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Machine and Deep Learning Approaches for Plant Disease Detection: A Comprehensive Review

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Abstract— People have been using edible foods since ancient times, and they continue to be an essential component of a healthy diet and traditional food systems today. Food crops as a major source of human energy intake, and the challenges they face due to biotic and abiotic stress factors, such as pollution, insects, bacteria, and unfavourable weather conditions. Detecting plant diseases in the early stage is critical for ensuring a stable supply of healthy food, and traditional methods of disease detection by experts are lengthy and have some limitations. The use of Machine and Deep learning is a key aspect of precision farming for crop growth monitoring. Plenty ML strategies, including random forest and support vector machines (SVMs), Convolutional Neural Networks, Deep learning as well as image processing have been used to precisely detect, classify, and predict plant diseases. By leveraging machine learning algorithms, farmers and agricultural experts can accurately detect and diagnose crop diseases, enabling them to take appropriate measures to control and prevent further spread of the disease. This article provides a comprehensive overview of the different AI approaches for plant disease identification and control, drawing on a range of research articles in the field. The application of machine learning in agriculture holds promise for improving crop health and increasing yields and represents an important area of innovation for sustainable agriculture in the future.

Keywords- Plant Pathogens, Artificial Intelligence, Deep Learning, Precision Farming.

I. INTRODUCTION

Based on the Food and Agriculture Organization infectious diseases of plants and insect infestations constitute two of the primary factors reducing food supply and food safety [56]. Depending on the type of crop, the climate, and the existence of an infectious agent, plant diseases change periodically. Crops may face stresses from the environment due to biological factors (insects, pests, weeds, viruses, etc.), abiotic factors (drought, water logging, salinity, etc.), or a combination of these causes [73]. In contrast, a pathogen is any organism responsible for causing disease, including viruses, bacteria, and fungi. Harm to crops can range from minor physiological flaws to plant death, depending on the illness and stage of establishment. In addition to these biological influences, the plant can suffer from diseases brought on by physical agents such as rapid climatic change.

The standard method for reducing the harm that these microbes inflict is to rely on pesticides [89]. The indiscriminate use of pesticides can result in the death of beneficial insects utilized in biological management and the establishment of genetic resistance, along with their detrimental impacts on the natural world [25].

Localizing diseased regions in plantations helps to cut down the application of chemicals. The traditional methods for identifying and locating plant illnesses include molecular analysis on leaf tissue or direct visual identification using visual detection of disease symptoms emerging on plant leaves. These procedures take a long time and involve many personnel [23].

Recently, effective approaches for illness detection and localization have been put forth employing automatic monitoring and identification systems. The identification and assessment of agricultural anomalies now have new avenues with the help of developed machine-learning techniques [24].

Stats gathered from the soil and cover of plants, sensors like remote sensing (RS), and ground devices, in additionally creating and evaluating algorithms that utilize machine learning, can all be accustomed to disease detection [50]. Economic viability, environmental sustainability, and conservation of land resources are maximized when management strategies are put into effect with decision tree, support vector machine. Overall, it makes it possible to give efficient therapy at an appropriate moment, place, and pace [44].

Several sensors for evaluating variables related to the plant's canopy, leaf markers derived from remote sensing imaging, and IoT sensors has offered to the farming sectors [81]. Data processing strategies are needed to compile such sorts of data provided the range of retrieved data in order to further comprehend crop growth circumstances and the emergence of disease signs. Additionally, machine learning and deep learning-mediated data integration have made significant strides and, when applied to agricultural data, will have a significant influence on the field of plant assurance, particularly in the areas of disease and prospective identification of disease. For this purpose, a variety of multi-sensor and remote sensing-based combining systems are being used [81].

In-depth study in the area of digital farming, particularly for plant surveillance, management, and security, has resulted in a sizable body. Research has been made possible by the utilization of agricultural-related data from various acquired technologies like machine learning, deep learning, etc. This review article highlights the causes of plant diseases and how AI-based methods are more effective than conventional techniques like biological diagnostics, mycological examination, microscopy, and visual inspection, and molecular methods for the detection of plant diseases. Machine and deep learning methods, like artificial neural networks, support vector machines, decision trees, and K-nearest neighbors, are employed for identifying diseases in plants, Convolutional Neural Networks, also deep learning algorithms like AlexNet, VGG-Net, and GoogleNet [22][81], are also emphasized in this review.

II. MATERIAL AND METHODS

An outline of the causes of plant diseases and their effects on agricultural crops was provided at the beginning of this extensive review. Pathogens cause infectious diseases to develop, and for a variety of causes, these infections can become epidemics that astound civilization and have incredibly damaging effects.

A. *Causes of Infectious Diseases*

In the case of floras, contaminated organisms, like fungi, protozoa, bacteria, viruses, insects, and parasitic vegetation, are the main causes of infectious diseases [30]. These contagious plant diseases have grown in importance as influencing variables on crop production and economic effectiveness as agriculture has developed [88]. These infectious agents can spread through a variety of channels, including airborne transmission, aquatic routes, transmission via animals, and transmission by people [50]. They can also continue to be infectious for a long time, frequently for months or years. Soil is a common place to find these pathogenic pathogens' natural repositories [6]. The essential and substantial phytopathogens are as follows

a) Fungi

Fungi belong to the Eukaryota domain and are distinct from bacteria due to their intricate cell structure, which includes a well-defined nucleus and mitochondria. Although fungal genomes have fewer similarities than those of a great deal of eukaryotes, they are considerably larger than those of prokaryotes [91]. The main components of the cellular wall of fungi are mannan, chitin, and chitosan, along with other lipids, proteins, and polyphosphates. These organisms create mycelium, structure made from a network of slender, branching hyphae. In certain instances, this mycelium does not have intercellular septa, resulting in the formation of a syncytium [71]. Fungi inhabit diverse ecological niches and can have both beneficial and harmful effects. They appear to have an evolutionary history older than that of plants, with their coexistence spanning an extensive period comparable to the era of higher plant development. Approximately Eighty percent of the world's current plant species engage in symbiotic relationships with fungi. But fungi have the ability to upset this delicate equilibrium and become biotrophic, hemibiotrophic, or necrotrophic plant pathogens [29]. Normally, pathogenic fungi gain entry into plants by exploiting wrecked pores and leaves. Nevertheless, in various instances, fungi generate particular spreadable bacterial form and enzymes designed to break down the plant's cell wall. Necrotrophs, capable of infecting a broad spectrum of hosts, induce swift cell demise through the coordinated activity of enzymes, contaminants and oxygen-reactive species. [69].

