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A Survey on Different Plant Diseases Detection Using Machine Learning Techniques

Sk Mahmudul Hassan [1], Khwairakpam Amitab [2], Michal Jasinski [3,*], Zbigniew Leonowicz [3], Elzbieta Jasinska [4], Tomas Novak [5] and Arnab Kumar Maji [2,*]

[1] Department of Computer Science and Engineering, Gandhi Institute of Technology and Management, Bengaluru 561203, Karnataka, India
[2] Department of Information Technology, North Eastern Hill University, Shillong 793022, Meghalaya, India
[3] Department of Electrical Engineering Fundamentals, Wrocław University of Science and Technology, 50-370 Wrocław, Poland
[4] Department of Operations Research and Business Intelligence, Wrocław University of Science and Technology, 50-370 Wrocław, Poland
[5] Department of General Electrical Engineering, Faculty of Electrical Engineering and Computer Science, VSB—Technical University of Ostrava, 708 33 Ostrava, Czech Republic
* Correspondence: michal.jasinski@pwr.edu.pl (M.J.); akmaji@nehu.ac.in (A.K.M.)

Abstract: Early detection and identification of plant diseases from leaf images using machine learning is an important and challenging research area in the field of agriculture. There is a need for such kinds of research studies in India because agriculture is one of the main sources of income which contributes seventeen percent of the total gross domestic product (GDP). Effective and improved crop products can increase the farmer's profit as well as the economy of the country. In this paper, a comprehensive review of the different research works carried out in the field of plant disease detection using both state-of-art, handcrafted-features- and deep-learning-based techniques are presented. We address the challenges faced in the identification of plant diseases using handcrafted-features-based approaches. The application of deep-learning-based approaches overcomes the challenges faced in handcrafted-features-based approaches. This survey provides the research improvement in the identification of plant diseases from handcrafted-features-based to deep-learning-based models. We report that deep-learning-based approaches achieve significant accuracy rates on a particular dataset, but the performance of the model may be decreased significantly when the system is tested on field image condition or on different datasets. Among the deep learning models, deep learning with an inception layer such as GoogleNet and InceptionV3 have better ability to extract the features and produce higher performance results. We also address some of the challenges that are needed to be solved to identify the plant diseases effectively.

Keywords: plant disease; machine learning; deep learning; transfer learning; image segmentation; feature extraction

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1. Introduction

Agriculture is considered as one of the main sources of the economy in India. Like human beings, plants also suffer from diseases which affect the normal growth of a plant [1]. Diseases can be in any part of the plant including leaf, flower, fruit and root. Due to the complexity and huge number of crops and cultivated plants, the number of diseases is also large [2]. Thus, a pathologist may often fail to diagnose a disease accurately. The precise and timely diagnosis of plant diseases protects crops from quantitative and qualitative loss [3–5]. Most farmers have a lack of knowledge about the effective detection of plant diseases [6]. The identification of plant disease by the naked eye is also time-consuming, requires continuous monitoring and is less accurate in nature. The automated identification of diseases reduces human effort and also provide accurate results [7]. An automated plant disease detection is highly beneficial to farmers, since they know less about plant diseases.

In the current era, many works are ongoing in the domain of machine learning, which can be used effectively in the field of health monitoring, the identification of diseases in plants, etc. This kind of system provides reliable, precise results and reduces the time, cost and manpower for maintaining and ensuring quality in real-time applications. In the field of agriculture, there are a lot of opportunities for researchers to apply machine learning techniques in many aspects, such as the identification of plants, early detection of diseases, pesticide, nutrition requirement, etc. In this paper, we consider the diseases which occur on the leaves of the plant. Several machine learning techniques are discussed in this paper, which were proposed by different researchers based on color, shape, texture features and deep learning models for detecting diseases in plant leaves.

The automated detection of diseases in plants has been studied largely in recent times. The identification of diseases in plants requires accurate and precise information regarding the quantitative measurement of diseases [8]. In [9,10], the authors studied potato and tomato diseases and showed how these crops were affected by viruses. In [11], authors surveyed several papers on the classification of rice diseases and also considered different criteria such as the dataset used, disease classes, preprocessing and segmentation techniques along with the classifier used. Prajapati et al. [12] conducted a survey on the classification of cotton plant diseases using machine learning techniques. Iqbal et al. [13] surveyed the classification of citrus plant diseases using image processing. Kaur et al. [14] conducted a survey on the identification and classification of plant diseases through leaf images. These studies discussed in [11–14] are based on handcrafted features. To classify the diseases using handcrafted features, there is a need for the preprocessing, segmentation and extraction of features from the images, which is laborious and time-consuming.

With the technological advancements, machine-learning-based artificial intelligence has gained a lot of attention in the development of new techniques and models in computer vision [15]. Deep learning models are used in fields such as image recognition [16], voice recognition [17,18] and other complex applications such as self-driving cars, machine interpretation, etc. The application of deep learning in agriculture [19] and particularly in the plant disease detection [20] domain is very much new and limited. In [21], the authors surveyed the identification of plant diseases based on deep learning techniques and essentially focused on the data sources, models and preprocessing techniques used in the proposed CNN models. In [22], the authors reviewed research works on the identification of diseases using several types of deep learning techniques. In these papers, the authors discussed mainly the different CNN models used in plant disease identification. However, the comparative advantages and disadvantages were not clearly highlighted in these works.

In this work, we survey the different methodologies for the identification of plant diseases using both handcrafted-features-based and deep-learning-features-based identifications. We also discuss several segmentation techniques used in the identification of plant diseases along with their advantages and disadvantages. This paper aims to address the drawbacks of the existing works on the identification of diseases based on both handcrafted features and deep learning approaches. We also consider the recent works on the identification of plant diseases which are based on deep learning models. We point out some of the challenging issues in the identification of diseases along with the advantages and disadvantages of using deep learning models.

This paper is organized as follows: Section 2 provides the basic steps in the identification of plant diseases from leaf images. Section 3 represents a comprehensive review on the identification of plant diseases along with their relative advantages and disadvantages. In Section 4, we discuss the different techniques and advantages of deep-learning- over handcrafted-features-based approaches. Different challenges that are faced during the identification of diseases and the areas that need to be focused on are discussed in Section 5. Finally, Section 6, provides the conclusion and future directions in the classification of plant diseases.

2. Basic Steps in Identification of Diseases from Leaf Images

For the effective identification of plant diseases from the leaves of a plant, several steps are required, and among all those, data collection and preprocessing are the first steps. After preprocessing, the next step in the identification of diseases is the extraction of features. Finally, the features are fit into different classifiers for classification.

2.1. Data Collection

The first step in plant disease identification is the collection of image data. Several standard plant diseases datasets are available online such as the PlantVillage dataset [23], Cassava dataset [24,25], Hops dataset [26], Cotton disease dataset [27] and Rice disease dataset [28,29]. The PlantVillage dataset consists of 38 different classes of 14 different plant species (vegetable and fruits) such as apple, blueberry, cherry, corn, grape, orange, peach, pepper, raspberry, potato, soybean, squash, strawberry and tomato. The diseases include apple scab, apple black rot, cedar apple rust, apple healthy, blueberry healthy, cherry healthy, cherry powdery mildew, corn gray leaf spot, corn healthy, corn northern leaf blight, grape black rot, grape black measles, grape healthy, grape leaf blight, orange huanglongbing, peach bacterial spot, peach healthy, pepper/bell bacterial spot, pepper/bell healthy, potato early blight, potato healthy, potato late blight, raspberry healthy, soybean healthy, squash powdery mildew, strawberry healthy, strawberry leaf scorch, tomato bacterial spot, tomato early blight, tomato healthy, tomato late blight, tomato leaf mold, tomato septoria leaf spot, tomato spider mites, tomato target spot, tomato mosaic virus and tomato yellow leaf curl virus. All the images were taken in a laboratory setup condition. The Cassava disease dataset consist of five different classes of diseases and the images are real-time field-captured images. Diseases in the Cassava dataset includes cassava mosaic disease, cassava bacteria blight, cassava brown streak disease, cassava green mite and cassava healthy. The Hops dataset consists of five different classes of diseases with nonuniform background conditions. Diseases include downy, powdery, healthy, nutrient and pest diseases. The Cotton dataset consists of healthy and diseased cotton leaves and plants. The Rice disease dataset consists of four different classes of diseases captured in field conditions. Diseases in the Rice disease dataset are bacterial blight, blast, brown spot and tungro. Some of the researchers built their own diseases dataset in their work. Table 1 shows the available standard datasets of images of plant diseases along with image environment.

2.2. Preprocessing

Preprocessing is one of the most important steps in the identification of plant diseases. Several preprocessing steps exist such as the resizing of the images to fit the model, the removal of noises, color transformation, morphological operations, the segmentation of the disease region, etc.

Different filtering techniques, such as the Wiener filter, median filter [30] and Gaussian filter [31], are used to remove the noises in the disease-affected image. Different color spaces are used in image processing, such as RGB, HSV, CIEL*a*b* [32], YCbCr. To find the region of interest (ROI)/disease area in the leaf images, different segmentation techniques are used such as color thresholding [33,34], the Sobel edge detector [35], Otsu's segmentation [36,37] and K-means clustering [38–40].

2.3. Feature Extraction

Features play an important role in machine learning. Features are used to describe the disease information in mathematical form, which makes the classification easier. For an effective classification, a feature should contain the necessary information that is required to differentiate the classes. Different types of features are used for the identification of diseases, and they can be classified as color features, shape features [31,41], texture features [35,41,42] and deep-learning-based features. Color features define the different color values of the disease region. The area, perimeter, minor/major axis length, eccentricity, etc., are some of the shape features. Texture-based features such as local binary pattern (LBP) [43], gray-level co-occurrence matrix (GLCM) [36], gray-level run-length method (GLRLM), Gabor texture features [32] are used for the identification of diseases. Figure 1 shows some of the features that are used in classification of plant diseases.

