REVIEW

Application of machine learning: a recent advancement in plant diseases detection

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Abstract

The world population, and thus the need for food, is increasing every day. This leads to the ultimate question of how to increase food production with limited time and scarce land. Another obstacle to meet the food demand includes the stresses a plant goes through. These may be abiotic or biotic, but the majority are biotic, i.e., plant diseases. The major challenge is to mitigate plant diseases efficiently, more quickly and with less manpower. Recently, artificial intelligence has turned to new frontiers in smart agricultural science. One novel approach in plant science is to detect and diagnose plant disease through deep learning and hyperspectral imaging. This smart technique is very advantageous for monitoring large acres of field where the availability of manpower is a major drawback. Early identification of plant diseases can be achieved through machine learning approaches. Advanced machine learning not only detects diseases but also helps to discover gene regulatory networks and select the genomic sequence to develop resistance in crop species and to mark pathogen effectors. In this review, new advancements in plant science through machine learning approaches have been discussed.

Keywords: diagnosis, disease, hyperspectral imaging, machine learning

Introduction

The food demand is scaling upward day by day to meet the demands of an increasing population. But food security is threatened by various factors like unpredicted climate change, biotic and abiotic stresses, etc. Of all the alarming factors, biotic stress due to pathogen attacks is the major one. Plants are vulnerable to many foreign pathogen attacks. Crop plants can be affected by more than one pathogen at a single time. The diverse nature of crop plants and the varied symptoms shown by the plants, onset of disease diagnosis are not possible by only optical observation. Sometimes a plant pathologist also faces problems identifying a disease correctly. Reports have shown that more than 50% of crop loss is mainly due to pests and diseases which can have negative consequences on all the entrepreneurs, industries, and mostly small farm holders whose entire livelihood depends on agriculture (Harvey *et al.* 2014). Additionally, more than half of the population of developing countries are hungry and poor, hence making developing countries vulnerable to pathogen-derived disruptions in the food supply chain (Sanchez and Swaminathan 2005). Hence, rapid detection, accurate diagnosis, and timely management of plant diseases can be the only solution for profitable agriculture. Therefore, in the modern era of agriculture, the inclusion of smart technologies can be a new frontier in plant disease detection and diagnosis.

Efforts have been made in past years to prevent crop loss through integrated pest management (IPM). Rapid and correct identification of diseases is the first and foremost step for an effective crop protection strategy (Ehler 2006). Many governments and non-governmental organizations (NGOs), agricultural institutions, extension officers, or plant clinics have been working for a long time in rural and urban areas to avoid crop loss. Recently, the launching of a wide range of digital platforms and online services has made it easier for both farmers and organizations to disseminate information more quickly (ITU 2015). Nowadays, the increasing use of the internet and mobile phones throughout the world has made a "one-click solution" approach for farmers. An automated computational plant disease detection system can facilitate and assist a pathologist with easy disease detection (Mohanty *et al.* 2016). A simple and user-friendly system could be a novel tool for all farmers of the world who are facing difficulties due to the scarcity of infrastructure. Entrepreneurs and industries having acres of land can also reduce time and labor costs with the use of smartphone-based approaches. Advanced HD cameras, extensive built-in software, and storage capacity have made it possible to create an effective plant disease diagnostic tool.

The discovery of various graphical processing units (GPU) and advancements in machine learning-based artificial intelligence has gained so much popularity due to the development of many improvised models and methodologies leading to the formation of a new category termed deep learning (LeCun *et al.* 2015). Both machine learning and deep learning fall under the broad category of artificial intelligence (AI). Deep learning is a sub-category and an updated version of machine learning. Machine learning (ML) uses a wide range of algorithms, analyzes and then make decisions. On the other hand, deep learning creates an 'artificial neural network' by organizing the data to make an intelligent decision.

Deep learning models have highly advanced and feasible sectors like voice and image recognition. It analyzes a high volume of data to assist other related applications (LeCun and Bengio 1995; Ciresan *et al.* 2011). Although the applications are limited, these models are used for easy and rapid detection of plant diseases. More exploration and incorporation of recent advanced techniques can open new ways in agriculture. Multiple tasks can be performed by these deep learning approaches such as leaf retrieval, image segmentation, deep analysis of high-volume data, and identification of the problem. The first step is leaf retrieval which is challenged by various factors. The 2nd step, image processing is the most important step since the accurate detection and identification of diseases mainly depend on this step. Image processing is carried out by the Chan-Vese algorithm which is the most effective one for proper segmentation. The last step is carried out by migration learning algorithms which analyze a set of data of diseased leaves to identify the disease.

Convolutional Neural Networks (CNNs), being a significant and powerful technique, can perform pattern recognition and can analyze a large volume of data. Thus, CNNs are one of the basic tools of deep learning used in agriculture. There is much evidence that these CNNs include effective systems to identify plants based on the morphological pattern of the leaves (Grinblat *et al.* 2016). In 2016, Sladojevic and his co-workers developed a model having a 91 and 98% success rate to detect 13 diseases of five different plants by using databases available on the internet (Sladojevic *et al.* 2016). Satisfactory performance was observed with the CNN model, developed by Fuentes and his co-workers for the detection of nine different tomato pests and diseases (Fuentes *et al.* 2017).