In contrast, the life cycle of biotrophs is intimately linked to that of their natural hosts. Through specialized biotrophic hyphae in the interphase region, they release effector molecules that suppress the plant's immune system and exhibit specificity in their interactions with the host [15]. These hyphae absorb biomolecules that the plant produces. fungus can also form specialized hyphal outgrowths known as appressoria, aiding in substrate attachment and the penetration of the plant's cell wall via the action of enzymes that break down the cell wall in combination with mechanical force. The Haustoria, which contains numerous mitochondria and ribosomes, penetrate the plant's cells through the damaged areas. Typically, haustoria are split by an invasion of the host's cell from the plant cell plasma membrane. It is important to highlight that increased plant defenses can result in a shift Necrotrophy replaces biotrophy. [51].

Plant health is seriously threatened by phytopathogenic fungi at every step of crop production. Fungicides are the most common way to combat these fungi, but there are significant risks to the environment and human health associated with this approach. These risks include resistance evolving, resistance genes spreading horizontally, and the emergence of species resistant to several fungicides [47]. Worldwide agriculture employs approximately 150 various substances having various modes of action that function as fungicides. Regretfully, resistance to almost all major classes of fungicides has been reported to date in a variety of phytopathogen types. Common indicators of fungal diseases in plants include symptoms such as wilting, spotting, the appearance of mold (identified by the fungus's mycelium and sporulation on affected organs), the development of pustules (containing concentrations of fungal spores), excessive growth, deformities, mummification resulting in rot, becoming darker, compaction, and reduction of the affected tissue [13].

It is worth highlighting that over 10,000 fungal species have been identified in association with plants to date. Consequently, it is not unexpected that diseases brought on by other pathogenic microbes are less harmful than those caused by fungal infections. [71].

Fungi stand out as the primary culprits among plant pathogens are those that cause the greatest damage to plants in both natural and agricultural environments. Fungal plant pathogens usually display complex life and disease cycles with several phases, occasionally up to five separate stages. [34]. Each of these phases present on an individual host plant is distinguished by totally different reproductive techniques. Each phase produces different fungal spores or propagules, each with unique mechanisms and tendencies for spreading and infecting hosts. The majority of fungi take on a thread-like structure called hyphae, which are made up of cells with thick chitin-rich cell walls [28]. These organisms make entry points for hyphae by applying physical pressure and enzymes, and can infiltrate the interiors of plants, subsequently establishing colonies and appropriating plant nutrients. In terms of their genetic makeup, during the majority of their entire life cycle, fungal genomes are diploid, though certain phases and propagules can occur in a haploid state. [77]. Fruiting bodies, which are reproductive structures, exhibit various forms depending on the fungal group. These include recognizable shaped-like cup structure in Ascomycetes, mushroom-like structures in Basidiomycetes, and simple, multi-tipped branches in fungi imperfection.

b) Bacteria

Bacteria inhabit virtually every corner of our world and can exhibit pathogenicity towards flora, fauna, and mushrooms. DNA is the genetic material that bacteria deposit, typically within a chromosome, and it's not uncommon for a single cell to contain multiple chromosomes. Plasmids are mobile genetic elements that are extrachromosomal and carried by cells of bacteria. They can carry essential virulence genes or, on the other hand, components for biological management [14]. Additionally, bacteria may house a prophage, representing bacteriophage DNA that has integrated into their genome. Most bacteria undergo division through the process of binary fission, typically involving the simultaneous replication of extrachromosomal components as well as chromosomal DNA. This division necessitates the presence for membrane potential [76]. It's worth noticing that bacteria can possess more than one plasmid, with some plasmids potentially being lost in the process of cell division. Pantoea stewartii, for example, can carry up to thirteen distinct plasmids. While plasmids are primarily transferred by bacteria within their own populations, genetic information is still frequently exchanged horizontally within the prokaryotic domain [12].

Bacteria possess a unique cellular architecture characterized by a crucial feature: the cell membrane, which acts as a barrier separating their inner cytoplasm from the external environment. This cellular division is significant as it helps classify bacteria into two distinct categories: Gram +ve and Gram -ve organisms, based on their distinguishing cell wall structures. Conversely, Gram -ve bacteria exhibit a slightly different architectural arrangement [82]. The presence of these cell walls is crucial for bacteria, as they require specialized secretion systems to eliminate harmful substances like xenobiotics and to release diverse proteins and virulence factors into their surroundings. These secretion systems exhibit diverse structural forms, with Gram-negative bacteria typically featuring at least six different types, Gram-positive bacteria having four exclusive types, and both groups sharing two. Surprisingly, these secretory mechanisms are also essential for phytopathogenic bacteria's virulence [32]. It is noteworthy to highlight an intriguing phenomenon during bacterial cell division, wherein a natural imbalance arises between mother and daughter cells. Typically, phytopathogenic bacteria exhibit slower growth rates compared to counterparts that are non-pathogenic and that were recently isolated from crops; they grow best in temperatures within 20 and 30°C. These bacteria are pathogens, and they have different kinds of genes, like virulence genes, which are pivotal for infection and subsidize considerably virulence, as well as disease-specific genes, crucial for the manifestation of diseases. A group of genes plays a crucial role in essential functions during the pathogenic process, encompassing host recognition, attachment of the pathogen on the surface of crop, the development of contagious architectures, infiltration into host tissue, and the subsequent colonization. Pathogenic components can either stay affixed on the surface of the bacteria or discharged into the surrounding environment [26]. While harmful microorganisms are accountable for causing numerous significant plant diseases worldwide, their impact is not as extensive as that of fungus or infectious microbe. Nonetheless, the financial toll that bacterial infections take is comparatively milder than those caused by fungi and viruses. Bacteria can disrupt various stages of crop production, posing challenges to agricultural productivity. Moreover, the escalating average annual temperatures provide reason to anticipate a growing threat from bacterial spot diseases and increased economic losses in the years ahead [61]. Anticipating a rise in summer temperatures by 3–4°C per year, there is an expectation that the occurrence of bacterial diseases will double, and plant infections could increase by 30–50%. This underscores the pressing need for proactive measures and research to mitigate the impact of bacterial pathogens on agriculture [67].