Table 1. Details of the datasets used.

Dataset Description	**Image Environment**	**Link**
PlantVillage dataset: 54,304 images of 14 different plant species and 38 different classes including healthy leaf images	Captured in laboratory setup condition	https://github.com/spMohanty/PlantVillage-Dataset (accessed on 15 February 2022)
Rice leaf diseases: 120 images of three different rice diseases	Captured on uniform background	https://archive.ics.uci.edu/ml/datasets/Rice+Leaf+Diseases (accessed on 25 February 2022)
Rice disease dataset: 5477 images of 3 different disease classes and 1 healthy class	Captured on white background	https://www.kaggle.com/shayanriyaz/riceleafs (accessed on 21 February 2022)
Rice disease dataset: 5932 images of 4 different disease classes	Field images	https://data.mendeley.com/datasets/fwcj7stb8r/1 (accessed on 27 February 2022)
Cassava dataset: 24,395 images of 5 different disease classes including healthy leaf class	Field images with complex background	https://www.kaggle.com/srg9000/cassava-plant-disease-merged-20192020 (accessed on 12 May 2022)
Hops disease dataset: 1101 images of 5 different diseases including healthy leaves	Field images with nonuniform background	https://www.kaggle.com/scruggzilla/hops-classification (accessed on 3 March 2022)
Cucumber disease dataset: 695 images of disease-infected leaves	Field images	https://www.kaggle.com/kareem3egm/cucumber-plant-diseases-dataset (accessed on 27 March 2022)
Cotton disease dataset: 2310 images of healthy and diseased cotton leaves and plant	Field images	https://www.kaggle.com/singhakash/cotton-disease-dataset (accessed on 5 March 2022)
Corn disease dataset: 4188 images of four different disease classes including healthy leaves	Laboratory condition	https://www.kaggle.com/smaranjitghose/corn-or-maize-leaf-disease-dataset (accessed on 18 March 2022)
Plant Disease dataset: 125,000 images of 10 different plants species containing 37 different categories of diseases	Laboratory condition and also complex background	https://www.kaggle.com/lavaman151/plantifydr-dataset (accessed on 12 April February 2022)
New Plant Diseases dataset (Augmented): 87,000 images of 38 different classes	Laboratory condition	https://www.kaggle.com/vipoooool/new-plant-diseases-dataset (accessed on 18 April 2022)

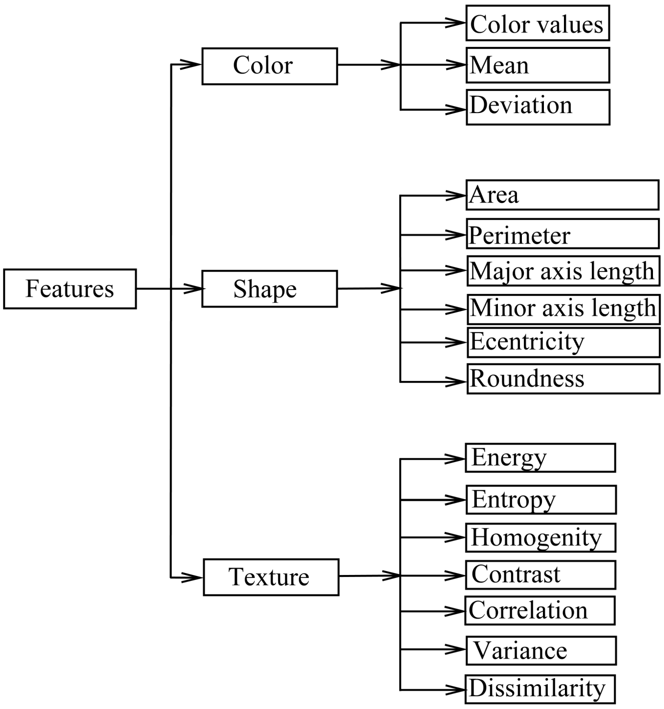

Figure 1. Some of the features used in plant disease detection.

2.4. Classification

Classification is the numerical analysis of various image features, and it organizes the leaf image data into some of the disease categories. Classification is categorized as supervised and unsupervised classification. Some of the commonly used classification techniques are K-nearest neighbor (KNN) [32], support vector machine (SVM) [34,36,44], logistic regression (LR), random forest (RF), decision tree (DT) [37], naive Bayes (NB), artificial neural network (ANN) [43] and probabilistic neural network (PNN) [43].

3. Different Existing Machine Learning Based Techniques for Plant Disease Detection

Numerous works have been conducted to date related to the identification of plant diseases. In this section, we discuss different methodologies that have been proposed by researchers for the detection of different plant diseases. It is found that the disease detection techniques based on machine learning can be classified by color-, shape-, texture-based features and deep learning models. Figure 2 shows the basic steps in the identification of plant diseases.

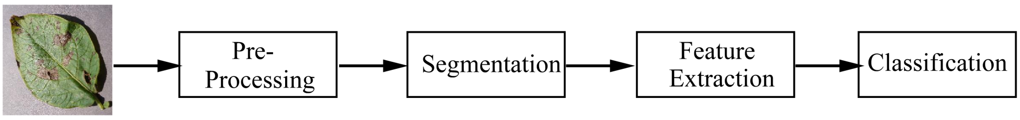

Figure 2. Basic handcrafted-features-based steps for identification.

3.1. Color-Features-Based Disease Detection

Disease detection by extracting color features was performed by Chaudhary et al. [45]. In their approach, they implemented YCbCr-, HSI- and CIE L*a*b*-based color models on a leaf image to extract the color features of a diseased leaf and then compared all these methods. From all of these color models, they chose the "A" component of the CIE L*A*B model for the initial segmentation of the diseased leaf. A median filter was used for preprocessing purpose. Hence, this method was affected by less noise from different sources. Finally, the diseased area of the leaf was segmented by applying Otsu's threshold on the "A" component of the color space .

Singh [46] used a color slicing technique to detect the blast disease of paddy. In their method, firstly they convert the RGB image to HSI and used color slicing to extract the diseased area and neutralize the rest of the portion. They compared their technique with disease boundary detection using the Sobel and Canny methods and obtained an accuracy rate of 96.6%.

Sghair et al. [47] used different color models to identify diseases in plants. Firstly, they transformed the images into different color models, followed by a noise reduction using a median filtering technique and finally segmented the diseased region from the leaf. They used three different color models: YCbCr, HIS and CIELAB. In their approach, they applied Kapur's threshold on the Cr component of the YCbCr model, the H component of the HIS model and the A component of the CIELAB model to segment the diseased spot.

Husin et al. [48] identified chili leaf diseases using different color features. They extracted the yellow, green and cyan color components from the leaves and used color matching techniques to identify the diseased and healthy leaves.

Pugoy et al. [49] identified two different rice diseases (brown spot, leaf scald) using a color analysis of the image. Threshold segmentation was used to segment the abnormalities, followed by a histogram intersection to isolate the segmented region. K-means clustering was used to assign the pixels into different clusters based on R, G and B color values. The classification of disease was done by comparing and matching the color values. Majid et al. [50] used fuzzy entropy to identify four different paddy (rice) diseases. A PNN was used as the classifier, and it obtained an accuracy rate of 91.1%. One of the major issue in their approach was that in the preprocessing step, they needed to crop the diseased region manually before extracting the features.

Shrivastava et al. [51] identified four different rice plant diseases using 172 color features. In their approach, the authors used 13 different color spaces and from each color channel, they extracted different color features such as mean, standard deviation, kurtosis and skewness. Seven different classifiers SVM, DC (discriminant analysis), KNN, NB, DT, RF and LR were used to classify the diseases and compare the performances. Among all the classifiers, SVM gave better a performance accuracy with 94.65%. The main issue in their work was that the images were already preprocessed and had a black uniform background.

The main disadvantage of disease detection using color values is that using a color component is not sufficient to detect all types of diseases. Table 2 summarizes the method with segmentation techniques and features used in the detection of diseases based on color features.

Table 2. Summary of implemented details along with features based on color based method.

Author	Plant/Disease	Segmentation	Feature Extraction	Dataset	Accuracy (%)
Pugoy et al. [49] (2011)	Rice	Thresholding	R, G, B color values	NA	NA
Chaudhary et al. [45] (2012)	Disease-affected area on leaf	Otsu's method	Different color components	NA	NA
Husin et al. [48] (2012)	Chili leaf disease	Color clustering	Yellow, green and cyan components	107 captured images	NA
Majid et al. [50] (2013)	Rice	NA	Fuzzy entropy with 256 gray levels	NA	91.4
Sghair et al. [47] (2017)	NA	Kapur's threshold	NA	NA	NA
Singh et al. [46] (2018)	Blast disease	Thresholding	Different color values H, S, V, R, G, B values	100 captured images	96.6
Shrivastava et al. [51] (2021)	Rice	NA	172 color features	619 captured images	94.6 (SVM)

In this table, NA indicates the information is not available.

3.2. Shape- and Texture-Based Disease Detection

In addition, diseases in plant can be detected by extracting the shape features of leaves. Dey et al. [52] used the number of pixels in the disease-affected area to detect the rot disease in betel leaf. Firstly, they converted the acquired RGB image into the HSV color space. Then, a threshold value was calculated by applying Otsu's method on the "H" component of the HSV color space for segmentation purpose. The segmented binary image consisted of the rotten area with white pixels. They calculated the total number of pixels in this rotten portion to detect the affected disease.

