information to bypass more than one layer, thus enabling direct flow of the input to the output. Hence, ResNet has been widely adopted and achieved state-of-the-art performance on various computer vision tasks, including image classification, object detection, and image segmentation.

The authors of [64] designed a smart web application for predicting crop diseases using ResNet50, achieving an impressive classification accuracy of 98.98%. This innovative tool offers farmers the capability to identify plant diseases by analyzing images of crop leaves. In another study, the authors of [59] developed a technique using ResNet9. The model considered the image shape, the diseased area present, and the general green area of the leaf for its prediction. The authors also used data augmentation and hyperparameter optimization to improve the performance of the model. The accuracy of 99.25% achieved by the model shows that ResNet is highly recommended for crop disease diagnosis.

The authors of [16] developed a tailored model for identifying and categorizing image leaves. They used ResNet50 to extract various features from plant leaf images, including color and texture features. To acquire optimized and salient features with reduced size of the MRDOA, the modified red deer optimization method was also implemented as an optimal feature selection technique. The PDICNet model achieved an accuracy performance of 99.73%.

The authors of [65] focused on developing an automated, unbiased, and effective diagnostic approach for identifying wheat illnesses. They employed a model in a greenhouse scenario that incorporated image-deep features and parallel feature fusion. This was achieved by utilizing an automated methodology that relies on image processing techniques to match crop images with the objective of targeting identical locations. To speed up the dataset development process, an automated web tool was utilized to generate the dataset from either image or automatically build the corresponding dataset from the other image. Furthermore, handcrafted features were extracted from each image format, and disease detection results revealed that parallel feature fusion was more accurate than features from either type of image. ResNet101, which was implemented with deep features and parallel feature fusion, outperformed the other DL models. It produced a classification accuracy of 74% on leaf rust and 84% on tan spots.

The authors of [27] developed a DL-based technique to classify diseases in cauliflower plants at an early stage. Their major objective was to enhance disease diagnosis and detection by employing deep transfer learning techniques. This study trained and analyzed 10 DL transfer learning models, namely EfficientNetB0, Xception, EfficientNetB1, MobileNetV2, EfficientNetB2, DenseNet201, EfficientNetB3, InceptionResNetV2, EfficientNetB4, and ResNet152V2. ResNet152V2 attained an accuracy performance of 66.50%.

The authors of [62] proposed a DL model that would be capable of crop disease classification. This was achieved by consideration of 10 DL pre-trained models that were each fine-tuned using the PlantVillage dataset. ResNet50 achieved an accuracy of 93.26% among other DL pre-trained models. The authors of [64] sought to determine the most appropriate ML/DL models for the PlantVillage tomato dataset and the classification of tomato diseases. Among the tested DL models, ResNet was inclusive, whereby the features were extracted using COLOR and GLCM. ResNet also produced the best accuracy of 98.97%.

Figure 15 and Table 10 show the classification accuracy of ResNet50-based crop detection techniques. The comparative performance analysis of the algorithms reveals exceptional accuracy across various datasets. Algorithm [59] achieves outstanding performance (99.25% accuracy, 99.33% F1 score, 99.33% recall, 99.67% precision) using two crops and two diseases. Similarly, the ResNet50 algorithm in [64] demonstrates impressive accuracy (98.98% accuracy, 98.98% F1 score, 99.05% recall, 98.99% precision) with three crops. The ResNet50 models developed in [27,64] achieve high accuracy (98.2% and 98.36%, respectively) with diverse dataset sizes (fourteen crops/thirty-eight diseases and one crop/six diseases). The algorithm developed by the authors of [65] shows modest accuracy (93.5%) with a single crop and two diseases. Algorithms [61,64] demonstrate competitive performance (96.49% and 98.2% accuracy) using 14 crops and 38 diseases. These results highlight ResNet50's robustness across diverse dataset sizes and complexities.