Plant infections caused by bacteria can be broadly categorized into two types: local bacterial blight, which damages the parenchymal tissues of specific plant organs, and systemic bacterial blight, which is characterized by the pathogen entering the plant's vascular system and spreading through conductive bundles and surrounding. [45].

The group of Phytoplasmas is different than group of spiroplasmas which is exceptionally tiny bacteria, with a diameter of approximately 1 µm, and are notably devoid of a cell wall. Instead, they rely on a cytoplasmic membrane to separate themselves from the external environment. These bacteria are accountable for inducing phytoplasmosis and growth retardation in plants. Comparable to mycoplasmas, a related bacterial genus, phytoplasmas seem to belong to some of the most primitive and self-replicating life forms [53]. Phytoplasmas typically have a genome size ranging from 0.5 to 1.3 million base pairs, whereas Mycoplasma genitalium have 0.58 million base pairs. Cultivating phytoplasmas in axenic cultures is challenging, highlighting their significant dependence on host metabolism [48].

Phytoplasmosis has a significant adverse effect on the crop's quality and production. Phytoplasmosis has a significant effect on harvest damage; losses for eggplants, tomatoes, peppers, potatoes, and cucumbers can be as high as 40%, 60%, 93%, and 100%, respectively. Plants with phytoplasmosis display virescence, phyllodia, and proliferation, among other reproductive organ dysfunctions.

Remarkably, positive phytoplasmosis is a rare occurrence, with only one documented case. This phenomenon has a beneficial impact on the economically valuable poinsettia, a popular seasonal ornamental plant [89].

On plant surfaces, a variety of bacterial plant pathogens form territories. They enter the plant only in favorable circumstances, usually through lenticels or stomata, thus initiating the disease process [84]. Certain bacterial pathogens, like spiroplasmas is entered directly into plant tissues through feeding insect vectors of plant. While bacteria rely on natural openings, wounds, or insect-feeding sites to access plant tissues [74]. Additionally, it's important to note that there are several significant differences between fungi and bacteria. Since bacteria are prokaryotic organisms, their cells have haploid genomes and no internal, membrane-bound organelles. Bacteria have the capacity for genetic material exchange, facilitating remarkable adaptability to change with changing environmental conditions than that of fungi [5].

c) Viruses

Small infectious agents called viruses, which lack cells, can only replicate inside live cells. They infiltrate a variety of living things, as bacteria, archaea, crops, and mammals. They may actively multiply and control the metabolic processes of the host inside the host, or they may fuse with the genetic material of the host and become an inert provirus. In addition to single-stranded and retroviruses that contain DNA, single-stranded and double-stranded RNA viruses are the most common forms of plant viruses [2]. Each virus has a unique reproduction cycle and life cycle as a result of its unique genetic makeup. A capsid, a protein that forms a protective shell, encases the nucleic acid molecule that makes up viruses. This capsid's lipids and proteins occasionally combine to form a lipoprotein membrane. An average plant virus is about 30 nanometers in size. [18].

These viruses can moves horizontally as well as vertically. Plasmodium-like passageways, or plasmodesmata, are used by viruses to enter nearby cells. By modifying these pathways, viruses frequently develop proteins that assure the flow of virions, promoting the propagation of infection to nearby cells. The beginning of local diseases in plants is caused by this process [16]. A few viruses can survive for extended durations in cells of plants and the products formed from them thanks to their amazing resistance to heat and stability. Additionally, they can spread passively by being transported mechanically from a single species to another. Nevertheless, the vast majority of crop infections actively spread from diseased to wholesome plants by a means of transmission, or carrier species [57]. These carriers can be classified into mechanical vectors, where the agent does not reproduce, and biological vectors, where a stage of the viral development process occurs. Plant-eating arthropods, nematodes, and fungi serve as the primary vectors for plant viruses [19].

Plant viruses present a substantial risk to a huge number of crops, causing financial loss second only to those induced by other pathogens. Furthermore, specific viruses can infect over a thousand distinct plant varieties spanning over eighty-five families. In numerous tropical and subtropical regions, viral infections can spread to crop losses as high as 98%. [62]. The influence of viral infections fluctuates based on the stage of development of crop, potentially causing significant damage during growth while resulting in minimal harm during harvesting, storage, and transportation. It's noteworthy that, in certain instances, plants can harbor viral infections without exhibiting evident symptoms [59]. Symptoms associated with There are five major categories of viral diseases: growth restraint, characterized by diminished overall plant growth or stunted branches; coloring; deformations; necrosis; and poor reproduction.