Phadikar et al. [53] used color and shape features for the detection of rice diseases such as leaf brown spot, rice blast, sheath rot, bacterial blight, etc. For segmentation purpose, they used a Fermi energy based technique and genetic algorithm (GA) for the extraction of a diseased leaf's shape features. Fermi energy based region extraction had an advantage over selecting a proper threshold value. For classification purpose, they used a rule generation technique. The advantages of the implemented method included a smaller computational complexity as it did not require a gain calculation of the rules.

Yao et al. [36] used both shape and texture features for detecting diseases in the rice plant. After segmentation, shape features such as area, perimeter, long axis length and width, along with texture features including contrast, uniformity, entropy, inverse difference, linearity and correlation were extracted from the GLCM of each image of a leaf from every orientation angle. For classification, they used an SVM classifier and got an accuracy rate of 97.2%. Though this method was effectively able to identify the diseases, it failed to correctly identify diseases having a similar texture, and thus performance decreased.

The method proposed by Islam et al. [33] aimed to detect and recognize potato diseases (late blight, early blight, healthy leaf). First, they masked out the background as well as the green region of the image using thresholding, by analyzing the color and luminosity component of a different region in L*a*b* color spaces. Then, they extracted the ROI which contained the disease-affected region. They used the GLCM to extract texture features such as correlation, contrast, homogeneity and energy. The mean, entropy, standard deviation, skew and energy were calculated from the histograms of the color planes. A multiclass SVM was used for the classification of potato diseases from the PlantVillage dataset. In the segmentation, it was difficult to set the threshold value in their method and the number of training image was also small. One of the disadvantages included that the images in the dataset were captured on a uniform background.

Camargo et al. [54] developed a disease segmentation algorithm to identify the diseased area by using the distribution of intensities in the histogram and finding the threshold according to the position in the histogram. Furthermore, they [31] identified the diseases in cotton plants using an SVM classifier. A set of features such as shape, color, texture and fractional dimension was extracted from the diseased area, and they obtained an accuracy rate of 93.1%. One of the disadvantages was that the extraction of features was time-consuming and identifying the proper set of features from a set of 54 features was challenging. The number of images in the dataset was small.

In [55,56], the authors identified different cotton plant diseases using color, shape and texture features. Chaudhari et al. [55] used K-means clustering for the segmentation and a wavelet transform for the feature extraction. To reduce the number of features and speed up the computation, a PCA was used as a feature reduction technique. A backpropagation neural network was used for the classification, and it obtained an accuracy rate of 97%. The advantage of using a wavelet transform was that it worked well on low-frequency components and also in high-frequency transients. Bhimte et al. [56] identified three different types of cotton plant diseases using image processing. A K-means clustering technique was used to segment the images into three clusters as background, foreground and diseased regions. Different color, shape and texture features were extracted from the segmented images and an SVM was used to classify the images and it achieved an accuracy rate of 98.46%. The number of images used to train and test the model was small. The selection of a proper set of features by the classifier was an important issue in the identification.

Wang et al. [57] identified two different grape diseases (grape downy mildew and grape powdery mildew) and two different wheat diseases (wheat stripe rust and wheat leaf rust) using a backpropagation (BP) network. In their approach, K-means clustering algorithm was used to segment the images and they extracted 21 color features, 4 shape features and 25 texture features from the segmented image, which were used for classification. One of the major issues in their paper was that the images were captured in a fixed condition. Seven different groups of feature combinations were used for the identification and therefore, finding the proper set of features combinations to get the optimal result was an important challenge.

Two different diseases in grapes, namely, downy and powdery mildew diseases, were identified by Padol et al. [41]. In that paper, firstly, the diseased region was extracted using K-means clustering techniques with three clusters. After the segmentation, nine color features and nine texture features were extracted from each cluster and an SVM was used for the classification. To train and test the model, they used 137 captured grape leaf images and achieved an accuracy rate of 88.89%. Later on, the authors [42] extended their work identifying the same diseases using both SVM and ANN classifiers. In order to improve the classification, a fusion classification was performed, which created an ensemble of classifiers from the SVM and ANN and reported a recognition accuracy of 100% for both downy and powdery mildew diseases. The feature set used for the classification consisted of nine color and nine texture features, as used in [41]. One of the issues was that only two different disease categories were considered, and the dataset used was too small. The extraction of features was time-consuming as the system used 54 different features for the identification.

Es-saady et al. [58] identified three pest insects damages (leaf miners, thrips and Tuta absoluta) and three pathogen symptoms (early blight, late blight and powdery mildew) using a serial combination of SVM classifiers. In that paper, the authors used a K-means clustering technique for segmenting the diseased area. From the segmented image, they extracted 18 color, 30 texture and 11 shape features. In their system, they used two SVM classifiers where the first SVM took the color features and the second SVM took the texture and shape features to classify the diseases. To train and test the system, they used 284 images captured on a uniform background and achieved an accuracy rate of 87.8%. Issues regarding their model were that the images were captured on a uniform background and the dataset size was very small.

In [59,60], the authors used a genetic algorithm (GA) to segment the diseased area from the leaf image. They showed that the GA had advantages over a simple thresholding-based segmentation or K-means clustering segmentation technique as the GA did not require user input or the number of clusters at the time of segmentation. In [60], the authors identified five different plant diseases using the minimum distance criterion (MDC) and an SVM classifier. Firstly, the classification was achieved using the MDC with a K-Mean clustering and they obtained an accuracy rate of 86.54%. The performance accuracy improved to 93.63% using the GA. Secondly, the classification was done using an SVM where the performance improved to 95.71%.

Two tomato diseases (TSWV, TYLCV) were identified in [61] with the help of some geometric and histogram-based features; the authors classified a diseased image using an SVM classifier with different kernel values. The dataset used was 200 captured images of both diseased and healthy leaves and they obtained an accuracy rate of 90%. One of the disadvantages in their approach was that the images containing more than one leaves needed to be cropped manually to extract a single leaf image, which made the process complex. In [37], Sarbol et al. identified six different types of tomato diseases from images of the leaf and the stem. Using Otsu's segmentation technique, they extracted the diseased area and different color, shape and texture features. They classified the leaves using a decision tree classifier and obtained a classification accuracy rate of 97.3%.

Six different tomato diseases were identified by Hlaing et al. [30] using model-based statistical features. From the preprocessed images, they extracted the SHIFT features and to reduce the computational time and complexity, they reduced the dimensions using a generalized extreme value (GEV) distribution. They used a 10-fold cross-validation to analyze the performance accuracy and reported an accuracy rate of 84.7% using a quadratic SVM. Furthermore, their proposed method took 56.832 s to train the classifier and achieved 12,000 predictions per seconds. The authors extended their work from [30] and identified the diseases using SHIFT features with a Johnson SB distribution as a dimension reduction technique [62]. They achieved a better performance accuracy of 85.1% and it took 33.889 s to train the classifier. In both papers, they used tomato disease images from the PlantVillage dataset, where the images were captured in a laboratory setup condition. Due to the loss of information for the classification, they did not perform a segmentation technique. One more advantage was that the implemented model was robust to various resolutions.

Later on, Titan et al. [63] developed an SVM-based multiple-classifier system (MCS) to improve the accuracy of classification, and they used color, shape and texture features for the identification of leaf diseases in wheat plant. They got an accuracy rate of 96.1%. The selection of appropriate features among all extracted features which gave the best classification accuracy was an important challenge in their approach.

Chouhan et al. [1] identified and classified plant diseases using bacterial-foraging-optimization-based radial basis function neural network (BRBFNN). They used the region-growing algorithm for searching and grouping the seeded region having common attributes which were used for the feature extraction. They worked on some fungal diseases such as common rust, cedar apple rust, late blight, leaf curl, leaf spot and early blight. The advantage of using region growing was the grouping of seed points having similar attributes, which increased the efficiency of the network. Bacterial foraging optimization assigned the optimal weight to the radial basis network, which made the network faster and also increased the accuracy of the network. The main issues in their approach were that it worked only for fungal diseases and it could not be extrapolated to identify other diseases in plants.

Kaur et al. [44] used a color feature, texture feature and a combination of color and texture features for detecting several diseases of soybeans, such as downy mildew, frog eye, septoria leaf blight, etc. They used three clustering techniques for training. In the first cluster, they found whether the leaf was affected by disease or healthy by calculating the number of connecting components. If a more-connected component was there, then its four neighbors corresponded to unhealthy leaf. They used an SVM classifier for classification. Training the network with real-time images was an important area that needed to be done.

Masazhar et al. [64] identified the palm oil leaf disease by extracting 13 texture features from the GLCM, and a multiclass SVM was used for classification purpose. First, they converted the RGB image to the L*a*b* color space and for segmentation purpose, they used the K-means clustering algorithm and evaluated the features from the segmented image. The main issues in their method were that it was limited to palm oil leaf disease only and the dataset used was very small.

Chuanlei et al. [34] used three different types of features such as shape, color, and texture features in the detection of diseases in apple leaf. Firstly, they removed the background using a histogram, and region growing was applied to separate the diseased leaf spots from the leaf image. They extracted 38 different features and reduced the dimensionality of the feature space by selecting the most valuable features from the combination of a GA and a correlation-based feature selection (CFS). Diseases were classified using an SVM classifier and they obtained an accuracy rate above 94%. One of the advantages of the model was that the dimensionality reduction reduced the time complexity of the model.