Application of machine learning and deep learning in plant-pathogen interaction

Applications of machine learning can be used for non-invasive plant disease detection, classification and prediction technology. Disease and pest severity and its estimated loss are easily calculated through machine learning (Popp *et al.* 2013). Image processing and remote sensing can give a high impact as light reflectance of a healthy leaf which will differ from that of a stressed leaf compared to visual analysis. These modern techniques can be very useful and accurate crop protection strategies. Chlorophyll fluorescence sensors and thermography are two important measures used in leaf surface temperature and in chlorophyll activity analysis. Both of the aforesaid sensors are very powerful for detecting stress responses, but different pathogens are not accurately distinguishable. Multispectral or hyperspectral sensors are considered to be two complementary techniques. Multispectral remote sensors construct relatively few bands. Radiometric and geometric adjustments of the data are required to classify symptomatology (Landgrebe 2003). Hyperspectral imaging constructs hundreds of narrow bands par pixel in the outcome image which accurately distinguish various symptoms (Lowe *et al.* 2017). Pre-processing and dimensionality reduction of hyperspectral imaging data is impactful to avoid the of dimensionality (Bruce *et al.* 2002). Inefficient technology costs, therefore increasing maximum storage capacity data through supercomputing is the trend of progress in this streamline (Table 1).

Table 1. Applied machine learning technology under different disease prediction models

Application	Model	Details	References
Septoria blotch disease on wheat	RF	The proposed model applied by Spectroradiometer, IR thermometer and Chl fluorescence for measurements. In this model 119 diverse vegetables were studied with respect to photosystem II, quantum quantity and leaf surface area	Odilbekov *et al*. (2018)
Rape oil seeds infected by *Alternaria* (under glass house conditions)	NN	The model consisting of two linear hyperspectral scanners and a thermographic camera. The wavelengths in the range of 430–2376 nm were employed for classification, with increments of c. 32 nm per pixel. The second derivative is practiced which estimates the switch in the slope of the curve	Baranowski *et al*. (2015)
Tomato infected with *Phytophthora infestans*	NN	Measurements of hyperspectral images from soil and canopies. Utilization of wavelength, soil value and mean spectral values	Wang *et al*. (2008)
Easily detect infected plants from clusture caused by the causal pathogen *Oidium neolycopersici*, by using thermal image screening	SVM	A thermal imaging camera and pair of visible light imaging cameras. Features utilized in classification are standard deviation of temperature values measured by luminance, mean values of cyan and yellow color and a channel as well as disparity (depth information)	Raza *et al*. (2015)
Plant disease detection and diagnosis with the application of deep learning to differentiate between 58 classes of plant species and diseases	CNN	The collected image data of leaves from open data resources of 25 plant species	Ferentinos (2018)
The pre-planting risk prediction of *Stagonospora nodorum* blotch	MR, NN, RF	Prediction using longitude, cultivar resistance, latitude, preceding crop, seed treatment, tillage type and wheat residue, seeding rate and 431 unique disease cases	Mehra *et al*. (2016)

Earlier studies have demonstrated the utilization of less than 100 to more than 10,000 images for the testing and training of different DL models (Moshou *et al.* 2004; Ferentinos 2018).

Application of machine learning based on wide genome scale

Machine learning has proven to be one of the major players in developing genomics such as whole genome sequencing driven by data explosion. In addition to this, the application of ML has spread to omic studies such as proteomics, metabolomics, structural genomics and regulatory genomics (Yip *et al.* 2013; Libbrecht and Noble 2015; Angermueller *et al.* 2016; Zou *et al.* 2019). The application and function of machine learning networks is also observed in the prediction of fungal and bacterial pathogen effector proteins, selection of resistance gene or genes against several pathogens and analyzing different gene regulations, etc. (Table 2). Several ML models can manage a wide range of "numerical algorithms" and algorithms which confer selection of resistance genes in plants, its function, rate of disease severity and some complex traits (Gonzalez-Camacho *et al.* 2018). Moreover, ML models include advance technologies like

hyperspectral imaging and genomic selection which have wider applications in plant science (Crossa *et al.* 2017).

Various models for plant disease detection

GoogLeNet

It is a 22-layer deep learning network and its architecture can solve computer vision tasks like object recognition and image classification, presented in the ImageNet Large-Scale Visual Recognition Challenge 2014. Nowadays, it is used for computer vision tasks such as adversarial training, face recognition, and detection. The input layer of this architecture takes an image of 224 × 224 dimensions. It achieves efficiency by simultaneously reducing the input image and retaining important spatial information. This architecture is a powerhouse with high computational efficiency. GoogLeNet architecture consists of nine inception modules and two max-pooling layers between inception modules. The main goal of these max-pooling layers is to downsample the input through the reduction of the width and height of the input data. Another effective process is reducing the input size by

Table 2. Machine learning models applied for the prediction of genomic data for plant pathogen interaction and effector proteins for sub-cellular localization

Description	Model	References
Forecast of bacterial type-IV secreted proteins by the application of 100 C-terminal residues. The negative training sets of non effectors were generated by arbitrarily choosing proteins from the organisms represented in the positive training set	SVM	Wang *et al.* (2014)
The creation of gene regulatory network of the pathogenic fungus *Fusarium graminearum* out of many transcriptomic datasets	BNI	Guo *et al.* (2016)
Molecular research for rust resistance by using genomics which encompasses example scripts of ML models for forecasting resistance against rusts in wheat	RF, SVM	Ornella *et al.* (2017)
It helps to identify effector proteins in the apoplast. It was found that effector has synonymous characterization with the localized proteins on the same loci. Thus, it can use larger amounts of training data from plants, neutralizing the low number of training examples of apoplastic effectors	RF	Sperschneider *et al.* (2018)
Assumption of bacterial type-III secreted proteins with application of deep learning trained on the 100 N-terminal residues. Negative training data belongs to type-I to type-VIII secreted proteins	DCNN	Xue *et al.* (2018)
A computational interactome for arranging vital genes correlated with complex agronomic characters/traits in rice (*Oryza sativa*) employing 485 transcriptomic datasets	RF	Liu *et al.* (2017)
Recognition of numerous stress conditions through stress-responsive genes and pinpoint candidate genes for broad resistance in rice (*Oryza sativa*). Classify if stress response is abiotic or biotic trained on contrastively expressed genes from 559 microarray samples from 13 stress situations	SVM	Shaik and Ramakrishna (2014)

lessening the networks' computational load. Gaining a proper understanding of GoogLeNet architecture is very crucial to knowing the advancement of deep conv networks within the deep learning field.