Viroids are another type of infectious agent. They are round RNA particles that cause a variety of plant and animal illnesses. They are taxonomically equivalent and are placed within the realm of viruses, particularly those belonging to the Pospiviroidae and Avsunviroidae families. Viroids, unlike viruses, are without a protein covering (capsid) and are made up of covalently bonded proteins, single-stranded RNA molecules, typically measuring 200–500 nucleotides in length, which is significantly shorter, about 50-80 times, compared to viral genomes. Viroids cannot encode proteins or replicate independently [58]. The precise molecular structure behind the effects of viroids remains not fully comprehended. Nevertheless, there is a theory suggesting that By binding to cellular kinases, viroids can change the phosphorylation status of gene products, altering the expression of genes involved in growth, stress, development, and protection. [21]. During an infection, viroids can stimulate the production of proteins linked to pathogenesis, instigate RNA interference can reduce gene expression post-transcriptionally, interfere with splicing, and start the demethylation of rRNA genes. It is noteworthy that even a single nucleotide substitution at a specific position can significantly alter viroid pathogenicity. In instances of infection with two viruses, these transport domains can exchange, potentially contributing to their further development [35]. The Avsunviroidae family of viruses lacks the central conserved area. They do, however, contain sequences required for the creation of ribozyme structures, which are required for the self-cleavage of RNA strands. The most common symptoms associated with viroid illnesses are as follows: diminished overall plant growth or specific parts, discoloration such as chlorosis and anthocyanosis, and deformities affecting various plant organs [52]. As a result, viruses and viroids collectively form a significant category of pathogens accountable for plant diseases.

d) Complex diseases

While it's commonly believed that a single species or strain of pathogen is responsible for causing crop infection, in nature, microorganisms primarily exist as part of complicated multi-species networks. The majority of laboratory research focuses on single strains grown in true cultures, however, this technique falls short of understanding the complicated evolution of specific illnesses in plants. As a result, infections involving more than one pathogen are frequently referred to as "complex" due to the complexities of their identification and care afterward. [42]. Pathogenic bacteria, viruses, and fungus can all have synergistic interactions. When cowpea is infected with both cowpea mosaic virus and cucumber mosaic virus, for example, virus-virus synergy is visible. [54], resulting in more severe disease and greater growth retardation compared to single-virus infections [87]. Fungus-fungus synergy is relatively common and leads to complex diseases like ascochyta blight in peas and mango malformation disease. Brown apical necrosis of walnuts caused by many pathogenic fungi and the bacteria Xanthomonas arboricola is an example of synergistic interaction between diverse pathogen groups. Such pathogen-pathogen synergism, which results in more severe illness symptoms than expected, is critical for understanding microbial pathogenesis and evolution, as well as establishing efficient treatment measures. [17].

e) Other Pathogens

Oomycetes: A distinct microbial group that is classified as fungi. These are responsible for the devastating late blight disease of potatoes during the 19th-century Irish famines. This pathogen is concerned with one of the greatest mass migrations ever documented [10].
Nematodes: Microscopic worms inhabiting soil, some of which cause plant diseases either by piercing crop coats with their styles to feed, or by infiltrating plant interiors, where they drive plant division of cells, leading to tumors. In both situations, they struggle with plant cells for nutrients and water. [33].
Protozoa: Although only a few protozoa are Some plant infections, such as Phytomonas, have serious consequences. Species of this family live in palm xylem channels and produce withering problems. This is especially harmful to tropical countries wherein palms of coconut are an important financial source for both the cultivation of fruits and tourism. [11].

B. *Approaches for Identifying Plant Diseases*

To control the harmfulness of pathogens in its initial phase is very significant [90]. Before the advancement of digitalization, the process of recognizing pathogens was done by using traditional approaches like visual inspection by experts [78], and microscopic or biological examination in the laboratories. While these traditional methods are costly and time-consuming (Table 1). Building more powerful techniques for plant disease detection has been made possible through some digital approaches such as, Image processing [80] Back Propagation in Neural Networks deep learning techniques [8][73].

TABLE 1. LIMITATIONS OF TRADITIONAL METHODS FOR PLANT DISEASE DETECTION.

Method	**Advantages**	**Disadvantages**
Visual Observation	1. Simple and non-destructive 2. Can detect symptoms such as leaf spots, wilting, etc	1. May require trained eye for accurate identification 2.Limited to visible symptoms 3. May miss early or latent infections Continuous crop monitoring is required
Microscopic Examination	1. Can detect pathogenic fungi, bacteria, and iruses 2. Can assess disease severity and progression	1. Some pathogens may be difficult to visualize under the microscope 2. Requires laboratory setup and skills, 3. Can identify specific pathogens 4. Time-consuming process
Biological Examination	1. Can confirm the presence of specific pathogens 2. Can determine pathogen races or strains Can be used for quarantine and certification purposes	1. Requires specialized skills and equipment to perform assays 2. Time-consuming process 3. Some assays may be expensive or require sophisticated equipment 4. Costly

Image processing along with machine and deep learning methods enable the detection for crop diseases at their early stage. By analyzing high-resolution images of crops, these technologies are efficient in finding subtle symptoms and similar patterns associated with diseases. Machine learning techniques like SVM, KNN, CNN, Faster R-CNN, and Yolo are trained on large volume of real and labelled dataset, which makes them to accurately classify and detect specific diseases [8]. This improves the accuracy of disease identification, minimizing misdiagnoses and false positives. Deep learning models, Convolutional Neural Networks, for example [36] [75], can automate The method for examining images and detecting diseases. This reduces the manual effort required for visual inspection, making disease detection more efficient and scalable. Techniques such as image processing, machine and deep learning can be used to remote sensing data, such as satellite imagery or aerial photographs. This enables remote monitoring of large agricultural areas, providing a comprehensive view of crop health and disease distribution. All these techniques are efficient, accurate, and timely detection of crop diseases. They enable proactive disease management, optimize resource allocation, and improve overall crop yield and quality, leading to a more sustainable and productive agriculture industry.