Pujari et al. [43] detected different fungal diseases that occur in different crops such as fruit, vegetables and commercial plants. For each category, they used different segmentation techniques to identify the diseased area, extract different features and also to identify the diseases. For fruit crops, they used K-means clustering, for vegetables, they used Chan–Vese and for commercial crops, they used a GrabCut segmentation technique. In the case of fruit crops, they used the GLCM and GLRLM for feature extraction. For classification, they used a nearest neighbor classifier and obtained an accuracy rate of 91.3%. For the identification of diseases in vegetable crops, they extracted LBP features from the disease-affected leaves and used an ANN for the classification; they obtained 95.1% accuracy. In their method, performance decreased in the case of a high variability among the diseases.

Zhang et al. [65] designed an automatic system to identify and classify the cucumber leaf diseases. Firstly, a superpixel operation was performed to divide the images into several compact regions. Secondly, logarithmic-frequency pyramid histogram of orientation gradients (PHOG) were extracted as features from the segmented lesion image, which was obtained using an expectation maximization (EM) segmentation algorithm. They achieved an accuracy rate of 91.48% using SVM classifier. Later on [66], the authors extended their work to identify the diseases through the Internet of things (IoT). In that work, the authors combined the architecture of the superpixel clustering and k-means clustering algorithms to segment the diseased regions. PHOG-based image descriptors were used, and they reported an accuracy rate of 92.15%. The running time of the implemented model was less, since the original image was divided into many small compact regions using superpixels and since the number of extracted features were reduced using PCA. Zhang et al. [67] proposed another work to segment the diseased region from the image using superpixels and EM techniques.

Dandawate et al. [68] identified soybean plant diseases from mobile captured images. In their paper, a color- and cluster-based segmentation and extracted SHIFT features were used. They recorded an accuracy rate of 93.79% using an SVM classifier. Some of the identification challenges such as background clutter, illumination, shadow, scale and orientation were addressed. One of the issues in their paper was that they did not consider individual disease classes. They considered only two classes, healthy and diseased.

Prajapati et al. [69] identified three different rice plant diseases using color, shape and texture features. Before extracting the features, they used different background removal and segmentation techniques and for the classification they used an SVM and achieved an accuracy rate of 83.80% and 88.57% using 5- and 10-fold cross-validations, respectively. Three different segmentation techniques were used, namely, Otsu's segmentation, LAB-color-space-based K-means clustering, and HSV-color-space-based K-means clustering. Among the used techniques, the HSV-color-space-based K-means clustering performed better. To evaluate the model performance, they extracted 88 features and built three different models with different feature combinations.

Prasad et al. [32] proposed a novel approach to identify the plant diseases using mobile devices. They used CIE's L*a*b*-color-based unsupervised segmentation technique. A Gabor wavelet transform (GWT) and the GLCM were used to represent the image mathematically and they achieved a maximum accuracy of 96.3% using a KNN classifier. The issues regarding their paper were that they considered only uniform background images. Segmenting the leaf images captured in a complex background with different lighting conditions may be a challenging issue for their method. The feature vector used was very dense and the computation cost was high.

Singh et al. [60] identified the diseases in five steps as follows. First, they took the input image, preprocessed the image followed by masking the green pixel, then segmented the diseased area using GA; finally, they computed the feature using the co-occurrence matrix and classified using an SVM classifier. We summarize the shape- and texture-based methods as follows:

- Before the extraction of features, a lot of preprocessing is required, which makes the model complex.
- Segmenting the diseased region from the images with a background object is challenging.
- The extraction of features and selecting the proper set of feature set giving the optimal result is an important issue.
- The dataset used in the majority of the paper is small and only a few disease categories is considered.
- The extraction of features in a large dataset is time-consuming as well as a laborious task.

Table 3 summarize the different segmentation techniques that were used to segment the diseased region along with their advantages and disadvantages. Table 4 summarizes the detection of diseases in plants using shape- and texture-based features with the preprocessing techniques, classifier and dataset used.

Table 3. Summary of different image segmentation techniques.

Segmentation	Type	Complexity	Advantages	Disadvantages
Color thresholding	Thresholding	Medium	Simple and powerful technique, easy to implement	Difficult to set the threshold value, more sensitive to noise
K-means clustering	Clustering	Low	Suitable for a large number of datasets, computation is faster, simple	Need to mention the clusters (K) at the beginning of the algorithm, difficult to choose the number of clusters
Sobel edge detection	Thresholding	Low	Simple and can detect the edges, efficient for high contrast disease images	For multiple edges, it does not give good result, image boundaries have to be very smooth
Otsu's segmentation	Thresholding	High	For two-class problem such as foreground and background this method works well	It considers only two classes in the histogram, does not work well with variable illumination
Genetic algorithm based	Stochastic	High	It supports multiobjective optimization, works well on a discrete problem	Time-consuming, designing an objective function is difficult
Fermi energy based	Thresholding	Low	Separates the infected and uninfected pixel accurately, nonuniform illumination images perform better	Calculating the energy value at each pixel position is complex

Table 4. Summary of implemented methods based on shape and texture.

Author	Preprocessing	Features	Classifier	Dataset	Accuracy (%)
Qing et al. [36] (2009)	Resizing, Otsu's segmentation method, fill the hole	Area, perimeter, GLCM, texture features	SVM	216 captured images	97.2
Camargo et al. [31] (2009)	Color transformation, Gaussian filter, thresholding-based segmentation	Color features, shape features, texture features	SVM	117 captured images	93.1
Anthonys et al. [35] (2009)	Thresholding, Sobel Edge detection	Color differences, area, roundness, shape complexity, length and concavity, longer axis, shorter axis	Membership function (MF)	50 captured images	70
Bashish et al. [38] (2010)	Color transformation, K-Means clustering-based segmentation	Angular moment, mean intensity level variation, correlation, contrast, entropy, sum and difference of entropies	ANN	192 captured images	93 (precision)
Tian et al. [63] (2011)	Thresholding-based segmentation	Color features, shape features, texture features	NA	200 captured images	95.16
Arivazhagan et al. [70] (2013)	Color transformation, masking pixel, thresholding	GLCM texture features	MDC SVM	500 captured images	94
Phadikar et al. [53] (2013)	Fermy energy based segmentation	Color features, shape features position	Rule mining	500 captured images	94.21
Chaudhari et. al [55] (2014)	Resizing, K-means-clustering-based segmentation	avelet transform	BP	NA	97
Mokhtar et al. [61] (2015)	Resizing, K-means-clustering-based segmentation	Geometric features, histogram-based features	SVM	200 captured images	90 (SVM) 91.5 (quadratic kernel)
Dandawate et al. [68] (2015)	Resizing, color transformation, color-based cluster-based segmentation	SHIFT features	SVM	120 captured images	93.79
Pujari et al. [43] (2015)	K-means clustering for fruit, Chan–Vese for vegetable, GrabCut for commercial crops	GLCM, GLRLM, local binary pattern, discrete wavelet transform	SVM ANN PNN	Not mentioned	Fruit 98.08 (block wise features), vegetable 84.11 (ANN) 91.54 (Neuro KNN), commercial crop 83.17 (Mahalanobis distance) 86.48 (PNN)
Singh et al. [39] (2015)	Filtering, contrast enhancement, K-means-clustering-based segmentation	Entropy, standard deviation	SVM	IRRI database	82
Anand et al. [40] (2016)	Histogram equalization, resizing, color transformation, K-means-clustering-based segmentation	GLCM, texture features	ANN	NA	NA
Prasad et al. [32] (2016)	Color space transform, noise removal, image normalization, CIE L*a*b*-color-based segmentation	Gabor wavelet transform (GWT) and GLCM	KNN	NA	93
Es-saady et al. [58] (2016)	Resizing, filtering K-means-clustering-based segmentation	Color features, GLCM-based texture features, shape features	two SVM	284 captured images	87.80
Padol et al. [41] (2016)	Resizing, Gaussian filtering, K-means-clustering-based segmentation	Shape features, color features, texture features	SVM	137 captured images	88.89

Table 4. *Cont.*

Author	Preprocessing	Features	Classifier	Dataset	Accuracy (%)
Padol et al. [42] (2016)	Resizing, Gaussian filtering, K-means-clustering-based segmentation	Shape features, color features, texture features	SVM ANN	137 captured images	88.33 (SVM) 89.17 (ANN) 100 (fusion)
Sabrol et al. [37] (2016)	Otsu's segmentation techniques	Shape features, color features, texture features	Decision tree	383 captured images	97.3
Hlaing et al. [30] (2017)	Color-thresholding-based segmentation, median filtering, region hole filling	Color statistics features, SHIFT-based texture features with GEV dimension reduction technique	SVM	3474 images from PlantVillage dataset	84.7
Mishra et al. (2017)	Remove distortion, genetic algorithm-based segmentation	Texture features	MDC SVM	NA	93.63 (MDC) 95.71 (SVM)
Monzurul et al. [33] (2017)	Masking, color threshold-based segmentation	GLCM, histogram color features	SVM	300 PlantVillage potato	95
Prajapati et al. [69] (2017)	Cropping, resizing, image conversion, masking, K-means-clustering-based segmentation	Color features, shape features, texture features	SVM	120 captured images	88.57
Zhang et al. [65] (2017)	Superpixel, expectation maximization (EM)	Pyramid of histograms of orientation gradients (PHOG)	SVM	300 captured images	51.83
Chuanlei et al. [34] (2017)	Color transformation, threshold-based background removal, region-growing segmentation algorithm	Color features, shape features, texture features	SVM	90 captured images	90
Zhang et al. [66] (2018)	Superpixel clustering, K-means clustering algorithm to segment	PHOG	SVM	150 apple, 150 cucumber captured images	85.64 (apple) 87.55 (cucumber)
Bhimte et.al [56] (2018)	Cropping, resizing, color transform, noise removal, K-means-clustering-based segmentation	GLCM	SVM	130 captured images	98.46
Hlaing et al. [62] (2018)	Color-thresholding-based segmentation, median filtering, region hole filling	Color statistics features, SHIFT-based texture features with Johnson SB distribution for dimension reduction	SVM	3535 images from PlantVillage dataset	85.1
Kaur et al. [44] (2018)	Resize, color space conversion, K-means clustering	Color features, texture features	SVM	4775 PlantVillage soybean	90

In this table NA denotes the information is not available. The term accuracy defines the ratio of the number of correct predictions to the total number of images used in the dataset.