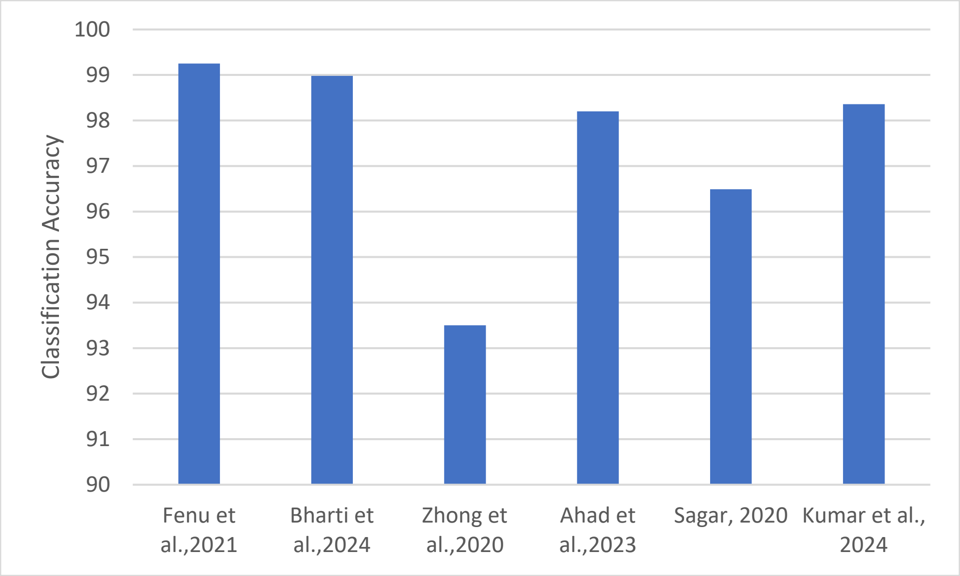

Figure 15. Classification accuracies of ResNet-based crop detection techniques. Data sourced from [27,53,61,63–65].

Table 10. Performance of ResNet50-based crop detection techniques.

Citation	Algorithm Used	Accuracy	F1 Score	Recall	Precision	Number of Crops Used	Number of Diseases
[53]	ResNet	99.25%	99.33%	99.33%	99.67%	2	2
[63]	ResNet50	98.98%	98.98%	99.05%	98.99%	3	
[65]	ResNet50	93.5%	-	-	-	1	2
[27]	ResNet50	98.2%	94%	94%	94%	14	38
[61]	ResNet50	96.49%	-	-	-	14	38
[64]	ResNet50	98.36%	-	-	-	1	6

Key observations include ResNet50's exceptional performance in crop disease detection and the importance of optimized architecture and training parameters. Future research should explore fine-tuning ResNet50 for specific crop disease detection tasks, data augmentation and preprocessing techniques, and ensemble methods. Comprehensive evaluations provide valuable insights into algorithm performance and inform optimization strategies.

4.4.4. Performance Analysis of DenseNet121 Crop Detection Techniques

The Densely Connected Convolutional Network (DenseNet) is another deep neural network architecture that has been able to address a few challenges by traditional deep neural networks, such as gradient vanishing and increased risk of overfitting as networks become deeper. This is made possible by its ability to establish feed-forward connections across all layers, whereby each layer receives direct input from all levels before passing along its own feature maps to all levels that follow. Despite having several of these blocks layered on top of one another, DensNet may be separated into dense blocks and transition blocks.

The authors of [52] suggested a classification method for crop diseases using ten pre-trained CNN models, specifically AlexNet, GoogleNet, VGG16, VGG19, ResNet50V2, Inception V3, Xception, MobileNetV2, InceptionResNetV2, and DenseNet121. The models were fine-tuned on the PlantVillage dataset. The fine-tuning was accomplished by unfreezing the last block of convolutional layers. The fine-tuning focused on improving the high-dimensional features extracted, aiming to affect the capture of additional details within these features by changing the weight parameter. In the study, DenseNet121 produced the best result, achieving a classification accuracy of 94.4% when all layers were frozen and 98.97% when only the last block's convolution layers were frozen. In another study, the authors of [65] employed DenseNet121 to identify apple leaf diseases. They used DenseNet121 with three regression multilevel classification algorithms and a focus loss function, and it obtained a classification accuracy of approximately 93%.

The authors of [27] conducted a comparison of rice classification using six CNN-based DL architectures: DenseNet121, InceptionV3, MobileNetV2, ResNext101, ResNet152V, and Seresnext101. This study utilized a database comprising nine of the most prevalent rice diseases. Additionally, a transfer learning approach was applied to DenseNet121, MobileNetV2, Resnet152V, and Seresnext101 to investigate whether transfer learning could potentially enhance accuracy.