C. The Machine Learning Techniques

Before identifying plant diseases earlier advancements of computers in terms of Image processing, AI, ML, and DL played a crucial role by enabling to provide of accurate, reliable, and scalable solutions for the identification of diseases, pathogens, viruses, and pests in plants sustainable agriculture sector. The early detection of plant disease helps for better quality and food production to train the machine learning model [83] [20], large and diverse datasets of plant images are collected. These datasets contain images of healthy plants as well as the ones infected with different diseases. However, these extensive large hyperspectral images required pre-processing as they contain a large number of bands and spot positions [64].

a) Image Processing

The various environmental factors like temperature, moisture content, etc. affect the images of plants in the dataset. However, the images are required to pre-process for better accuracy where numerous image processing techniques such as segmentation of images, image improvement, and classification of images can be used, and Feature extraction is used to identify the relevant features of the image. These features can be visual or numerical representations of prominent patterns, textures, colors, or shapes present in the image.

Image Segmentation: The entire image is separated into numerous portions, or segments, during image segmentation. This separation into sections is crucial because there may be certain areas of the image that are empty of data. As a result, processing of such photos may require more time if they are not segmented. Therefore, by splitting a picture into segments, we may only employ the most crucial ones for image processing, which saves time and processing power [27]. It simplifies The interpretation of an image and makes it easier to analyze by grouping regions that share similar properties as color, intensity, texture, or spatial proximity. Image segmentation can be challenging due to factors like noise, occlusion, varying lighting conditions, and complex object structures. Thus Segmentation can be performed on various levels, ranging from single-band to dual-band processing [56] [64]. Different image segmentation methods are used like threshold, region-based, edge detection, clustering, and watershed transform.

The collected input image is denoised and converted into to grayscale by using a simple threshold value [56] involves selecting a threshold value and classifying pixels based on whether their intensity values [27] are above or below that threshold. Accurate Image segmentation is an essential difficulty of computer vision. The region-Based Segmentation approach groups pixels into regions based on their similarity in terms of color, texture, or other features. It involves techniques such as region growing, region splitting and merging, and graph-based segmentation. In region-based object detection, a spot is separated into several areas called (K) as described by eq. (1). nonetheless, each pixel (p) for the image (I) only belongs to one area, as determined by its region-correspondence variable (Gould, Gao, and Koller n.d.),

$$Rp \in \{1,... ,K\}. \qquad (1)$$

The set of pixels Pr given by eq. (2) whose region-correspondence variable equals r, or the r-th region, is then all that remains.

$$Pr = \{p : Rp = r\} \qquad (2)$$

The image is separated into two smaller parts by the modified region-based active contour models (ACM), and then among the numerous subregions, the image is further separated into two smaller areas. before the ending condition is met [49]. Edge detection identifies boundaries between different objects in an image. It relies on detecting sudden changes in pixel intensity or gradients. This approach takes into account both the intensity of the surrounding pixels as well as the current pixel intensity value. Sobel operator, Canny operator, and Robert's operator are three widely used edge-based approaches [27]. Based on their closeness in feature space, pixels are organized into clusters in clustering-based segmentation [63]. Non-hierarchical clustering like K means is the most frequently applied clustering algorithm for picture segmentation. Instead, of representing a picture with hundreds of pixels, image segmentation uses a few key regions. Additionally, in the clustering technique for image segmentation, pixels that fulfill the criteria are grouped into one cluster, while pixels that don't are spread across several groups, as illustrated in fig. (1).

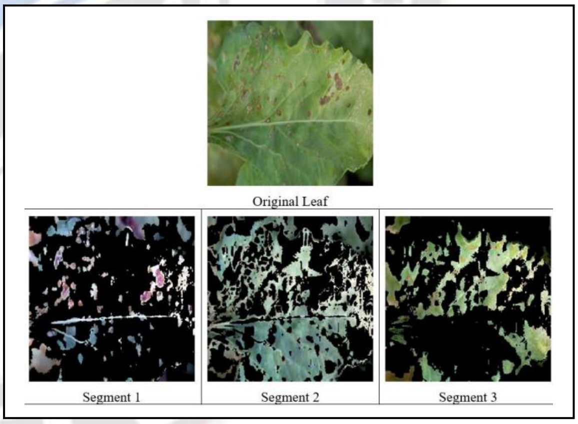

Fig.1 Clustering-based image segmentation [3]

One approach is utilizing the Watershed Transform for image segmentation in image processing which separates an image into various areas according to its color or intensity characteristics. The Watershed Transform is a mathematical morphological operation that treats the image as a topographic relief map [43], where the intensity values represent the height of the terrain. The Watershed Transform starts by identifying the local minima in the image, which are considered as the "seeds" for the catchment areas. Then, a flooding process is performed, where neighboring pixels are iteratively assigned to the catchment areas based on their intensity values. As the flooding process proceeds, the catchment areas gradually expand and merge, until all the pixels in the image are assigned to a specific catchment area.

Image Augmentation: Image enhancement techniques are essential in image processing to improve visual quality, enhance visibility, highlight important features, remove noise and artifacts, prepare data for analysis, and to restore degraded images [46]. These techniques play a vital role in fields like, agriculture, healthcare, surveillance, remote sensing, and many other applications where clear and high-quality images are crucial for analysis and decision-making. Techniques in the spatial and frequency domains are two different approaches used in image processing and analysis [46].

Spatial domain methods: The representation of an image is a continuous function of pixel intensities over space. The pixel values are directly operated upon by spatial domain algorithms and their neighborhood relationship in the image. Image Filtering like blurring filters, sharpening filters, and edge detection filters are convolution-based filters applied to an image to suppress specific features. Contrast stretching, histogram equalization, and dynamic range compression are employed to boost the total visual fidelity of the image by adjusting the pixel intensities. Depending on the sort of disturbance and how deeply it is ingrained in the image, noise will have an effect upon the image's quality. Digital photographs typically contain the noise categories Gaussian, Salt & Pepper, Speckle, Poisson, and Quantization. Using filters like the Mean, Median, and Wiener filters, noise, distortions and other traces are eliminated from photographs during the restoration process to be able to retrieve the original information [46].