3.3. Deep-Learning-Based Identification of Diseases

Recently, deep learning (DL) has achieved an exponential growth in the field of computer vision tasks such as object detection, pattern recognition, classification and biometry. DL models exhibit outstanding performance in image recognition task such as the ImageNet challenge. This image recognition idea extended to the agricultural field plant identification [71], disease detection [2,72–74], pest recognition [75,76], fruit identification [77,78] and weed detection [79]. In DL, there is no need for segmentation and feature extraction as a DL model has the ability to learn the features automatically from the input images.

Kawasaki et al. [80] identified two different types of cucumber diseases, i.e., melon yellow spot virus (MYSV) and zucchini yellow mosaic virus (ZYMV) using a CNN. In their paper, they used a rotation of images to increase the data size and showed that increasing the number of images increased the performance. The accuracy obtained with the proposed DL model was 94.9%. In [81], the authors extended their previous work to identify seven different types of cucumber diseases using two CNN architectures with a large dataset. In the dataset, they considered the a variety of images aspects such as the distance, angle, background, and a nonuniform lighting condition. Three data augmentation techniques, namely, shifting, rotation and image mirroring were used to increase the size of the dataset. The CNN configuration was based on VGG Net [82] and the Caffe framework [83]. The performance of CNN-1 decreased more in the case of a bad image condition than that of CNN-2 as the CNN-2 model was trained with both good and bad condition images. They attained an accuracy rate of 82.3% with fourfold cross-validation.

Sladojevic et al. [84] used pretrained fine-tuned CaffeNet model for the identification of 13 different plant diseases. To train and evaluate the performance of the model, they used 4483 internet-downloaded images and a data augmentation technique to increase the data size. A 10-fold cross-validation technique was used to evaluate the performance accuracy of model and they achieved an accuracy rate of 96.3%. Pretrained AlexNet and VGG16 net were used by Rangarajan et al. [85] to identify six different tomato leaf diseases. The classification accuracy obtained was 97.29% for VGG16 net and 97.49% for the AlexNet architecture.

Mohanty et al. [72] used two eminent established architecture of CNN, AlexNet and GoogLeNet, in the classification of 26 different diseases in 14 crop species using 54,306 images. To keep track of model overfitting, they split the dataset into different sets of training and testing ratios. Three different image data (color, grayscale, segmented) were used and the highest training accuracy of 99.35% was achieved on RGB images using GoogLeNet. Several issues existed in their method, including that the entire process was exclusively done in laboratory setup images, not in real-time images from cultivation fields. Performance decreased to 31% when the model was tested on images from different sources. One more limitation was that these models were based on the classification of front-facing single leaves on homogeneous background images.

Multiple CNN architectures were used by Nachtigall et al. [86] to identify six different apple leaf diseases. The best result were obtained using the AlexNet [87] architecture and an accuracy rate of 97.3% was achieved. In order to compare the CNN results, they used a multilayer perceptron (MLP) as an MLP can achieve a high recognition accuracy in image classification [88]. The Caffe [83] and DIGITS tools were used to design the CNN architecture. A LeNet [89] based deep CNN architecture was used by Amara et al. [90] to identify banana leaf diseases. Their proposed approach was effective under challenging conditions such as the illumination, a complex background, different resolutions, sizes, poses, and orientations of real scene images. To evaluate the performance, they used both color and grayscale images and recorded an accuracy rate of 98.61% and 94.44%, respectively.

The fusion of shape- and texture-based features such as Hu's moments [91], Zernike moments [92] with a CNN was used by [93] to identify olive leaf diseases. After 300 epochs, the authors [93] reported an accuracy rate of 98.61%. A fine-tuned AlexNet architecture was used by Atole et al. [94] to identify rice plant diseases and they achieved an accuracy rate of 91.23%.

Ferentinos et al. [2] used five different deep CNN architectures (AlexNet, AlexNetOWTBn, GoogLeNet, Overfeat and VGG) for the identification of plant diseases through leaf images of healthy and diseased leaves. The dataset used consisted of 58 different classes of images and they achieved the highest accuracy rate of 99.53% using the VGG [82] architecture. The dataset used was the largest available plant disease dataset, which included partial shading on leaves, images with different objects such as hands, finger, shoes, etc. The average time required to train these models was much more. One of the issues related to their method was the expansion of the existing database to incorporate a wider variety of plant species and diseases. Another issue was that the testing dataset used for the classification of the models was part of the same database that constituted the training set.

Five different eggplant diseases were identified by Rangarajan et al. [95] using a pretrained VGG16 network. To evaluate the result, they also used three different color spaces of the images, namely, HSV, YCbCr and grayscale. They obtained an accuracy rate of 99.4% with the RGB and YCbCr images. Images used to train and test the network were captured by mobile devices in both laboratory and field conditions. Six different pretrained network were used in [96] to identify 10 categories of several crop (eggplant, beans, lime, ladies finger) diseases. Among all the models, VGG16 gave the highest accuracy of 90%. We summarize the above papers as follows:

- The use of a pretrained deep learning model eliminates the preprocessing and feature extraction in the identification of disease.
- A fine-tuned and transfer-learning approach where the model is pretrained with a large dataset performs better than learning from scratch.
- RGB images give better performance accuracies than other formats of images.
- The number of parameters used in LeNet, AlexNet, VGG and GoogLeNet is large and hence the computation takes longer.
- The required training time is much longer in these models and requires high-power GPUs to train the model.

Lee et al. [97] used the VGG16, InceptionV3 and GoogLeNetBN architectures to identify diseases in plants. In their paper, they examined and compared the performances of these models based on a transfer-learning approach. They proved that disease detection using a pretrained model reduced the overfitting impact. Picon et al. [98] extended the work from [99] for the identification of three different wheat diseases based on mobile devices. A modified ResNet50 architecture was used in that paper. Firstly, a 7×7 convolution layer of ResNet50 was replaced by two consecutive 3×3 convolution layers. Secondly, a dense layer with a softmax activation function was replaced by a sigmoid function, which was able to detect multiple diseases on the same leaf. They obtained an improved accuracy rate of 87% using a superpixel segmentation approach and images containing the artificial background used in training.

Fuentes et al. [73] designed a practical and applicable solution in the real-time detection of tomato diseases and pests recognition using a robust deep-learning-based method. Furthermore, their model was able to deal with some of the complexities such as illumination conditions, object dimension and background variation. In their approach, they used a meta-architecture of CNNs, such as Faster R-CNN, SSD and R-FCN models; for the extraction of features, VGG16 [82], ResNet-50 [100], ResNet-101 models were used. A smooth L1 loss function was also used. They obtained an accuracy rate of 83%. In their model, they also included the stage of a disease on the leaves and the position where it occurred.

Ramcharan et al. [24] used an image-based DL method for the identification of diseases in cassava plants. They used a transfer-learning approach on the InceptionV3 model to train the network for the identification of three diseases and two pest damages. They used two different datasets, namely, the original cassava dataset consisting of multiple leaves on a single image and the leaflet cassava dataset consisting of single leaf images. There was an improvement in the accuracy for the leaflet dataset in comparison with the original cassava dataset. To analyze the performance, they used a softmax layer, SVM and KNN classifiers and obtained the maximum accuracy of 98% using an SVM classifier.

Ahmad et al. [101] identified four different tomato diseases using pretrained deep learning models, namely, VGG16, VGG19, ResNet and InceptionV3. They also fine-tuned the network to obtain the optimal result. The authors used two datasets, one of images in laboratory conditions, and another of self-collected field images; They observed that the laboratory images performed better. Among the DL models, InceptionV3 gave the best performance accuracy of 99.60% and 93.70% on laboratory and field images, respectively, after fine-tuning the parameters.

Oyewola et al. [25] identified five different cassava plant diseases using a plain convolution neural network (PCNN) and a deep residual network (DRNN) and showed that the DRNN outperformed the PCNN by a margin of 9.25%. A MobileNet CNN-based model was used by Elhassouny et al. [102] to identify the 10 most common types of tomato diseases and they obtained an accuracy rate of 90.3%.

Li et al. [103] identified ginkgo leaf diseases using VGG16 and InceptionV3 with images under both laboratory and field conditions. Between the two models, InceptionV3 gave better a performance accuracy on field images and VGG16 gave a better performance accuracy on laboratory images. The InceptionResNetV2 architecture was used by Yong Ai et al. [104] to identify different crop diseases and insect pests in crops. They built an Internet of things (IoT) platform in remote areas, such as mountains, and identified diseases and insect pests with an accuracy rate of 86.1%. We summarize the above the papers as follows:

- Extracting multiple features from different filter sizes in parallel improves the model performance.
- A CNN with residual connection can train a large model without increasing the error rate.
- A residual connection handles the vanishing gradient issue using identity mapping.

A pipeline CNN architecture was used by DeChant et al. [105] to identify maize plant diseases. Three layers of CNNs were trained: firstly, several CNNs were trained to classify small regions of images that contains the lesions; secondly, the predictions of the first layer were combined into a separate heat map; and finally, they were fed into the CNN layer to classify whether it was affected by the disease or not. A Faster R-CNN was used by Ozguven et al. [106] to identify sugar beet diseases and a correct classification rate of 95.48% was obtained.