Cifar-10

Cifar-10 is a collection of images used in several computer vision algorithms and machine learning. This dataset can be used to train a computer to recognize several objects. It contains 60,000 color images of 32×32 in 10 classes. There are 10,000 test images and 50,000 training images. It carries five training batches and one test batch. The training batches do not contain evenly distributed images and are in random order. The images in this dataset are of low resolution and allow researchers to try different algorithms.

AlexNet

This is a convolutional neural network architecture, introduced in 2012 for the composition of a consecutively stacked convolutional layer. This trained network uses graphical processing units (GPUs). It has eight layers, of which five are convolutional layers and three are fully connected. The special features of AlexNet are Multiple GPUs, ReLU Nonlinearity, and overlapping pooling. The multiple GPUs system carries half of the model's neurons on one GPU while the other half is on another GPU. It also requires less training time than other models. Similarly, this model uses a standard

function, i.e., Rectified Linear Units (ReLU) which takes less time and is six times faster than CNN using tanh function. Overlapping pooling can cause a reduction of error of 0.5% and can be harder to overfit.

ResNet-20

This model, Residual Network, was proposed in 2015 by Microsoft researchers. It requires skipping connections and connects directly to the output by skipping training of a few layers. The major advantage of this type of connection is, if any layer disturbs any of the performance, then it will be skipped through regularization. ResNet is far more accurate than other systems which also use skip connection such as highway networks, LSTM, etc. The approach behind this network is to allow the network to fit the residual mapping.

VGG16

VGG16 is a CNN model which was proposed by K. Simonyan and A. Zisserman from Oxford University. The whole dataset is comprised of more than 14 million images belonging to 1,000 classes. AlexNet is usually preferred by substituting large kernel-sized filters with multiple kernel-sized filters. The major disadvantage of this model is that it is very slow to train and has large bandwidth. This model is 533 MB which is a drawback. But still, it is used in many deep learning image classification problems.

Support vector machine (SVM)

SVM stands for support vector machine which uses classification algorithms for two group classification problems. It is an array of learning methods employed for regression, classification and outlier's detection. Its major advantage is its versatile nature which means several kernel functions can be specified. This module is effective in high dimensional spaces and effective where no samples are smaller than any of the dimensions. This module is memory efficient since it utilizes a portion of training points in the decision function. The major drawback is that this module's calculations use expensive fivefold cross-validation.

LeafNet

It is a plant identification system (Barré *et al.* 2017) that can recognize leaf images for species identification. This is a CNN-based identification model which has the ability to generate a better representation of leaf images than that of hand-crafted customized systems. This model can reduce the time spent by researchers to identify different species by recognizing their more domain-specific characters such as leaf venation, leaf edges, etc. The identification can be up to 850 leaf images per millisecond. The only drawback of this module is that it is very time-consuming to train this model for an extensive data set.

The process of machine learning

Lately, neural networks have been employed in many diversified domains as a paradigm of end-to-end learning. The neural network has produced diseased crops, associated diseases and disease progress maps since its output is very efficient. In the neural network prediction model, it needs numerical data input about disease incidence or disease severity and a disease progress model. Deep NN model can map from the insert layer to exit or output layer with accurate nodal values in successive chains. The main challenge of the NN model is to get accurate nodal and edge values by which a disease prediction model can be established properly. Modulation of the network parameters can alter the mapping area and direction for the training process (Mohanty *et al.* 2016). These processes are very computationally energizing and have been revamped drastically by both conceptual and engineering innovations (Le Cun *et al.* 2015 Schmidhuber 2015). In order to develop precise image classifiers for plant disease diagnosis, a standardized dataset of images of diseased and healthy plants is necessary. Until now, no such dataset has been freely available to the public. Therefore, after recognizing the problem, the PlantVillage project was initiated by accumulating 10,000 images of both diseased and healthy crop plants (Hughes and Salathe 2015). It has also made the dataset accessible to everybody. Mohanty and co-workers reported 26 diseases in 14 crop species employing 54,306 images with an enlarged neural network approach. They computed the performance of different models based on their potentiality of anticipating the crop disease pair very precisely and also reported 38 classes. The model accomplished a mean F_1 score of 0.9934 (overall accuracy of 99.35%) and hence it has been identified under three different headings: dataset description, measurement of performance, and visualization techniques. A schematic outline of machine learning procedure is shown in Figure 1.
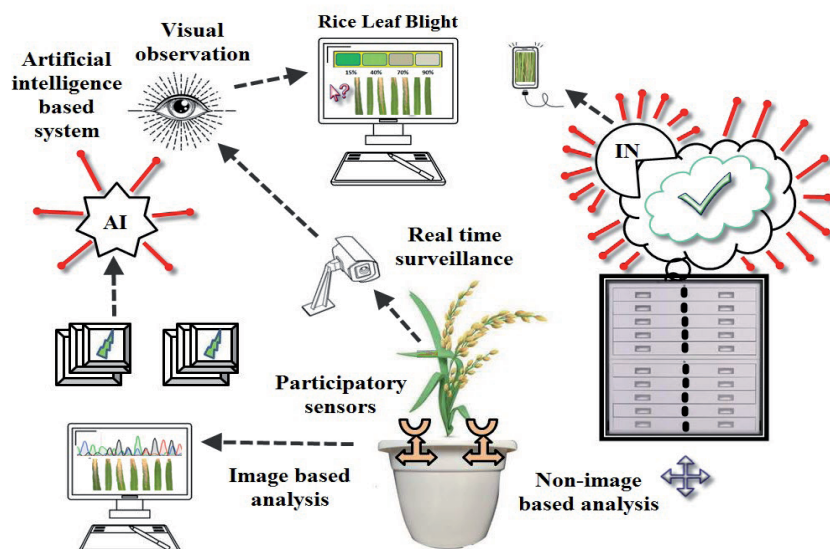