To compare the original transfer learning and ensemble approaches, a DEX ensemble model built on DenseNet121, EfficientNetB7, and Xception networks was used, which gave an accuracy of 98%. DenseNet121 achieved an accuracy performance of 97% in the detection of rice diseases. The authors of [16] used a pre-trained neural network model, DenseNet121, that was imported from the Keras library, to train DenseCNN, which was used for classification. In this study, DenseNet121 has been used to classify twenty-nine different diseases for seven crops and also extract features. This DL model was able to achieve 98.23% theoretically and practically 94.96%, outperforming the previously proposed state-of-the-art techniques.

The authors of [63] developed advanced DL techniques for predicting early diseases in cauliflower plants, with the primary objective of enriching comprehension of the importance of identifying and detecting crop diseases in rural agriculture, employing sophisticated deep transfer learning methods. This was achieved by examining the performance of 10 deep transfer learning models with regard to precision, F1 score, and accuracy, to mention but a few. Remarkably, among the ten models, EfficientNetB1 achieved the highest validation of 99.90%, with DenseNet121 giving 98.48%.

The authors of [20] implemented a DL-based approach for detecting leaf diseases in crops using images tailored for agricultural applications. The authors accomplished this objective by employing pre-trained CNN models and focusing on fine-tuning the hyperparameters of well-known models, including DenseNet121, ResNet50, VGG16, and InceptionV4, for efficient crop disease identification. The models' efficacy was evaluated through metrics such as classification accuracy, sensitivity, specificity, and F1 score. It was found that DenseNet121 exhibited the highest classification accuracy, reaching an impressive 99.81%. This superior performance is attributed to DenseNet121's thin and compact design, where the feature maps from preceding layers are directly linked to subsequent layers, resulting in a reduction in the number of channels in a dense block.

The authors of [18] introduced a methodology aimed at facilitating early diagnosis and mitigating potential crop losses through precise and resilient disease detection in tomato crops. This was accomplished by leveraging DenseNet121, chosen for its recognized performance resulting from its innovative utilization of dense skip connections across layers. These connections help alleviate the gradient vanishing problem by enabling a direct flow of gradients. The proposed approach incorporates DenseNet121 to enhance the performance and convergence of disease detection models. The resulting classification accuracy achieved by DenseNet121 was 98.30%.

Figure 16 and Table 11 show the classification accuracies of the reviewed DenseNet121 models. The comparative performance analysis of the models reveals exceptional accuracy across various datasets. The DenseNet model in [20] achieves outstanding performance (99.81% accuracy, 99.8% F1 score) using 14 crops and 38 diseases. Similarly, the DenseNet model in [62] demonstrates impressive accuracy (98.97% accuracy, 98.97% F1 score, 98.97% recall, 99.00% precision) with the same dataset configuration. Furthermore, the models in [10,18] achieve high accuracy (98.30% and 97%, respectively) with a single crop and nine diseases. The DenseNet model in [16] shows moderate accuracy (94.96%) using seven crops and twenty-nine diseases. The model developed in [46] demonstrates relatively lower accuracy (93.71%) with a single crop and six diseases.