Oppenheim et al. [107] detected four different potato diseases using a deep CNN. In that paper, the database of images used contained potatoes of different shapes and sizes and the images were labeled manually by experts. Several dropout layers were used to deal with the problem of overfitting, and the dataset was split into different training and testing ratios; the best accuracy of 96% was achieved with a 90%–10% training and testing ratio.

A nine-layer deep convolution neural network was used by Geetharamani et al. [108] to identify different plant diseases. In that paper, they showed that increasing the size of the dataset using data augmentation techniques such as image flipping, noise injection, gamma correction, color augmentation, scaling and rotation increased the validation accuracy from 91.43% to 96.46%. They also compared their results with traditional machine-learning-based approaches and showed that a deep-learning-based approach outperformed traditional approaches.

Wang et al. [109] used a deep convolution network fine-tuned by transfer learning for the detection of apple leaf diseases. They compared two architectures, namely, building a shallow network from scratch and transfer learning by fine-tuning. The shallow network consisted of some convolution layer with some filters, and there were two fully connected layers and one softmax layer to predict the output. Transfer learning is a useful approach to build powerful classification network using few data, by fine-tuning the parameters of a network pretrained on a large dataset, such as ImageNet [110].

The CNN-based architectures GoogLeNet and Cifar10 were used in [111] to identify nine different types of maize leaf diseases. In that paper, the authors used data augmentation techniques to increase the data size and improved some hyperparameters by changing the pooling combinations, adding dropout operations and rectified linear unit functions. In the GoogLeNet model, the average identification accuracy obtained was 98.9%, and the Cifar10 [112] model achieved an average accuracy of 98.8%.

A novel deep convolution network based on the AlexNet and GoogLeNet architectures was used by Liu et al. [113] to identify four different apple leaf diseases using leaf images. In their model, they replaced the fully connected layer of AlexNet by a convolution layer and an inception layer, which reduced the model parameter by a large number with a higher accuracy rate of 97.62%. The optimizer used in their paper was Nesterov's accelerated gradient (NAG).

Later on Ramcharan et al. [114] extended the work in [24] into a mobile-based cassava disease detection. They utilized the single-shot multibox (SSD) model with the MobileNet detector and classifier, which was pretrained on the COCO dataset [115]. To evaluate the performance, they used both image and video files of diseased leaf images. In total, 2415 images of six different diseases were used to train the CNN network and they obtained an accuracy of 80.6% and 70.4% in the case of image and video, respectively.

Toda et al. [116] designed a deep CNN based on the InceptionV3 [117] architecture. In their approach, they used attention map and identified and removed several layers which were not contributing to the identification. The removal of the layers reduced the number of parameters by 75% without affecting the classification accuracy and a top accuracy of 97.1% was achieved.

Lu et al. [118] proposed a novel deep CNN method inspired from LeNet and AlexNet to identify 10 different rice diseases. To achieve the optimal result, different convolution filter sizes and pooling operations were carried out. The maximum accuracy obtained using stochastic pooling was 95.48% and 93.29% using a 16 × 16 convolutional filter. Stochastic pooling has the advantages of max-pooling and also prevents the model from overfitting. One of the advantages of these models is that their computation time decreases as the number of layer used is less.

A SqueezeNet [119] architecture was used by Durmus et al. [120] to identify tomato leaf diseases. They used a robot to detect the diseases on the plants autonomously in the field or in the greenhouse and obtained an accuracy rate of 94.3% using the SqueezeNet architecture. They compared their performance with that of the AlexNet architecture, whose size is 227.6 MB, while the size of SqueezeNet is 2.9 MB.

A modified Cifar10 quick CNN model was used by Gensheng et al. [121] to identify four different tea leaf diseases. In their paper, the standard convolution was replaced by a depthwise separable convolution, which reduced the number of parameters. They also compared their results with traditional machine-learning-based techniques and some classical CNN models such as LeNet-5 [122], AlexNet and VGG16 [109], and achieved an improved accuracy rate of 92.5%.

Bi et at. [123] proposed a low-cost mobile deployable model to identify two different common types of apple leaf diseases. They used the MobileNet deep learning model and compared its performance with that of ResNet152 and InceptionV3. The dataset used were collected by agricultural experts. The authors achieved accuracy rates of 73.50%, 75.59%, and 77.65% for MobileNet, InceptionV3 and ResNet152, respectively. The average handling time in MobileNet was much less than that of InceptionV3.

Rice and maize leaf diseases were identified by Chen et al. [74] using the INC-VGGN method. In their approach, they replaced the last convolution layer of VGG19 with two inception layers and one global average pooling layer. In their model, basic features were extracted using a pretrained model and high-dimensional features by the inception layer. They obtained an accuracy rate of 92% and 80.38% in rice and maize, respectively.

Atila et al. [124] used an EfficientNet architecture to identify different diseases in plant. The performance of their model was compared with that of other CNN models such as AlexNet, ResNet50, VGG16 and InceptionV3 and it showed that EfficientNet outperformed the other CNN models. The highest accuracy rate of 99.91% was obtained using EfficientNetB5 on the original dataset and 99.97% using EfficientNetB4 on the original dataset. The number of parameters generated in the EfficientNet model was much less that that of the other deep learning models and hence it required less time to train the network.

A. Tuncer [125] used a hybrid CNN approach to identify plant leaf diseases. In that paper, the author used an inception network with a depthwise separable convolution, which reduced the number of parameters and computational cost of the model. Using a k-fold cross-validation, the model achieved a maximum accuracy of 99.27% and an average accuracy of 99% on the PlantVillage dataset. We summarize the above papers as follows:

- Removing convolution layers, changing the filter sizes, replacing the standard convolution by a depthwise separable convolution reduce the number of parameters.
- An attention network which focuses on a particular region reduces the complexity of the network.
- The time required to train the network is much less.

- It is easy to implement on small devices and the computation time is reduced.

In [126], the authors used CNN, VGG and Inception architectures to identify plant leaf diseases. In their approach, they used 15% images of the PlantVillage dataset and some real-time captured images to evaluate the accuracy and obtained an accuracy rate of 98% and 95%, respectively, with the CNN architecture. Pretrained AlexNet and GoogleNet [127] were used in [128] to detect three different soybean diseases from healthy leaf images with some modified hyperparameters such as minibatch size, max epoch and bias learning rate. In [129], the authors classified the maize leaf diseases from healthy leaves using deep forest techniques. In their approach, they varied the hyperparameters of the deep forest, such as the number of trees, number of forests, number of grains, and compared their results with traditional machine learning models such as SVM, RF, LR and KNN. The deep forest model achieved an accuracy rate of 96% and a maximum F1 score of 0.96 among all other classifiers.

Using the principles of deep learning, a fully connected CNN model was built by Sibiya et al. [130] to classify maize leaf diseases. The model was able to recognize three different types of maize diseases with an accuracy rate of 92.85%. A multilayer CNN was used by Singh [131] to identify mango leaf diseases and obtained an accuracy rate of 97.13%.

Different CNN architectures, such as AlexNet, VGG16, VGG19 and ResNet, were used in [132] to identify the diseases in plant. In their approach, they used the camera-captured images of eight different diseases to train the model. For the feature extraction, they used these CNN models and for classification purposes, they used different classifiers such as KNN, SVM and extreme learning machine (ELM). They achieved a maximum accuracy rate of 97.86% using the ResNet architecture. A NASNet-based deep CNN architecture was used in [133] to identify leaf diseases in plants and they obtained an accuracy rate of 93.82%.

A shallow CNN (SCNN) was used by Yang Li et al. [134] for the identification of maize, apple and grape diseases. First, they extracted the features from the CNN and then classified the diseases using SVM and RF classifiers. In their approach, they claimed that the combination of a shallow CNN and classic machine learning classification had a good ability to identify plant diseases and the kernel SVM and random forest had the ability to overcome overfitting. A number of deep CNN architectures were used by Sethi et al. [29] for the identification of four different rice diseases. In their approach, they extracted the features from the deep learning model and classified the diseases using an SVM classifier; they showed that the SVM performed better compared with the deep learning classifier. We summarize the above papers as follows:

- The extraction of features using a CNN model and the classification using different machine learning classifiers also give higher performance accuracies.
- A CNN model extracts better features, which make a classifier such as an SVM or RF give better performance results.
- An SVM and RF can tackle the overfitting issues.
- A CNN model is used only for extracting the features and hence the training of the model is not required.

Table 5 summarizes the DL models along with the dataset used to identify the diseases in plants with their class and labels. Table 6 shows the limitations of some of the implemented deep-learning-based techniques for the identification of plant diseases. From Table 6 it is seen that most of the researchers used the same dataset to train and test the DL models. It is also seen that the number of works on the identification of plant diseases having multiple diseases on a single leaf is also relatively small.

Table 5. Summary of deep-learning-based implemented methods.