Fig. 1. Schematic representation of machine learning procedures

Dataset description

As previously mentioned, there were 54,306 images of plant leaves utilized for the dataset which were labeled into 38 classes. Each class label signifies a crop disease pair by submitting the image of the plant leaf. Images of 256 × 256 pixels were resized to conduct both the model optimization and assessment on these downscaled images. Throughout the experiments, they used three various versions of the PlantVillage dataset. They started with the colored version of PlantVillage data followed by the gray-scaled version and finally, they ran all the experiments of the segmented version of PlantVillage dataset. Minimization of the biases was done with a regulated collection of data by eliminating the subsidiary background information. Segmentation was performed automatically with the help of a script adapted in their dataset. They chose a technique based on a series of marks produced by scrutiny of color, brightness, and the saturation labels of different parts of the images in various color spaces. Fixing the color casts during processing was found to be very helpful in eliminating a few potential biases. This experiment was planned to evaluate whether the neural network learns the "notion" of the plant disease or if it simply learns the inherent biases in the dataset.

Measurement of performance

To confirm whether the whole approach suits the new data exactly and to make sure that there is no overfitting, they run the experiments on different ranges of test-train set splits, namely 20–80 (20% of the dataset as a whole for testing and 80% for training), 40–60 (40% of the dataset as a whole for testing and 60% for training), 50–50 (50% of the whole dataset used for testing and 50% for training), 60–40 (60% of the dataset as a whole for testing and 40% for training) and finally 80–20 (80% of the dataset as a whole for testing and 20% for training). It is important to note that in many cases, the PlantVillage dataset has several copies of images of the same leaf (taken from various angles), and has the mapping of 41,112 images of similar cases out of 54,306 images. Among all the combinations of the test-train splits, it was expected that all the images of the same leaf go either in the testing set or in the training set. Moreover, for all the experiments the mean F_1 score, mean precision, mean recall together with the overall precision were determined over the total period of training at regular intervals (i.e., at the peak of every epoch). They employed the mean F_1 score for the comparison of results across the series of experimental configurations.

Approach

There are two popular systems, AlexNet and Google-Net. Both of the aforementioned servers are used under the networking system. Krizhevsky *et al.* (2012) and Szegedy *et al.* (2015) used them to assemble a path named Image Net data base (Deng *et al.* 2009, Russakovsky *et al.* 2015). The design of the AlexNet architecture is similar to that of the LeNet-5 (LeCun *et al.* 1989) architecture. Usually, the LeNet architecture variants are comprised of an array of stacked convolution layers followed by connected layers. The ReLu non-linear activation units are connected with the normalization layer and a pooling layer of the convolution layers. AlexNet is comprised of five convolution layers, subsequently three completely connected layers, and eventually closed with a SoftMax layer. The first two convolution layers are connected (conv[1,2]) and are directly linked to a normalization and a pooling layer. The last convolution layer (conv5) is connected to a single pooling layer. The fully connected layer (fc8) of the adapted version of the AlexNet is comprised of 38 outputs which are identical to the number of classes in the dataset, which finally feed the SoftMax layer. The SoftMax layer can rapidly normalize the whole input which it receives from fc8, hence generating distribution of values over all 38 classes which add up to 1. Subsequently, the values can be explicated as the confidences of the neural network that submitted the input image denoted by the respective classes. All seven layers of AlexNet consist of a ReLu non-linearity activation unit linked with them, and the first two connected layers (fc[6, 7]) contain a dropout layer cognate with them, having a dropout ration of 0.5.

GoogleNet architecture is exceedingly deeper as well as wider with 22 layers. However, it has a noticeably lower number of parameters (~5 million parameters) than AlexNet (~60 million parameters). The important characteristic of GoogleNet architecture is the application of 'network in network' architecture (Lin *et al.* 2013) in the form of an inception module. Inception modules utilize parallel convolutions of dimensions: 1 × 1, 3 × 3, 5 × 5 including a parallel max-pooling layer, empowering it to hold diversified features in parallel. Lastly, a filter concatenation layer causes the output to connect with all the parallel layers. It treats one inception module out of nine inception modules all of which were employed in the version of GoogleNet architecture utilized in the experiment (Szegedy *et al.* 2015). The execution of both networks on the PlantVillage dataset were conducted by training the model from scratch in the first case, followed by adapting already trained models in the second case on the ImageNet dataset employing transfer learning. The re-initialization of the weights of the layers fc8 is

present in case of AlexNet and loss classifier layers are (1,2,3) present in case of GoogleNet. Sometimes in transfer learning, we do not limit .the learning of any of the layers while training the models. The vital point of difference between the two learning approaches, i.e., transfer vs. training from scratch, is that the initial state of weights of some layers allows the transfer learning method to employ a large quantity of visual knowledge which was already studied by the pre-trained GoogleNet and AlexNet models developed from ImageNet. Sixty experiments were conducted. Each experiment ran for a total of 30 epochs. One epoch is defined as the number of training duplications in which the specific neural network has completed a whole pass of the total training set. Based on empirical observations of all the experiments it was concluded that each time the learning converged well within 30 epochs. To compare all the findings from every experiment, the standardization of the hyperparameters such as stochastic gradient descent (solver type), 0,005 (base learning rate), learning rate policy: step (decreases by a factor of 10 every 30/3 epochs), 0.9 (Momentum), 0.0005 (weight decay), 0.1 (Gamma), Batch size: 24 (GoogLeNet), 100 (AlexNet) were employed in each experiment.