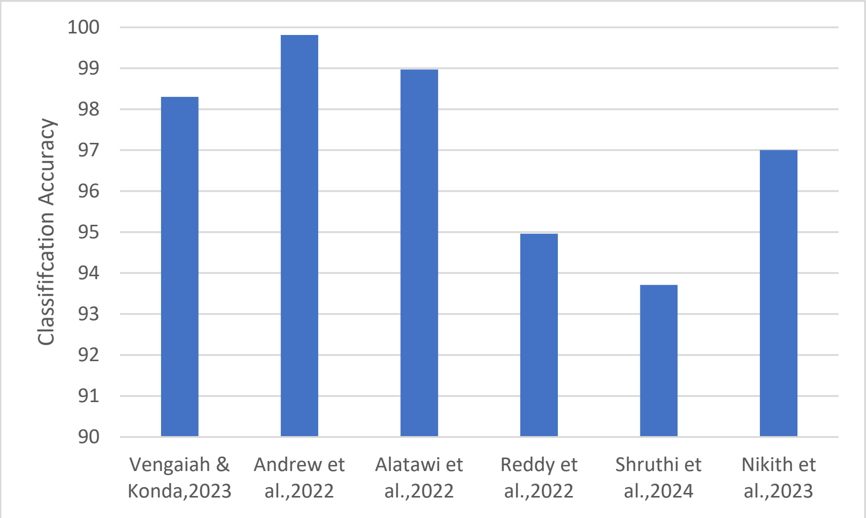

Figure 16. Classification accuracies of DenseNet121-based crop detection techniques. Data sourced from [10,16,18,20,46,62].

Table 11. Performance of DenseNet121-based crop detection techniques.

Citation	Accuracy	F1 Score	Recall	Precision	Number of Crops Used	Number of Diseases
[18]	98.30%	99%	99%	98%	1	9
[20]	99.81%	99.8%	-	-	14	38
[62]	98.97%	98.97%	98.97%	99.00%	14	38
[16]	94.96%	-	-	-	7	29
[46]	93.71%	-	-	-	1	6
[10]	97%	96.88	96.63%	96.75%	1	9

Key observations include DenseNet121's robust performance in crop disease detection, the benefits of using larger datasets, and the importance of optimized architecture and training parameters. Future research should explore fine-tuning DenseNet121, data augmentation, and ensemble methods to further enhance crop disease detection accuracy

5. Results and Discussion

This section presents and discusses the performance of all the ML and DL techniques reviewed in this paper.

5.1. Comparative Performance Analysis of ML-Based Techniques

In general, ML has performed admirably in a variety of domains, revolutionizing industries and research fields. As shown in the survey, the performance of ML algorithms can be measured using several criteria, including accuracy, speed, scalability, interpretability, and robustness, which vary based on the specific tasks, the characteristics of the dataset, and the data quality training.

Whereas some algorithms excel at image recognition or natural language processing, others may excel at anomaly detection or time-series forecasting. Finally, ML algorithms have demonstrated impressive performance across a wide range of applications, driving innovation and efficiency across a wide range of industries. Furthermore, ongoing research and development efforts aim to improve the capabilities and performance of these algorithms for future challenges.

The previous sections present the performance of SVM-based, KNN-based, and RF-based techniques; as shown in these sections, all the techniques achieved a classification accuracy ranging from 90% to 100%. Moreover, most of the best-performing techniques achieved a classification accuracy that is above 97%. This shows that most of the models only misclassified less than 3% of the images in the dataset, which is quite remarkable. This also shows that SVM, KNN, and RF are effective ML algorithms that can be used to design crop detection diagnosis systems.

Figure 17 shows the performance of the best ML-based and DL-based techniques reviewed in this study. The KNN model developed by [32] produced the best classification accuracy of 100%. Although the KNN model outperformed all the compared techniques, it may not have good generalization performance compared to the other techniques, as it was trained on small-scale datasets. This shows that building a robust ML model requires the model to be trained on a large-scale dataset with relevant features. Also, the KNN model developed by [32] achieved the second-best result. The authors of [32] developed a hybrid technique using CNN, K-means clustering, DWT, GLCM, and PCA. Histogram equalization and K-means clustering were employed to enhance the quality and segment the leaf images. Moreover, they used DWT, PCA, and GLCM for the extraction of informative regions or sample features. This shows that image preprocessing techniques, feature extraction, and image segmentation can improve the performance of ML and DL models. Constructing a model with very good generalization performance is very important, because industrial players are more interested in models that can generalize well to new diseases and models that can detect a large number of crop diseases.