Author	Plant/Disease	Model	Dataset	Class	Accuracy (%)
Mohanty et al. [72] (2016)	Multiple	AlexNet, GoogLeNet	54,306 images of PlantVillage dataset	38	99.35
Sladojevic et al. [84] (2016)	Apple, grape	Fine-tuned CNN architecture	4483 internet-downloaded images	4	96.3
Nachtigall et al. [86] (2016)	Apple	AlexNet	1450 captured images	6	97.3
Wang et al. [109] (2017)	Apple	VGG 16 with transfer learning	2086 images of PlantVillage dataset	1	90.4
Fuentes et al. [73] (2017)	Tomato	Faster R-CNN (ResNet)	5000 images from farm	10	83
Durmus et al. [120] (2017)	Tomato	Alexnet, SqueezeNet	Images of tomato diseases from PlantVillage data	10	95.65 (AlexNet), 94.3 (SqueezeNet)
Lu et al. [118] (2017)	Rice	Multistage CNN	500 captured images	10	95.48
Cruz et al. [93] (2017)	Olive	Lenet hybridized with shape, edge, Hu's moments, Zernike moments features	299 captured images	3	98.60
DeChant et al. [105] (2017)	Maize	Layers of CNN architecture	1796 captured images	2	96.7
Amara et al. [90] (2017)	Banana	LeNet	3700 captured images	3	98.61 (color image), 94.44 (gray image)
Ramcharan et al. [24] (2017)	Cassava	Inception V3 based on GoogLeNet	2756 captured images	6	98
Ferentinos et al. [2] (2018)	Multiple	AlexNetOWTBn, VGG	87,848 images	58	99.49 (AlexNet), 99.53 (VGG)
Atole et al. [94] (2018)	Rice	AlexNet	857 captured images	3	91.23
Rangarajan et al. [85] (2018)	Tomato	AlexNet, VGG16	13,262 images of PlantVillage data	6	97.29 (ALexNet), 97.49 (VGG16)
Liu et al. [113] (2018)	Apple	AlexNet with inception layer	13,689 captured images	4	97.62
Ramcharan et al. [114] (2019)	Cassava	MobileNet	2415 images	7	80.6
Adedoja et al. [133] (2019)	Multiple	NASNet	54,306 images of PlantVillage dataset	38	93.8

Table 5. *Cont.*

Author	Plant/Disease	Model	Dataset	Class	Accuracy (%)
Turkoglu et al. [132] (2019)	8 different plant diseases	Different DL model with SVM, ELM, KNN	1965 captured images	8	95.5 (ALexNet), 95 (VGG16)
Ozguven et al. [106] (2019)	Beet	Faster R-CNN	155 captured imaged	4	95.48
Gensheng et al. [121] (2019)	Tea	Modified Cifar10	134 captured images	4	92.5
Singh et al. [131] (2019)	Mango	Multilayer CNN	1070 captured images	2	97.13
Elhassouny et al. [102] (2019)	Tomato	MobileNet	7176 images of PlantVillage data	10	90.3
Arora et al. [129] (2020)	Maize	Deep Forest	400 image	4	96.25
Lee et al. [97] (2020)	Multiple	VGG16, InceptionV3, GoogLeNetBN with Transfer learning and Training from scratch	54,306 images of PlantVillage dataset	38	99.09(GoogLeNetBN), 99.00 (VGG16), 99.31 (Inception V3), 99.35 (GoogLeNet)
Zeng et al. [135] (2020)	Rice, cucumber	SACNN	AES-CD9214, MK-D2	6	95.33 (AES-CD9214), 98.00 (MK-D2)
Chen et al. [74] (2020)	Rice, maize	INC-VGGN	500 rice images, 466 maize images,	9	92.00
Li et al. [75] (2020)	Cotton pest	CNN	NBAIR	50	95.4
Sethy et al. [29] (2020)	Rice	Different DL model with SVM	5932	4	98.38 (F1-score)
Li et al. [134] (2020)	Maize	Shallow CNN with SVM, RF	2000 images from Plant Village dataset	4	94
Ahmad et al. [101] (2020)	Tomato	VGG16, VGG19, ResNet, InceptionV3	2364 laboratory images 317 real-time images	6	93.40 (lab), 85.00 (real)
Bi et al. [123] (2020)	Apple	MobileNet	334 captured images	2	73.50
Atila et al. [124] (2021)	Multiple	EfficientNet	55,448 images of PlantVillage data	39	99.91
Oyewola et al. [25] (2021)	Cassava	DRNN	5656 images of cassava plant	5	96.75
Tuncer et al. [125] (2021)	Multiple	Hybrid CNN	50,136 images of PlantVillage dataset	30	99

Table 6. Limitation of deep learning models for the identification of plant diseases.

Author	**Limitations**					
	Large Number of Images in Dataset	**Large Number of Species Considered**	**Accuracy on Testing Field Images**	**Multiple Diseases on Same Image**	**Consider Complex Background**	**Train/Test Data Are from Different Datasets**
Mohanty et al. [72]	yes	yes	low	×	×	×
Ferentinos et al. [2]	yes	yes	low	×	×	×
Liu et al. [136]	×	×	×	×	×	×
Amara et al. [90]	×	×	×	×	×	×
Fuentes et al. [73]	×	×	yes	yes	yes	×
Geetharamani et al. [108]	yes	yes	×	×	yes	×
Barbedo et al. [137]	yes	yes	low	yes	×	×
Cruz et al. [93]	×	×	×	×	×	×
Sladojevic et al. [84]	×	yes	×	×	yes	×
Brahimi et al. [138]	yes	yes	×	×	yes	×
Ozguven et al. [106]	×	×	×	×	×	×
Wang et al. [109]	×	×	×	×	×	×
lee et al. [71]	yes	yes	yes	×	yes	×
DeChant et al. [105]	×	×	×	×	×	×
Ramcharan et al. [114]	×	yes	yes	×	yes	yes
Oyewola et al. [25]	×	yes	×	×	yes	×
Ramcharan et al. [24]	×	yes	×	×	yes	×

In this table large images in a dataset are considered yes when the number of images is more than 1000/class.

4. Discussion

From our survey, we showed that deep-learning-based techniques outperformed the traditional classification approaches such as KNN, SVM, RF, LR, ANN and others. In deep learning, features are learned automatically from the networks, which is more effective and gives more accurate results at the time of classification than the traditional feature extraction approaches relying on color, shape, SIFT, texture-based, GLCM, histogram, Fourier description, etc., features. A large number of deep learning architectures are used for the identification of plant diseases. We summarized these deep learning models in Figure 3. From Figure 3, it is seen that AlexNet, VGG16, GoogleNet and InceptionV3 are the most frequently used DL models. VGG19 and ResNet50 are the next most used DL models. A summary of different DL models along with the number of layers, number of parameters and the size of each DL model is shown in Table 7. Figure 4 gives the number of research papers with respect to individual plant classes. Multiple plants are included in the PlantVillage dataset, which consists of 14 different plant species and 38 categories of diseases and is the most frequently used plant dataset by researchers. Rice and tomato are the next most-used plants in plant diseases identification areas. Figure 5 shows the histogram representation of the discussed papers published from 2009 to 2021 in the field of the identification of plant diseases. From Figure 5, it is seen that the identification of plant diseases has gained much attention after 2016. There are several advantages of using a DL model over a handcrafted-features-based approach. The extraction of hand-engineered traditional features requires extra effort and is time-consuming; moreover, searching for features that give the most precious results is not an easy task. DL-based features reduce this effort and gives the best results [109]. A DL model is robust under some challenging issues such as a complex background, illumination, size and orientation [73]. DL models are robust in scenarios containing challenging images, several intra and extraclass variations and they have the ability to deal with complex scenarios from a plant's surrounding area.

Table 7. Different DL models with respect to number of layers and parameters and size.

Model	No. of Layer	Parameters (Million)	Size
LeNet	5	0.06	-
AlexNet	8	60	240 MB
VGG16	23	138	528 MB
VGG19	26	143	549 MB
InceptionV1	27	7	51 MB
InceptionV3	48	23.85	93 MB
Xception	126	22.91	88 MB
ResNet50	50	23	98 MB
ResNet101	101	50	171 MB
ResNet152	152	44	232 MB
InceptionResNetV2	572	55.87	215 MB
DenseNet121	121	8.06	33 MB
DenseNet201	201	20.24	80 MB
NASNetMobile	-	5.32	23 MB
Squeezenet	69	1.23	5 MB
Shuffle Net	-	3.4	-
MobileNetV1	88	4.2	16 MB
MobileNetV2	88	3.37	14 MB
EfficientNet B0	-	5.33	29 MB
EfficientNet B1	-	7.85	31 MB

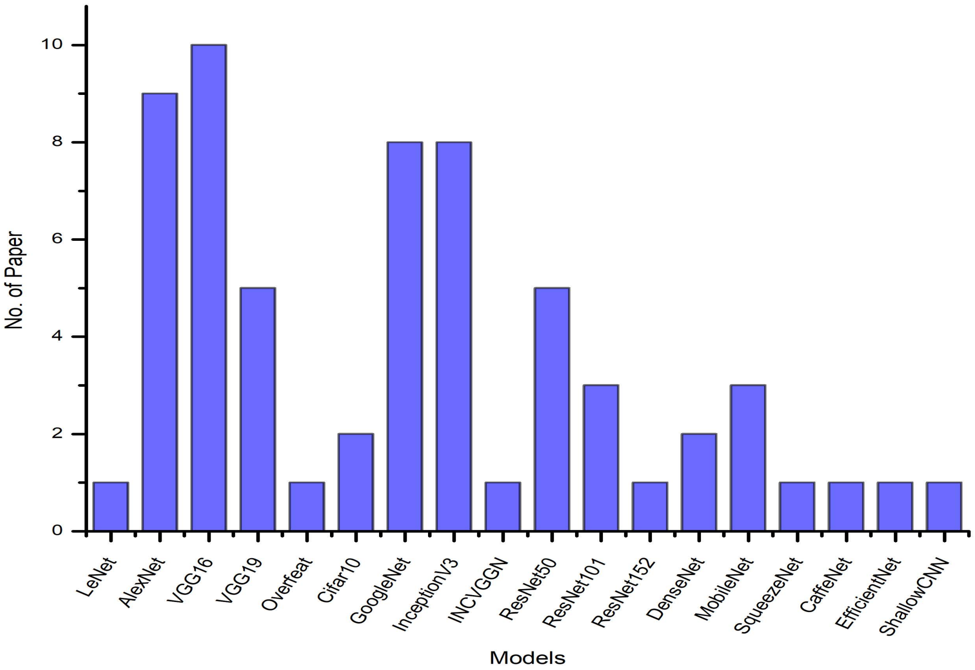

Figure 3. Number of research papers for various deep learning models.