Each experiment was performed employing its own fork of Caffe (Jia *et al.* 2014) which is a rapid, open-source framework for deep learning. For results, the overall accuracy can be repeated utilizing a standard instance of Caffe.

Significance of deep learning (DL) models in plant disease detection

The DL module was developed after the introduction of AlexNet for detection, segmentation, and classification. Thereafter, the modified or improved DL architectures has gradually evolved with better results in visualization of the input image for distinct identification and classification of disease. Of the modified DL methods, the PlantVillage dataset has been more widely accepted and practiced since it consists of 54,306 images of 14 various crops having 26 plant diseases. The implementation of DL models is performed by two visualization techniques, Without Visualization Technique and Visualization Technique, which are described below.

Visualization techniques

Without Visualization Technique

Sibiya and Sumbwanyambe (2019) reported that the classification of disease in maize plants was carried out by employing CNN and histogram techniques to justify the model. Zhang *et al.* (2018a) reported that the identification of disease in tomato was done by using AlexNet, GoogleNet, and ResNet. After using every

model of CNN architecture, ResNet was regarded as the best. The execution of LaNet models for detection of banana diseases employed the F1-score and CA for the evaluation of the model in both the color and grayscale (Amara *et al.* 2017). Of all CNN-based modules, only five models were applied, AlexNet, AlexNetOWTbn, GoogleNet, Overfeat, and VGG architecture, of which the VGG was found to be superior over the remaining four models (Ferentinos *et al.* 2018). Eight different plant diseases were detected and identified by applying DL models, GoogleNet, ResNet-50, ResNet-101, Inception-v3, and InceptionResNetv2 along with three classifiers, K-nearest neighbor (KNN), Support Vector Machine (SVM), and Extreme Learning Machine (ELM) (Türkoğlu and Hanbay 2019). After a fair comparison of all the combinations of models and classifiers, ResNet-50 was found to be the best along with the SVM classifier based on the performance metrics of sensitivity, specificity, and F1-score. The identification and detection of diseases in cassava were done with a novel DL model called inception-v3 (Ramcharan *et al.* 2017). Different diseases of cucumber were classified by using two versions of CsNN with the highest accuracy being 0.823 (Fujita *et al.* 2016). Ancient plant disease identification and classification methods were substituted with the super-resolution convolutional neural network (SRCNN) (Yamamoto *et al.* 2017). Based on accuracy, of all the DL models, AlexNet architecture in particular was found to be effective for the classification of tomato plant diseases (Durmus *et al.* 2017). A comprehensive comparative analysis was done and it was found that six tomato diseases were detected by employing AlexNet and VGG-16 DL architectures (Rangarajan *et al.* 2018; Too *et al.* 2019). Hence in this technique, there was no visualization of identification of disease symptoms.

Through image visualization procedure

This technique utilizes the visualization of any symptoms on the leaf of diseased plants and hence we can better classify and identify the diseases (Brahimi *et al.* 2018). Visualization was performed with a saliency map which identified and detected 13 various diseases with the help of CaffeNet CNN architecture and attained classification accuracy of up to 96.30% which was much better than the SVM model (Sladojevic *et al.* 2016). To distinguish the spot of disease symptoms, a number of filters are used by CNN architectures like AlexNet and GoogleNet with the help of the PlantVillage dataset (open accessed) (Mohanty *et al.* 2016). Performance was determined by using F1 score, precision (P), recall (R) and gross accuracy. Grayscale, color and segmentation were used for the examination of performance and to make a vibrant comparison between two CNN architectures such as GoogleNet and

AlexNet. GoogleNet was found to be better. Activation of the visualization of the first layers significantly visualized disease spots. Olive plant diseases were detected and identified with the modified LeNet model which utilizes edges and segmentation maps to locate the spot of the disease (Cruz *et al.* 2017). Four cucumber diseases were successfully identified and classified and the accuracy was compared with random forest, support vector machines, and AlexNet models in which images were analyzed and disease symptoms identified accurately. A unique deep learning technique was developed which is referred to as a teacher or student network. It put forward an innovative visualization method to detect symptoms of plant diseases. The prediction percentage was calibrated by employing different detectors such as SSD, Faster-RCNN and RFCN. These were executed with well-known architectures such as AlexNet, VGG, GoogLeNet, ResNet-50, ZFNet,and ResNetXt-101 for relative learning and indicated that the best models of all architectures was the ResNet-50 model. Three CNN models, namely, ResNet-50, Inception-V2, and MobileNet-V1, were used to identify banana diseases and pests along with two detectors such as Faster-RCNN and SSD (Selvaraj *et al.* 2019). Different combinations of the CNN models were input with diseased plant images such as heat maps to anticipate the occurrence of a specific disease (De Chant *et al.* 2017). LeNet architecture was standardized to detect and classify diseases of the soybean plant (Wallelign *et al.* 2018). The occlusion technique was developed with GoogleNet which triggers the identification of symptomatic regions of the disease. GoogleNet outperformed the AlexNet model which was also used to try to detect tomato plant diseases (Brahimi *et al.* 2017). The identification and classification of wheat diseases were performed with two models, namely VGG-FCN and VGG-CNN, for the visualization of all the features in each block (Lu *et al.* 2017). The clustering method of the VGG-CNN model was utilized for the detection of fusarium wilt in radish (Ha *et al.* 2017). For detection of individual symptoms/spots of diseases, a DL model was developed and employed and also for identification, classification, and quantification of eight soybean stresses a deep CNN network was employed successfully (Ghosal *et al.* 2018; Barbedo 2019). Patches of symptoms on rice plants were identified by using CNN which implements future maps. There was a novel mobile application designed by using the deep residual neural network in which there was easy identification of diseases with the help of hot spot (Picon *et al.* 2019). A customized hot spot technique was designed based on the algorithm in which all the hotspots present are pooled by alteration in the segmented image to get color constancy. Moreover, all the procured hot spots were described with two descriptors, which can estimate the color of a particular disease and detect the texture of the hot