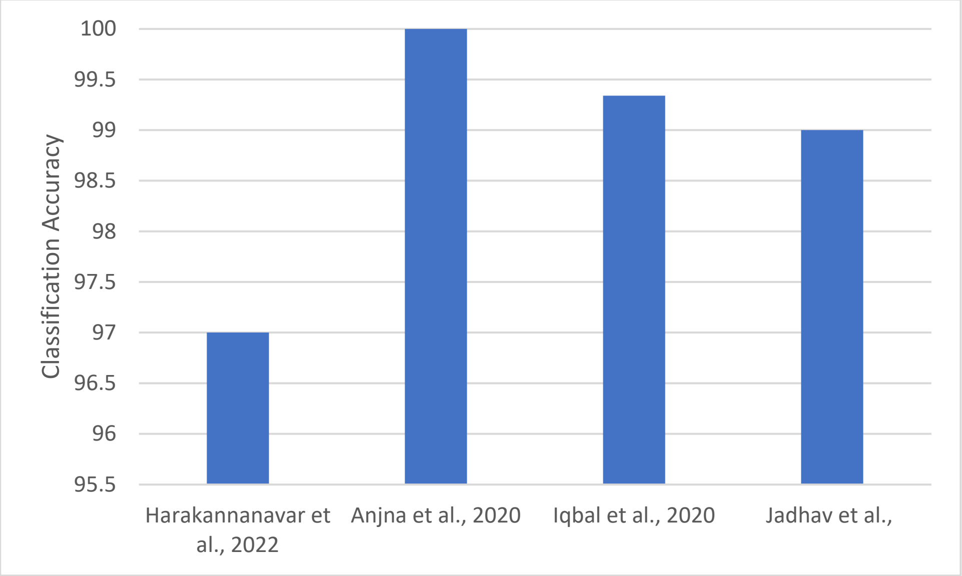

Figure 17. Classification accuracies of the best-performing ML-based crop detection techniques [31,35,36,43].

The best-performing ML algorithms for crop disease diagnosis, such as SVM, KNN, and their hybrid implementations with CNNs, exhibit notable effectiveness due to a combination of advanced feature extraction, segmentation, and classification techniques. These algorithms leverage various image processing steps, like K-means clustering for precise segmentation of infected leaf regions, as well as attention-based feature extraction in models like ViT, which captures positional and chromatic features. In particular, SVM models utilizing Green Chromatic Coordinates with RGB channel analysis show improved classification accuracy by enhancing the model's sensitivity to subtle color variations associated with disease symptoms. Meanwhile, combining CNNs with feature extraction methods like GLCM enables a more detailed representation of texture and structure within diseased areas, enhancing the model's overall accuracy and robustness.

Furthermore, KNN-based approaches benefit from hybrid feature selection, allowing them to integrate a compact yet comprehensive feature set, which reduces computational complexity without compromising accuracy. These models often incorporate dimensionality reduction techniques like PCA alongside spatial descriptors such as discrete wavelet transforms (DWTs) to capture high-level representations that are instrumental for identifying specific disease patterns. This combination of precise segmentation, optimized feature extraction, and feature selection allows KNN and SVM models to consistently achieve high accuracy in disease detection, often exceeding 97% in classification tasks. Such approaches are highly applicable in practical, field-based scenarios, as they not only perform well with limited image data but also exhibit adaptability to varied image acquisition conditions. Figure 18 shows the performance of the techniques that did not produce very good results. As shown in the results, SVM and KNN models did not produce very good results. The models could perform better if they are trained on features derived from feature selection techniques, such as GLCM and LBP.

Moreover, the results show that SVM performs better when trained on a balanced dataset with relevant features, while RF outperforms the other algorithms when trained on an imbalanced dataset. This shows that the choice of ML model to be used should be determined by the size, balance, and quality of the dataset used for training. Furthermore, as shown in the analysis, DL-based techniques produced very good results. The authors of [62] presented a performance analysis of ten DL-based crop detection techniques, and all of them produced a classification accuracy of over 98%. Also, the authors of [18] presented a performance analysis of four DL-based models, and they achieved a classification accuracy of over 92%. This demonstrates the potential for employing deep DL algorithms in creating efficient systems for diagnosing crop diseases in agriculture. DL algorithms possess the capability to acquire hierarchical data representations and extract pertinent features from crop images across various abstraction levels. With this capability, they can understand complex patterns and correlations in the data, making them well suited for agricultural disease detection systems.