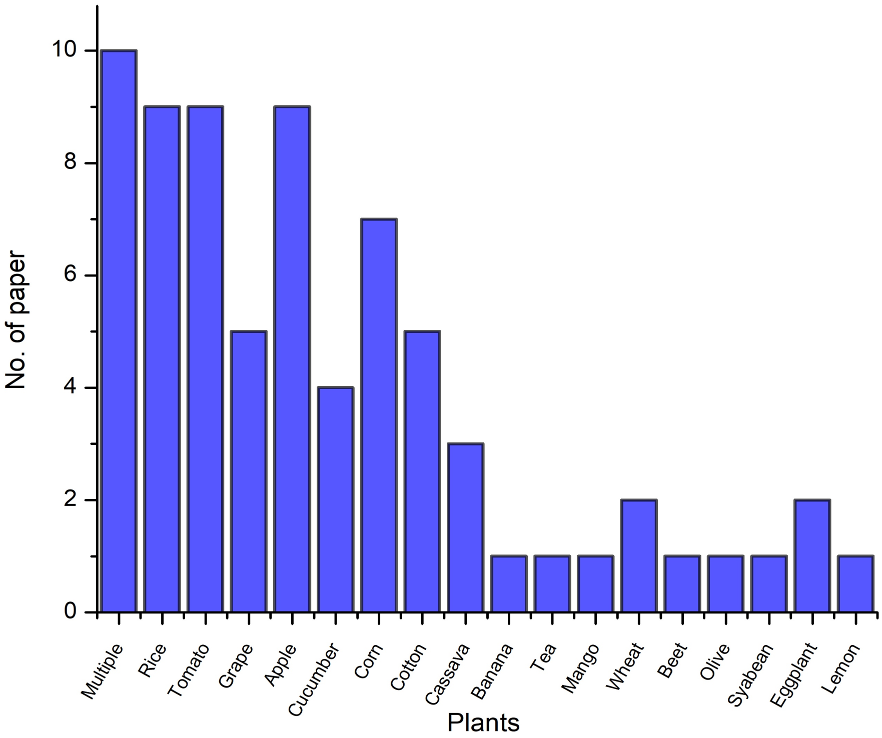

Figure 4. Number of research papers for different plant categories.

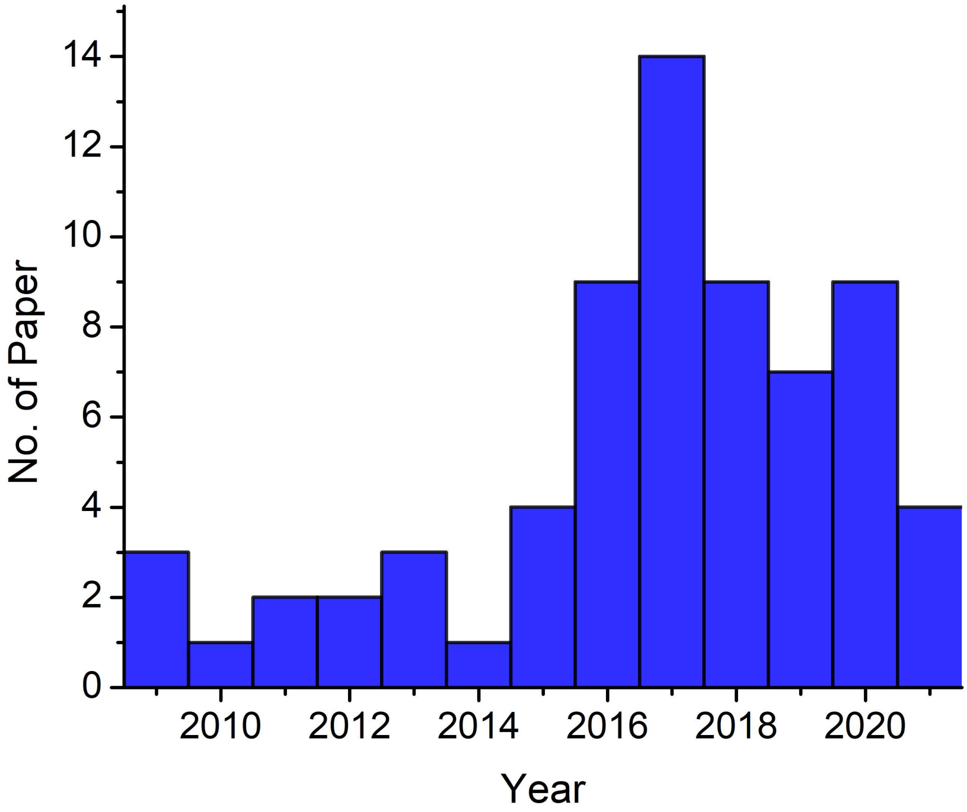

Figure 5. Histogram of number of papers published with respect to years.

5. Challenges

The identification of diseases in plants from the leaf image faces some challenges. Resolving these challenges and issues is a key point to design a practical plant disease identification system on real-time images with diverse field conditions. In this section, we discuss some of the unresolved issues in the identification of diseases in plants.

5.1. Dataset of Insufficient Size and Variety

In many papers and articles, the main limitation is the dataset used to train the CNN network, which leads to a worse performance accuracy for the identification of disease. In DL, there is a need for a large dataset with a wide variety of images. The PlantVillage [23] and Image Database of Plant Disease Symptoms (PDDB) [137] dataset are the only freely available large diseases dataset at the present time. The images available are from a laboratory setup and were captured with a uniform background. However, the collection of images from the field is expensive, and it requires agriculture expertise for the accurate identification of diseases.

5.2. Image Segmentation

Segmentation consists in finding the region of interest from the image. Two approaches exist in segmentation, a traditional approach and a soft-computing-based approach. K-means clustering and color thresholding are traditional and fuzzy logic, artificial neural network and region growing are soft-computing-based segmentation techniques. Segmenting a leaf image from a complex background is a challenging issue for the identification of diseases. The segmentation of the leaf region can improve the performance accuracy. Images with many illegitimate elements often cause difficulties in the identification.

5.3. Identification of Diseases with Visually Similar Symptoms

Some of the diseases have similar symptoms, which even experts often fail to distinguish properly by the naked eye. Sometimes one disease symptom may vary due to geographic locations, crop development stage and weather condition. Until now, no work has been found in the literature that incorporates these issues in the identification of plant diseases.

5.4. Simultaneous Occurrence of Multiple Diseases

Most of the plant disease identification model assumes that there is only one type of diseases in the image. However, multiple diseases as well as some nutritious disorders may occur simultaneously. This can affect the identification of diseases. From the survey, we can see that few works exist in the field that identify multiple diseases. Fuentes et al. [73] only considered the identification of multiple diseases in tomato leaves.

5.5. Identification of Diseases from Real-Time Images

From the literature, we observed that most papers are based on the identification of diseases using laboratory images. The performance of a model decreases in the case of a real-time identification of diseases. In [72], the authors obtained an accuracy rate of 99.35% on the PlantVillage dataset and the model performance decreased to 31% when the model was tested with a different dataset. In [2], the authors recorded an accuracy rate of 99.53% on a wide variety of datasets. When the model was trained solely on laboratory images and identified field-captured images, the success rate decreased to 66%. Therefore, the effective identification of diseases in real-time field images is an important challenging issue.

5.6. Design a Light Deep Learning Model

Most of the deep learning architectures that were implemented in the literature are based on AlexNet, VGG, GoogleNet, ResNet, DenseNet and InceptionV3. Deep learning requires high-performance computing devices, expensive GPUs and hundreds of machines. This increases the cost to the users. Small CNN models will be highly desirable especially in embedded, robotic and mobile applications where real-time performance and a low computational cost are required. It requires a very large quantity of data in order to perform better than other techniques. It is extremely expensive to train due to complex data models.

6. Conclusions and Future Directions

In this paper, we presented a survey of different machine learning approaches for the identification of plant diseases using leaf images. As in humans, plants suffer from different diseases which affect their normal growth. This survey consisted of the identification of diseases using handcrafted-features-based method and DL-based methods. We compared the performance in terms of the preprocessing and segmentation techniques used, the features used to classify the diseases, along with the dataset used in each paper. Through the survey of the identification of diseases using shape- and texture-based features, we can conclude that preprocessing and segmentation techniques play a major role in increasing accuracy. The SVM was the most widely used classification technique for the identification of diseases. From the survey, it was observed that the performance of deep learning models outperformed traditional handcrafted-features-based techniques. From the accuracy of different deep learning models, we can say that the ResNet50, InceptionV3 and DenseNet201 architectures are suitable for the identification of plant diseases. MobileNetV2 and SqueezeNet are suitable architectures for lightweight devices such as mobile phones.

The early detection of diseases would help farmers to improve the crop yield and the problem of the expensive domain expert. Several gaps are there in the existing literature and some are highlighted as future research work for the identification of diseases in plants. The collection of large datasets with a wide variety of images and images from different geographical locations is an important research issue. From the survey, we also conclude that if the disease symptom changes significantly during different stages of infection, then the reliability of detecting diseases will be less. Future work includes developing a reliable lightweight deep CNN model and adopting these models for mobile devices.

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