spots (Johannes *et al.* 2017). An advanced visualization method was developed with correlation coefficient and deep learning architectures VGG-16 and AlexNet (Khan *et al.* 2018). The dilation CNN model can be used for the identification and classification of cucumber diseases (Zhang *et al.* 2019b). LeNet (CNN model) was very effective for the identification of grape diseases which utilizes color space and different vegetation indices (Kerkech *et al.* 2018). For practical implementation of a more precise DL model there must be an actual/real background/environment. However, in most of the above-mentioned approaches, the chosen dataset considered plain background which is not an actual and naturalistic condition for the identification and classification of plant diseases (Amara *et al.* 2017).

Novel/customized deep learning (DL) models for disease detection in plants

There have been some reports that novel/customized DL models get better/distinct detection of plant diseases, namely, upgraded GoogleNet and Cifar-10 models whose efficiency compared with AlexNet and VGG. It was also reported that there was an exceptional overall accuracy of 98.9% (Zhang *et al.* 2018b). Liu *et al* (2017a, b) reported a new DL model which was pioneered to acquire higher levels of accuracy, i.e. 97.62% for proper identification of plant diseases than other models such as GoogLeNet, VGG-16, ResNet-20, SVM and AlexNet. The extended dataset covers 13 different factors such as brightness and sharpness, horizontal symmetry, rotation to different angles, alteration, etc. The complete dataset was transformed into PCA (principal component analysis) jittering and Gaussian noise. Moreover, the correct selection or choice of the dataset should be done in such a way that it must be possible to extend the dataset. A novel CNN architecture called LeafNet, developed to detect and classify diseases of tea, attained much more precision than MLP (Multi-Layer perceptron) and SVM (support vector machine) (Chen *et al.* 2019a). Two new DL models were commenced, namely, modified MobileNet and reduced MobileNet whose precision level was almost equal to the VGG model, whereas the reduced MobileNet achieved a classification precision of 98.34% and also had a lesser number of parameters than the VGG models which showed time efficiency (Kamal *et al.* 2019). PlantDiseaseNet is exceptionally valuable for the complex environment of the agricultural ecosystem (Arsenovic *et al.* 2019). A CNN model, known as VGG-inception architecture outperformed several DL models such as several versions of ResNet, VGG, GoogLeNet, and AlexNet. They can

also be used for inter-object/class detection for which the clear and distinct vision of symptoms of five various types of diseases in apple trees was possible (Jiang *et al*. 2019).

Modelling and algorithms

Solution framework

The whole plant disease identification model skeleton works on three basic deep learning steps: the localization of plant leaves, the segmentation of images, the extraction of plant disease, and the identification of disease (Fig. 2). To locate the diseased leaf in the complex environment the RPN algorithm is employed to train the leaf dataset, followed by formulating the regression neural network and classifying the neural network. The second step is the diseased leaf segmentation which is performed by Chan-Vese algorithm. This algorithm is based on the zero-level set and minimum energy function and with the help of iterative computation, the leaf contour is attained. Training of the pretrained transfer learning architectures is used to get diseased leaf recognition on a simple background.

Leaf localization

To classify neural network, the pivotal work is to detemine if the image within the boundary box is background or an object. During training Intersection over Union (IoU) is taken as a yardstick of classification, the

boundary box found to be IoU greater than 0.5 is denoted as an object and IoU less than 0.1 is considered to be background. IoU calibrates the relevance between the pretended leveled boundary box and the predicting boundary box. The formula of IoU is shown below:

$$IoU = S_1/S_2,$$

where: S_1 signifies the overlap region of predicting boundary box and S_2 signifies the total region of it.

Leaf segmentation

After obtaining the data of the previous steps the model does leaf image segmentation with the Chan-Vese algorithm. This algorithm aims at lessening the energy functions and getting blade profiles by using iterative calculations. The Chan-Vese algorithm works by the level set to fabricate the energy function to compel the region as a whole rather than to regulate the surface transformation with the help of explicit control speed *F*. The minimum summation of the variances between the gray values of the image outside and inside the contour and the length of the contour improved to make it coincide and is known as the energy function. The procedure for leaf segmentation is illustrated in the form of a flow chart (Fig. 3).