Frequency domain Methods: The use of the Fourier transform method, portrays an image through its frequency components. It changes an image's spatial representation into a frequency representation, enabling depth-in-frequency content for the image. This technique breaks an image down into its constituent frequencies and reveals details about global patterns and frequency-related characteristics. In order to denoise, blur, or sharpen images, filters can be built and used in the frequency domain to selectively enhance specific frequencies. Filters, including Gaussian, bilateral, or high-pass ones, to enhance certain aspects of an image or get rid of undesirable artifacts. While using techniques like the Discrete Cosine Transform (DCT) to remove unnecessary data and take advantage of frequency redundancies, the image is compressed into a more compact representation [32].

Classification of Images: The separation of images involves grouping or identifying captures according to their visual content into many set-in-stone groupings. It entails educating a deep learning or machine learning model to spot patterns and features in images that are characteristic of particular classes. A dataset of tagged images is given to an algorithm or model, and each image is assigned to the appropriate class. The model develops a decision boundary between several classes and learns to extract pertinent features from the images throughout the training phase. The model then assigns new, unseen images to the appropriate class using these learned attributes.

b) Decision Tree

A supervised ML approach called a decision tree is adapted to solve problems related to regression and classification. The structure it creates is a A tree mimics a schematic, with each internal node representing a characteristic, each branch representing a decision rule, and every node in the leaf representing the result or class label [66]. The algorithm selects the feature that offers the best split at each node in a way that maximizes information gain or minimizes impurity at each node [85], leading to the purest leaf nodes (homogeneous samples). It does this by using a training dataset to partition the data recursively based on various features. Numerous measures, including Gini impurity by eq. (3), entropy by eq. (4), and misclassification error by eq. (5), are used to quantify the impurity or classification error.

$$\text{Gini}(n) = 1 — \sum(p\_i)^2 \tag{3}$$

$$\text{Entropy}(n) = — \sum(p\_i * \log2(p\_i)) \tag{4}$$

$$\text{Misclassification error}(n) = 1 — \max(p\_i) \tag{5}$$

where the probability of class i at a given node is denoted by p_i, and n is the node.

Root Node (R): The topmost node in the tree, which represents the initial decision.

Internal Node (I): Nodes that make decisions based on a feature and have child nodes.

Leaf Node (L): Terminal nodes that represent the final decision or a class label.

The mathematical structure of the decision tree is represented as a binary tree.