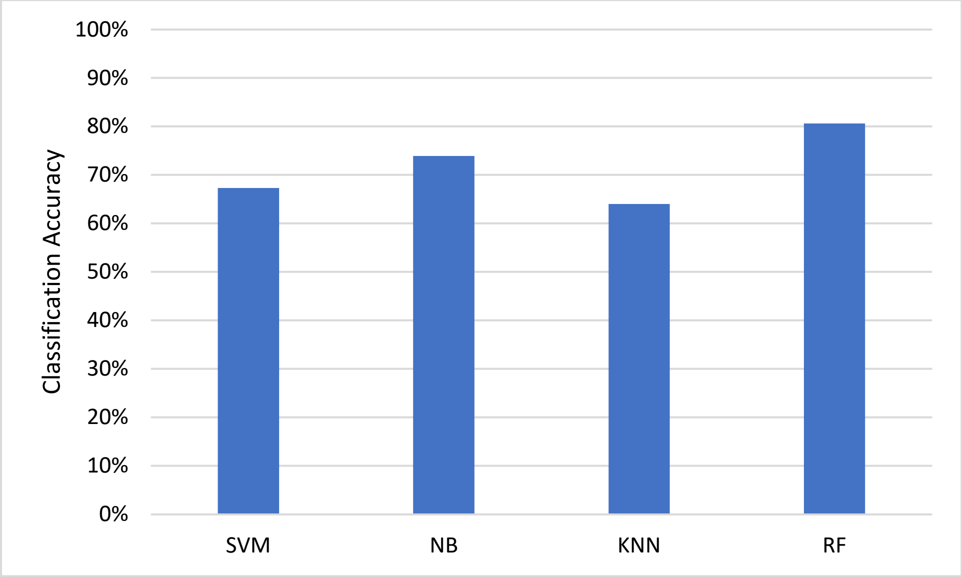

Figure 18. Comparison between the least-performing ML-based crop detection techniques.

5.2. Comparative Performance Analysis of DL-Based Techniques

Figure 19 displays the performance comparison of the top nine DL techniques. As shown, most of the pre-trained models exhibit highly favorable outcomes. This success can be attributed to their prior training on the ImageNet dataset, which comprises more than 1.2 million images. These models have acquired the ability to extract significant features from a vast array of images, recognizing patterns, edges, and shapes. Leveraging these pre-trained features allows the models to generalize effectively when applied to new sets of crop images. Additionally, as illustrated in Figure 17, VGG16 attained the highest classification accuracy of 100%. DenseNet121 and ResNet50 also produced promising results, indicating the models' importance in assisting farmers or agricultural specialists in detecting crop diseases.

The top-performing DL-based crop detection techniques excel due to specific features and optimizations that enhance their accuracy and robustness in handling complex plant image data. For instance, ResNet9 leverages an efficient architecture of four convolutional blocks and two residual blocks, optimized with a Tree-structured Parzen Estimator (TPE) for hyperparameter tuning, which effectively prevents overfitting and captures intricate details in disease patterns. This fine-tuning, supported by a large dataset and data augmentation techniques, allows ResNet9 to generalize well to varied conditions, resulting in high classification accuracy even in scenarios that closely mimic real-world conditions. DenseNet121, another high performer, uses its deep, dense architecture to address vanishing gradient issues, and the large convolutional layers enable it to learn complex features across diverse, real-life crop images. Extensive data augmentation techniques, like rotation, flipping, and zooming, further reinforce the model's adaptability and robustness, preventing overfitting and enhancing its capability to identify disease patterns accurately across different plant species and image acquisition methods.