Disease leaf identification

In this method, training is completed quickly and carries out disease identification in a simple environment, decreasing the need for deep learning algorithms for
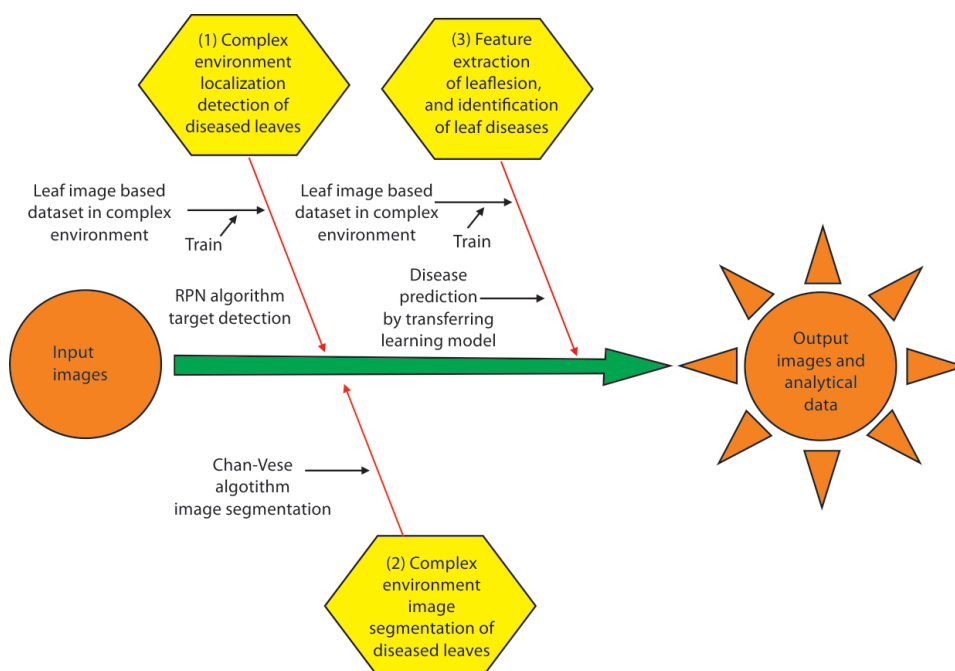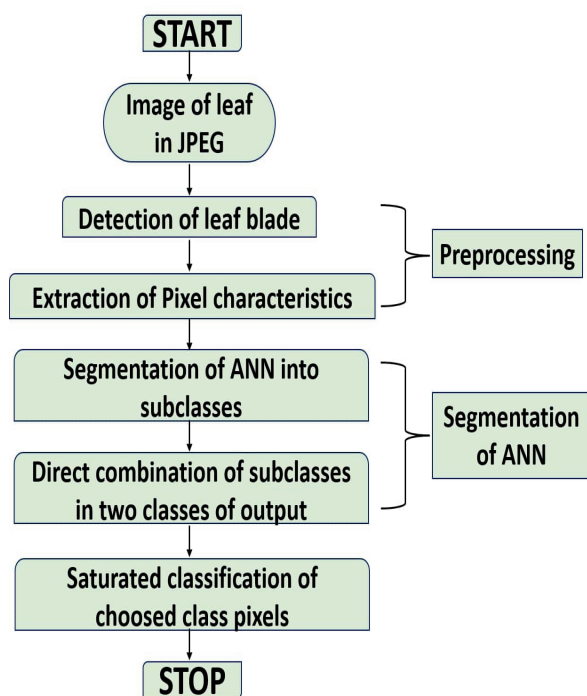

Fig. 2. Schematic representation of model frameworks

```
                    START
                      │
              Image of leaf
                in JPEG
                      │
         Detection of leaf blade ──┐
                      │            ├─ Preprocessing
       Extraction of Pixel characteristics ──┘
                      │
        Segmentation of ANN into ──┐
              subclasses           ├─ Segmentation
                      │            │    of ANN
      Direct combination of subclasses ──┘
          in two classes of output
                      │
       Saturated classification of
          choosed class pixels
                      │
                    STOP
```

Fig. 3. Flow chart on procedure of segmentation of leaf images (ANN – artificial neural network)

the hardware essentiality. By employing the transfer learning mechanism, the shallow neural network for the source task is changed to the neural network for a target task due to the reality of the shallow network which has equal features for different learning objects. The performance of transfer learning surpasses the new learning practices in convergence and ultimate findings.

Hyperspectral imaging in plant disease detection

Several imaging techniques such as multispectral imaging (Veys *et al.* 2019), thermal imaging, fluorescence, and hyperspectral imaging (Signoroni *et al.* 2019) have been developed to detect plant disease at early stages (Mahlein *et al.* 2019). Among all the imaging techniques the hyperspectral imaging technique has been the most relevant and effective one. The hyperspectral imaging (HSI) system can identify the region of interest, and a feature ranking-KNN (FR-KNN) model can generate adequate results which can differentiate diseased and healthy plants (Xie *et al.* 2017). The so-called redundancy problem was overcome by a separate selection procedure called orthogonal subspace projection (OSP) (Shuaibu *et al.* 2018). The HSI can identify all diseases that occur on the leaf of groundnut

by employing the sensitive bands and hyperspectral vegetation index (Chen *et al.* 2019b). The hyperspectral imaging can also detect tomato diseases by SVM classifiers whose performance was judged by sensitivity, specificity, F1 score and overall accuracy (Moghadam *et al.* 2017). HSI has been employed successfully in machine learning models for identifying disease (Hruska *et al.* 2018). The multispectral imaging techniques with the combination of the random forest (RF) classifier achieved a precision of 89.3% for wheat disease identification (Su *et al.* 2018). Plant diseases were detected by SVM based on the hyperspectral data and obtained an accuracy of up to 86% (Rumpf *et al.* 2010). Hyperspectral imaging of leaf blight of rice (causal organism – *Xanthomonas oryzae* pv. *oryzae*) and its severity detection is illustrated in Figure 4. Disease severity was scaled on a five-point scale followed by three times input and four times screening with the healthy leaves.