Algorithms: DT

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At the root node:
If (Feature A <= Threshold X): child node in left
Else: visit the child node in the right
At the child node in the left:
If (Feature B <= Threshold Y): Go to a leaf node with a predicted value/class
Else: Go to another internal node or leaf node
At the child node in the right:
Visit another leaf node
```

c) Support Vector Machine

Regression analysis and classification are two applications for the supervised machine learning method known as Support Vector Machine (SVM). Both binary and multi-class classification issues shown in Fig. (2) and fig. (3) can be solved using it [60]. In a high-dimensional feature space, SVM creates a hyperplane [40] or a collection of hyperplanes [1]. The data points are divided into various classes using these hyperplanes [68]. Finding the ideal hyperplane that maximally divides the classes and performs well on previously unknown data [39].

The training dataset with N data points each represented by a feature vector X and a corresponding label Y. In binary classification, Y can take two values -1 or 1, representing the two classes. SVM seeks to locate a hyperplane in the feature space that separates the data elements of different classes with maximum margin. A weight vector P defines this hyperplane. and a bias term a as described in eq. (6). n:

$$P.X + a = 0 \quad (6)$$

where "." dot is the product between two vectors.
Now, for each data point (X_i, Y_i) in the training set, define the constraint as mentioned in eq. (7).

$$Y\_i * (P. X\_i + a) >= 1 \quad (7)$$

This constraint ensures that the point of data lies on the appropriate side of the decision boundary with a margin of at least 1. The goal of SVM is to identify the optimal values of W and b that satisfy these constraints and maximize the margin.
To find the optimal values, formulate the SVM problem as an optimization problem with the objective function as described by eq. (8)
minimize (1/2) * ||P||^2
subject to
Y_i * (P.X_i + a) >= 1 for all i = 1…….n (8)
While adhering to the limitations, this objective function seeks to minimize the weight vector W's norm. Since it's a convex optimization issue, methods like gradient descent and quadratic programming can be used to solve it quickly.

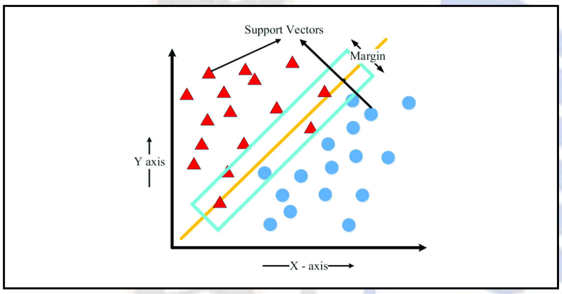

Fig. 2 SVM-based binary classification [79]

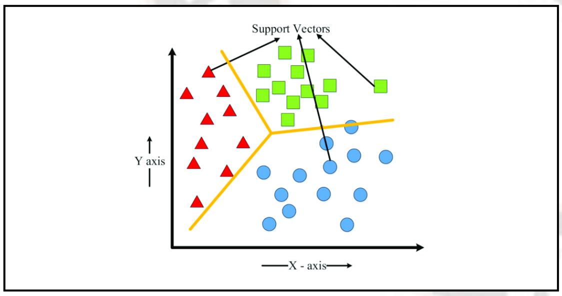

Fig. 3 SVM-based Multiclass classification [79]

d) KNN Classifier

a non-parametric method that operates without assuming anything regarding the distribution of the underlying data. The "K" in KNN stands for the quantity of closest neighbors that are taken into account while generating predictions [9]. It operates under the tenet that comparable data points typically have comparable target values or belong to the same class. The algorithm measures the similarity between data points using a distance metric, like the Euclidean distance [9] [92]. The steps involved in finding the optimal K-nearest point as shown in Fig. (4)

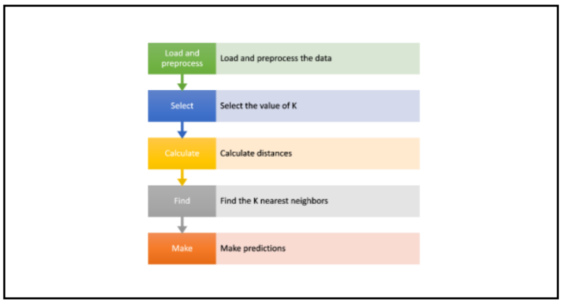

Fig. 4 Steps in KNN Classifier

D. *Deep Learning Techniques*

a) ANN

Deep learning is an artificial neural network-based subset of machine learning. ANN, often called as Neural Networks, which are employed for a variety of tasks, including classification, regression, clustering, and pattern recognition [41][55][72]. ANN is made up of nodes that are interconnected and structured in layers, and each node applies a mathematical function to the weighted total of its inputs to produce an output. an artificial neuron takes multiple inputs, multiplies each input by a corresponding weight, sums up these weighted inputs, applies a non-linear activation function, and produces an output given by eq. (9).

$$y = f\sum([i = 1]^n w_i . x_i) + b \quad (9)$$

where:
- y is the neuron's output.
- The function of activation is f.
- Weight connected to input x_i is denoted by w_i.
- The biassed referrals is b.

Numerous fields, including pattern recognition, natural language processing, image processing, epert systems, robotics, gaming, drug discovery, and genomics, use Artificial Neural Networks of various types, including single-layer, multi-layer perceptrons, ,probabilistic neural networks, and Convolutional Neural Networks radial-basis function networks [31].

b) CNN

CNNs are designed to automatically and adaptively learn spatial hierarchy characteristics from input data [83]. They consist of multiple layers, each performing a specific task in the process of feature extraction and classification [79] [1] as shown in fig. (5).
Convolutional Layers: These layers apply convolutional filters to the input elements. Each filter scans a small area of input to detect specific features. As the filters convolve across the input, it produces feature maps that capture different patterns and structures.
Feature Map (also known as an activation map) from the previous layer, denoted as F_in, with dimensions (P_in x Q_in

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x Q_in), where P_in is the height, Q_in is the width, and R_in is the total number of inputed channels.

Pooling Layers: These strata diminish the multifaceted nature of space of the feature maps produced by the layers of convolution. Pooling can be done through operations like max pooling, where only the maximum value within a pool is retained, or average pooling, where the average value is computed. Pooling helps to extract and retain the most crucial elements while minimizing computational complexity.

Activation Functions: These functions introduce non-linearities to the outputs of the convolutional and pooling layers described in eq. (10). Common choices incorporate the function of the Rectified Linear Unit, which assign minus values to zero, softmax functions [79].

$$F\_i(c, d) = \max(0, F\_i(c, d)) \qquad (10)$$

where c and d are spatial coordinates and F_i is feature map.

Fully Connected Layers: These layers establish connections between each neuron in a layer and every other layer's neuron., mimicking a traditional neural network. To learn high-level representations based on the extracted features, fully connected layers are usually positioned towards the end of the network.

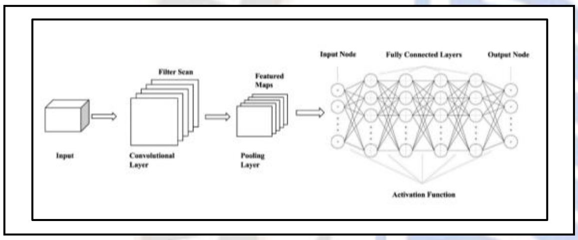

Fig.5 Layers involved in CNN

c) AlexNet