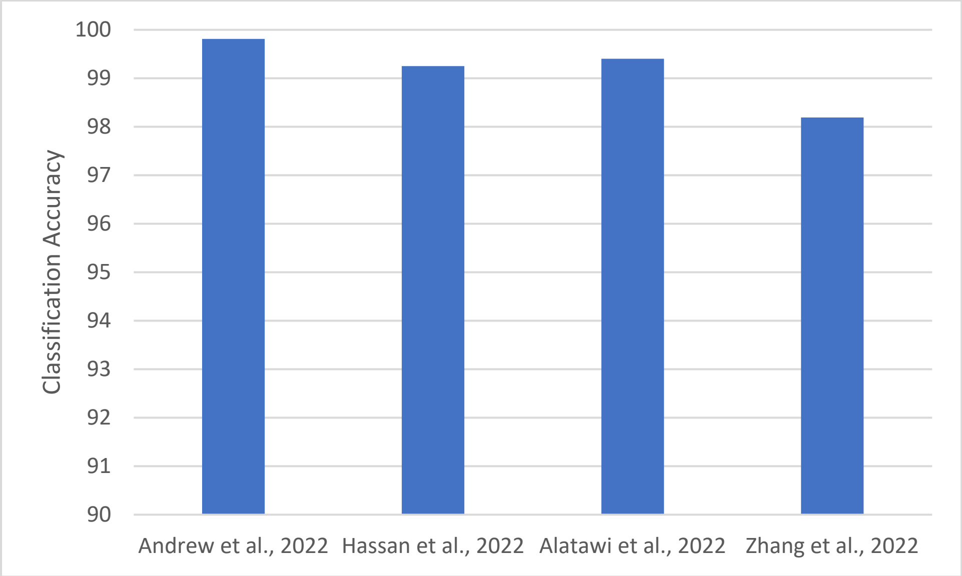

Figure 19. Classification accuracy of the best-performing DL-based techniques. Data sourced from [20,49,58,62].

Models like VGG16 also benefit from feature selection techniques, such as using a three-parent genetic algorithm (3PGA) that extracts the most relevant features from the data, boosting accuracy while reducing computational overhead. The model's success also stems from its use of diverse color spaces (RGB, HSV, YCbCr, and grayscale) to capture luminance and chromatic information, enabling effective disease recognition across varied environmental and lighting conditions. Additionally, CNN models designed with multiple convolutional, pooling, and dropout layers effectively capture and classify disease features with high accuracy while avoiding model overfitting. These CNN architectures, especially with large public datasets, create robust frameworks for plant disease diagnosis that can be applied globally, even on devices like smartphones, facilitating widespread use in real-time crop monitoring and disease management.

5.3. Discussion of Findings

The findings from this review highlight several key observations regarding ML models used in sustainable agriculture. First, the PlantVillage dataset, a widely used resource, presents significant challenges due to its imbalance in image distributions. Notably, the dataset contains a higher number of healthy images compared to diseased ones, as well as an overrepresentation of fungi images, while mites and molds are underrepresented. This imbalance can hinder model generalization, making it inadequate for robust ML models without preprocessing steps. Furthermore, studies demonstrate that feature extraction techniques, such as using ViTs in combination with Green Chromatic Coordinates, significantly improve classification accuracy, achieving up to 99.69% when hybridized with SVM.

The comparative performance analyses of various ML algorithms (ResNet50, VGG16, CNN, KNN, RF, and SVM) for crop disease detection reveal several key observations. The analysis shows that SVM tends to perform better with balanced datasets, while RF exhibits better results on imbalanced datasets. Techniques like KNN and CNN also deliver high accuracy; however, KNN's generalization capabilities may be limited on small-scale datasets. Moreover, the incorporation of preprocessing techniques, such as K-means clustering, DWT, and PCA, as demonstrated by [31], significantly boosts model performance. DL models like VGG16 and DenseNet121 have shown excellent results, indicating their potential to aid in disease detection for sustainable agriculture.

DL architectures (ResNet50, VGG16, and CNN) consistently demonstrate exceptional accuracy (95–99%) across diverse datasets, highlighting their robustness in handling complex image data. In contrast, traditional ML algorithms (KNN, RF, and SVM) show varying performance, with accuracy ranging from 80 to 98%. Notably, dataset size and diversity significantly influence algorithm performance. Optimized architecture and training parameters, transfer learning, and data augmentation techniques emerge as crucial factors in achieving high accuracy. Ensemble methods and fusion of different approaches also show promise. Furthermore, comprehensive evaluations (F1 score, recall, precision) provide valuable insights into algorithm performance and inform optimization strategies. The analyses also underscore the importance of considering the number of crops and diseases in the dataset, as larger datasets tend to yield better performances. These findings suggest that the choice of model and techniques should be based on the specific characteristics of the dataset and the desired application.

6. Summary and Future Research

This section presents a summary of the performance analysis conducted, along with proposed future research directions based on the findings.