The deep learning approach based on the HSI was suggested by the contextual details which provide spectral and spatial characteristics (Ma *et al.* 2015). The novel 3D-CNN model was used for an accurate, fast, and efficient approach, which was formerly known as CNN techniques, assured the employment of both spatial as well as spectral data (Paoletti *et al.* 2018). The feature extraction protocol of the CNN model for HSI classification employed the dropout and L2 regularization method to avoid overfitting (Chen *et al.* 2016). The deliberate combination of DL models with the HSI by researchers enable them to distinctly see disease symptoms. Thereafter, a hybrid method was designed and standardized. It was comprised of DCNN, LR, and PCA and eventually had better findings (Yue *et al.* 2015). Several DL models such as 2D-CNN-LSTM/ GRU, LSTM/GRU and 1D/2D-CNN (2D-CNN had better results) were compared for better precision and to prevent overfitting. Consequently, to prevent overfitting, an innovative and advanced method, i.e. 2D-CNN-BidLSTM/GRU was proposed for the HSI which executed a 0.75 F1 score and 0.73 accuracies for identification of wheat diseases (Jin *et al.* 2018). To detect symptoms before their complete appearance on the tomato plant, there was a novel DL technique called generative adversarial nets (GAN) (Wang *et al.* 2019). For detection of potato infecting viruses, the DL on HIS attained remarkable values of recall (0.88) and precision (0.78) (Polder *et al.* 2019). Symptomatological characterization of wheat leaf, using Dl architecture called multiple Inception-Resnet models which analyze both spatial as well as spectral information, attained an accuracy of 85% which is substantially higher than that of the RF-classifier (77%) (Zhang *et al.* 2019a). The schematic representation of hyperspectral imaging is provided in the form of a flow chart (Fig. 5).
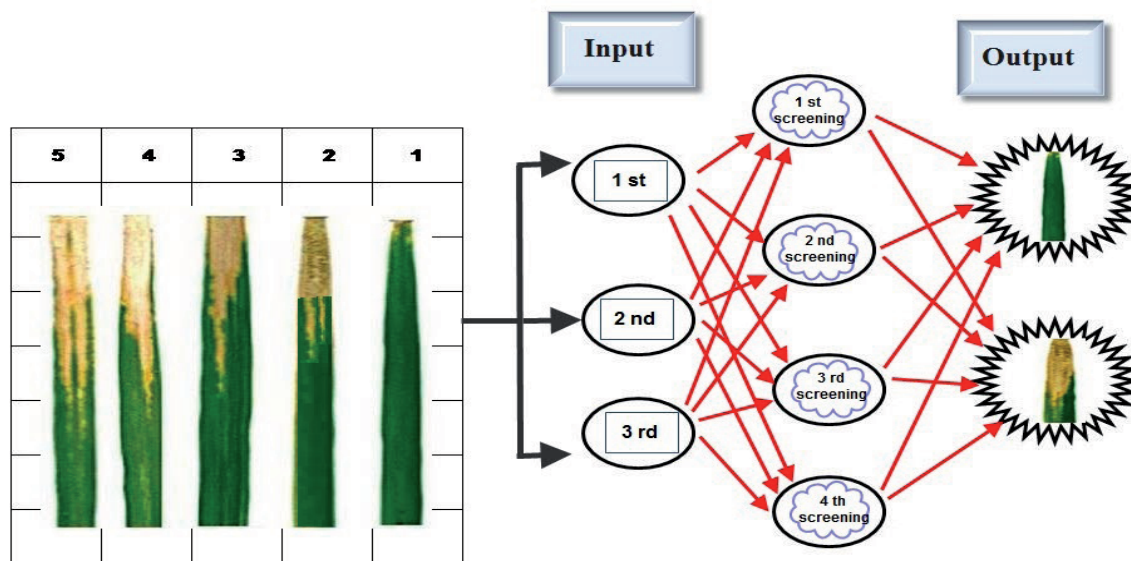
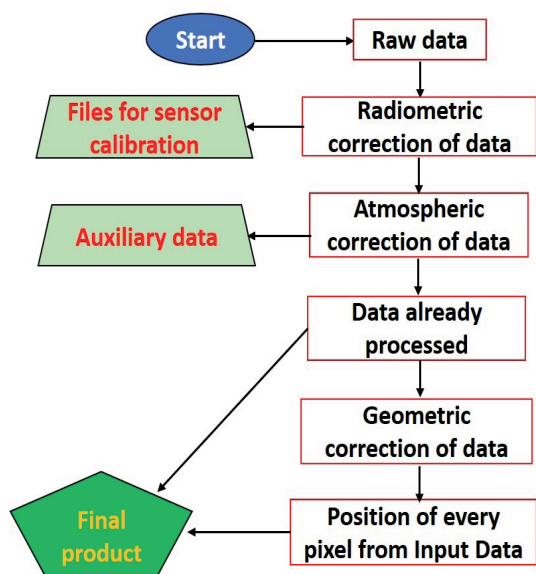**Fig. 4.** Schematic representation of hyperspectral imaging on model disease detection

Fig. 5. A flow chart on hyper-spectral imaging

Conclusion and future scope

The models based on deep learning have features of fast, high precision, high training efficiency, unsupervised and universal acceptability. However, there are many challenges such as accuracy feasibility and overfitting in the detection of plant diseases under very complex and diverse environmental conditions. To solve these issues novel deep learning models combined with RPN algorithm, CV algorithm, and TL algorithm have been developed. Compared to traditional approaches modern approaches are superior in terms of robustness, and faster convolutional neural networks. They also minimize the number of parameters that are essential for obtaining better results. Under field conditions, the main challenge is to nullify the effect of complex and diverse environmental conditions to get better results through a deep learning architecture. Hence, researchers can know the effect of climatic complexity in obtaining better information about diseases in the field. So, DL models can act as information technology in agricultural production which eventually favors sustainable agriculture. Most researchers have especially utilized the PlantVillage model as their standard DL model where it consists of many images with a simple/plain background but practically a realistic background is needed. Hyperspectral/multispectral imaging technology is robust and effective in the detection of different diseases provided it is utilized with the most efficient DL models. Deep learning models save time and promote the need-based application of pesticides since they can identify diseases before symptoms appear. Therefore, it avoids the indiscriminate use of agricultural chemicals which are hazardous to mankind and the environment as well. DL models should be developed in such a way that they can also detect disease severity throughout the entire cycle. There is also a need for comprehensive research to standardize the DL model for many diseases with much-enhanced accuracy.

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