The deep CNN architecture known as AlexNet was created by Geoffrey Hinton, Ilya Sutskever, and Alex Krizhevsky. AlexNet comprises five convolutional layers among its eight layers, followed by three fully connected layers which was winner of ILSVRC-2012 competition. The network uses rectified linear units (ReLU) as activation functions, which helps in training faster compared to traditional activation functions like sigmoid or tanh. It uses data augmentation and dropout techniques, which enhances generalisation and limit overfitting.

d) VGG-Net

The Visual Geometry Group Network or VGG-Net [4], is an intricate CNN design intended for image classification applications. In 2014, the Visual Geometry Group at Oxford University developed it. With the addition of some max polling and dropout layers, VGGNet was created to increase the depth of CNN to thirteen convolutional layers, hence improving the performance of AlexNet. In contrast to AlexNet, which placed second in the ISLSRVC-2014 competition, VGGNet changed the size of its filters [22]. There are other variants of VGG-Net, however the most often used one is called VGG-16. It includes 16 weight layers, consist of three fully connected layers and thirteen convolutional layers [7], In addition, VGG-19 has nineteen weight layers.

e) GoogleNet

GoogleNet released The term "inception modules," also known as inception V-1, refers to a grouping of several convolutional filter sizes combined into a single layer. This enables the network to simultaneously recognize features at many scales and record various spatial information levels. GoogleNet has a novel 22-layer network architecture that includes a stack of several inception modules. In comparison to earlier architectures, it greatly lowered the quantity of parameters and still obtained good accuracy on the ImageNet dataset. Because of its effectiveness, GoogleNet used for real-time applications on devices with limited resources.

The table provided shows the results of the evaluated performance comparison between baseline CNN, AlexNet, VGGNet, and GoogleNet for the nine tomato plant disease types (tomato leaf mould, tomato early blight, tomato late blight, tomato mosaic virus, tomato target spot, tomato bacterial spot, and viral leaf curl yellowing). The increase in CNN layers leads the deep learning algorithm perform better, as seen in fig. (6).

TABLE 2. PERFORMANCE AND ERROR RATE MEASUREMENT OF DL ARCHITECTURES [22]

DL Architecture	**No. of CNN-Layers**	**Performance**	**Error Rate**
Baseline	2	84.58%	0.47
AlexNet	5	91.52%	0.51
GoogleNet	22	89.68%	0.30
VGGNet	13	95.24%	0.17

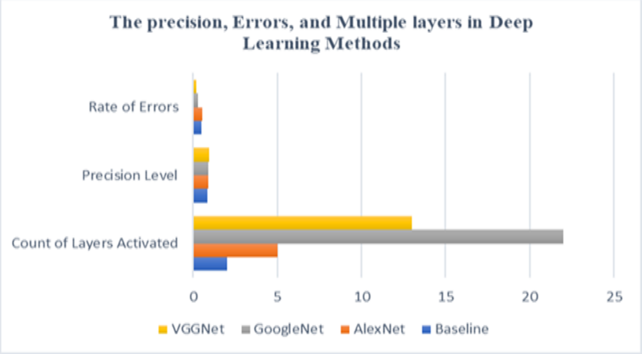

Fig.6 Precision, errors, and multiple layers in deep learning methods

III. RESULTS AND DISCUSSION

The results of several machine and deep learning techniques that are utilized by many researchers to diagnose plant diseases are listed in Table 3. These algorithms use pattern recognition and classification to identify and diagnose a range of plant diseases, either singly or in combination, to construct plant disease detection systems. The comparative study assesses the efficacy of different algorithms and approaches in a comparable space, as shown in Figure (7) and (8).

TABLE 3. REVIEW OF ML AND DL TECHNIQUES

Sr. No	Method Used	Accuracy	Plant	Infected with Disease
1	GLCM [70]	91.37%	Mango	Anthracnose, Powdery Mildew, Doney Mildew
2	GLRM [70]	86.71%	Mango	Anthracnose, Powdery Mildew, Doney Mildew
3	Decision Tree [37]	97.58%	Khasi Mandarin Orange plants	Citrus Tristeza Virus (CTV)
4	Enhanced-Decision Tree[37]	98.10%	Soybean	stem-blight
5	SVM [68]	76.00%	Soybean	Brown spots and bacterial blight, Soybean Mosaic Virus, Downy Mildew.
6	SVM [40]	90.00%	Chilli	cucumber mosaic
7	SVM [38]	88.10%	Tomato	Spetoria Leaf Spot, Leaf Mold, and Late Blight
8	SVM [3]	92.85%	Sevral Plants	Alternaria, Alternata, Anthracnose, Bacterial Blight, and EarlyLeaf Spot
9	KNN [37]	99.36%	Khasi Mandarin Orange plants	Citrus Tristeza Virus (CTV)
10	KNN [68]	64.00%	Soybean	Brown spots and bacterial blight, Downy Mildew, Soyabean Mosaic Virus
11	KNN [9]	89.90%	Citrus	Citrus Tristeza virus
12	Mahalanobis Classifier [70]	83.17%	Chilli	Gray mildew, smut, red hot, leaf spot.
13	ANN Classifier [70]	84.11%	Beans	Rust, early and late blight dot
14	CNN [68]	96.00%	Soybean	Soybean brown patches and bacterial blight Mosaic Virus, Downy Mildew
15	CNN- Three-layer classifier [56]	89.00%	coffee plants	Cerscospora, Leaf Rust
16	CNN- SDGM [79]	99.60%	Rice	Blast, Brownspot, Tungro
18	AlexNet [22]	91.52%	Tomato	Mosaic virus, late blight, leaf mold, and target spot
19	GoogleNet [22]	89.68%	Tomato	Mosaic virus, late blight, leaf mold, and target spot
20	VGGNet [22]	95.24%	Tomato	Mosaic virus, late blight, leaf mold, and target spot
21	SVM and CNN [1]	95.00%	Potato	Early and late spot

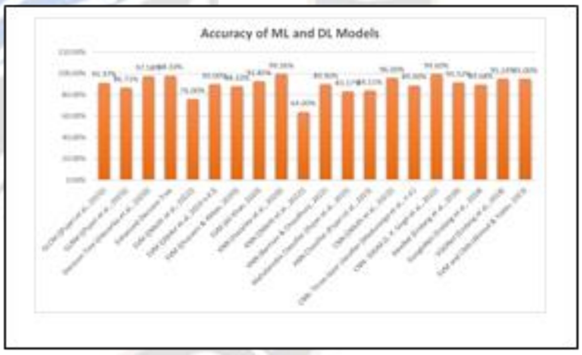

Fig. 7 Comparative analysis of ML and DL algorithms

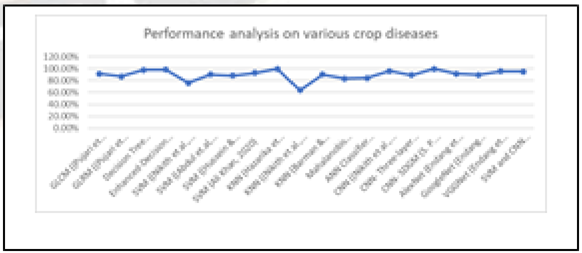

Fig.8 Performance analysis of ML and DL models on various crop diseases detection

IV. CONCLUSION

The various AI approaches most likely machine and deep learning strategies strongly applied for plant disease detection have been condensed into this review article. Furthermore, this article classifies techniques based on their level of accuracy, making it easier for researchers to utilize individual or conjunction methods for effective outcomes. These techniques are constantly growing and improving with advancements in the fields of research on machine and deep learning, enabling greater precision and effectiveness in the detection and management of plant diseases. Following an in-depth assessment, it emerged that deep learning methods have shown the best results in plant disease detection compared to traditional machine learning algorithms. With their ability to automatically extract intricate features from plant images, deep learning models can achieve higher accuracy and faster processing times. The future scope of deep learning algorithms for plant disease identification is promising. As technology advances, more sophisticated deep learning architectures can be developed that are specifically tailored for plant disease detection. These models can leverage larger datasets and utilize more advanced deep learning techniques. Deep learning algorithms can be combined with other techniques which provides the accuracy and reliability of disease detection can be further improved.

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