6.1. Summary

This study underscores the vital role of crop disease diagnosis in enhancing agricultural sustainability, food security, and farmers' livelihoods worldwide. By evaluating various ML and DL algorithms, the research highlights the strengths and limitations of different methods in disease detection, focusing on accuracy, sensitivity, specificity, and computational efficiency. Key findings reveal that feature selection and preprocessing are crucial for optimizing model performance, with techniques like image segmentation significantly improving results. High-quality, well-labeled datasets are essential for robust model performance, and involving agricultural stakeholders in the development process is vital for long-term accuracy and real-world effectiveness. Notably, the study found that SVM models perform well on balanced datasets, RF models excel on imbalanced datasets, and DL-based techniques (VGG16, DenseNet121, ResNet50) achieve exceptional accuracy rates (up to 100%). Overall, ML and DL models hold promise for improving crop disease management and agricultural sustainability but require careful consideration of dataset quality, model selection, and stakeholder involvement.

6.2. Future Research Directions

The following are some future research directions:

1. Future research may focus on developing more robust ML and DL models by integrating supplementary data modalities such as hyperspectral imaging, drone-based imagery, and environmental sensor data. These modalities provide richer and more diverse information, which can enhance the accuracy and robustness of crop disease diagnosis techniques, especially in cases where image data alone are insufficient for distinguishing between different disease types. Additionally, multi-sensor data fusion techniques could be explored to combine these diverse data sources more effectively.
2. Transfer learning, where pre-trained models are adapted to specific crop disease datasets, remains a promising area for future exploration. Given the high cost and time involved in manually labeling large datasets, transfer learning can significantly reduce the need for large amounts of labeled data while still improving the model's generalization capabilities. Exploring domain adaptation techniques for transfer learning would further enable the model to perform well across different crop types, environmental conditions, and geographical locations.
3. The deployment of crop disease detection models on edge devices such as drones, IoT devices, or mobile phones could pave the way for real-time, on-field applications that work with limited or no internet connectivity. Future research could explore the optimization of models for edge computing by reducing their complexity without sacrificing accuracy. Techniques like model quantization, pruning, and lightweight architectures (e.g., MobileNet) could be used to ensure efficient deployment of these models in resource-constrained environments.

4. Integrating crop disease detection with precision agriculture practices presents a promising avenue for future research. This combination could lead to more efficient use of agricultural inputs such as pesticides and fertilizers, reducing the environmental footprint while improving yield. Research could focus on creating models that not only detect crop diseases but also recommend precise interventions tailored to specific environmental conditions and resource availability. This could be particularly useful for smallholder farmers who rely on minimal resources for crop protection.
5. Given the limitations of imbalanced datasets such as PlantVillage, future work should investigate techniques for balancing datasets either through data augmentation, synthetic data generation, or advanced sampling strategies. Generative Adversarial Networks (GANs) could be employed to generate synthetic images to augment underrepresented categories such as bacterial or viral infections, improving model generalization across various diseases. Future research can also investigate the impact of class imbalance, noise, and high-dimensional data on algorithm performance.
6. Future research can explore hybrid techniques that combine ML algorithms with features extracted from state-of-the-art DL models like ViTs and Capsule Neural Networks. Recent studies have shown that combining SVM with features extracted from ViTs and chromatic indices can yield high classification accuracy. Investigating how these hybrid models perform across larger, more diverse datasets and applying them to other crops could open new avenues for improving both ML and DL model performance in agricultural applications.
7. Another promising direction is the exploration of instance selection and hyperparameter optimization techniques tailored to crop disease detection. Models like KNN, while achieving high accuracy on small datasets, may suffer from poor generalization. Research could focus on developing scalable instance selection techniques that allow models to generalize better across larger, real-world datasets. Additionally, exploring automated hyperparameter tuning methods like Bayesian optimization or evolutionary algorithms can optimize model performance without requiring manual intervention.
8. Future research should also focus on improving image preprocessing and feature extraction techniques. Methods like histogram equalization, K-means clustering, and dimensionality reduction techniques (e.g., PCA) have shown to improve model performance. Researchers could investigate the efficacy of combining multiple preprocessing techniques, such as combining discrete wavelet transforms (DWTs) with texture-based features like GLCM and LBP, to enhance the extraction of informative regions from leaf images.

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