Plant Curl Disease Detection And Classification Using Active Contour And Fourier Descriptor

M. Bala Naga Bhushanamu[1], M. Purnachandra Rao[2], K. Samatha[3]

[1]Research Scholar, [2]Retd. Professor, [3]Professor
Dept. of Physics, Andhra University, Visakhapatnam, Andhra Pradesh, India

Abstract: ***Automatic plant leaf curl detection is an important step towards the development of Computer-aided crop damage analysis systems. It helps in analyzing the health condition of the plants through leaf images. Image processing techniques are recently being used to analyze the condition of the leaf and identify the disease that inflicted the crop. Leaf curl disease can be identified by analyzing the edges of the leaf. This paper presents a procedure to identify the curl disease occurring in plant leaves using active contour, Fourier feature descriptor, and deep learning. Active contour is used to identify the shape of the leaf. The edge contour of the leaf is then given to the Fourier feature descriptor. The feature extracted using the Fourier descriptor is invariant to the angle and size of the leaf. The same feature vector is produced in any given angle and size of the leaf in the image. The features are trained using 1D CNN. The model can then be used to classify new images and automatically identify the leaf have curl disease or not. The experimental results prove that the proposed algorithm produces good results in identifying the leaf curl disease.***

Keywords: Detection, Classification, Segmentation, Feature extraction, 1DCNN.

1. INTRODUCTION

The unusual phase of the plants is included the diseases that destructs the plants' growth normally. Several losses to the production of crops are caused due to the several types of plant diseases [1]. By depending on the growing of varieties of crops and favourable conditions of environment, the pathogen is presented which causes the plant diseases' occurrence and prevalence. To decrease the losses in fields and improve the quality of grains, there are different programs of plant disease management [2]. The contribution of research is specifically included the recognition and classification of plant diseases from the three or four decades greatly. To restrict the losses in producing high-quality crops, early detection of plant diseases will assists to achieve the production with great good grains. Recently, the major concern is involved the diseases of plants' image recognition which improves the visual applications that will be useful for development of digital technologies. By using the techniques of image processing, different methods are proposed for a quantification and automatic recognition of plant diseases [3]. With the use of features of plant diseases, the system of automatic diagnosis is reduced the relying of the concerned area by experts. Based on the image processing techniques, extraction of characteristic features of plant diseases is done from the disease affected images' diseased region. With the techniques of pattern recognition, the disease-infected plant is identified. However, those techniques are "support vector machine", "neural networks", etc. From the plant diseases' digital images, the

extraction of features is determined which includes “shape”, “color”, and “texture” and so on. In many horticulture plants, it’s found that different types of diseases’ are recognized through the image processing techniques for easily detect and diagnosis the plant diseases automatically. Here, in this study, three kinds of plant diseases are considered such as bacterial, fungal, and virus of tomato plants by taking the plant leaf images. The study is included the fungal disease of plant septoria leaf spot and plant late blight, virus of plant leaf curl, and bacterial diseases of bacterial canker and bacterial leaf spots. Seven types of steps for classification of tomato plant diseases are mentioned some steps

Step 1 and step 2: contains total six types of disease and healthy images, shown in figure 1.

Step 3: training and testing datasets are created and mentioned.

Step 4 and 5: By utilizing the method of Otsu, the segmentation is performed based on training and testing dataset.

Step 6: total number of 24 types of features are extracted, that means the features like texture, color, and shape are derived from the tomato plant with healthy and unhealthy of segmented images.

Step 7: the input and target data is provided which is used for classification. Based on classification tree, final classification is made.

To make a classification of healthy and unhealthy images of different kinds of tomato plant, the classification tree is utilized [4-5].

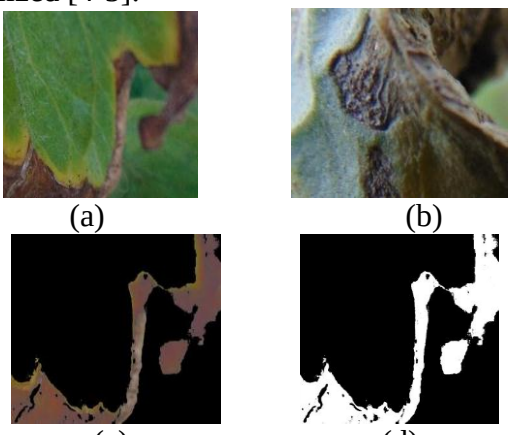


Figure. 1. a) & b) Late blight affected tomato leaves
C) Color Segmented Image D) Binary segmented images.

The training samples of n observations are involved in the “classification tree” which is based on I variable classes included the prediction values X1…Xj and the values 1,2,3…j. The classification tree’s main objective is to determine the best prediction values for Y using the new predicted values of X. In the figure different effected tomato leaves and segmentation methods.

The work reported in this article was undertaken to assess the relative contributions for the curl disease experienced by guava and a peach crop that arises.

This paper is structured as 5 sections. The section 1 describes the introduction of the plant disease detection. The section 2 explains the literature work. The section 3 describes the proposed Leaf disease detection methodology. The section 4 is description of experimental results. And the finally in section 5, the conclusion of this work were discussed.

2. LITERATURE SURVEY

The tomato apical leaf curl virus (ToALCV) is proposed by the author Carlos G. Vaghi Medina et.al [6] for this species. For the coat protein (CP) and the replication associated

protein (Rep), different evolutionary relationships are suggested for phylogenetic inferences. Capulavirus is similar to the products of complementary-sense gene (RepA, Rep, and C3) according to the analyses of the sequence similarity network (SSN) protein along with the viron-sense gene products (CP, MP, and V3) are operating similar to curtovirus, topocuvirus, and becurtovirus. With the recombination origin, the "modular organization" is supported to appear in genome of ToALC according to the presented data. The nine subgroups are defined the geminiviruses CP's based on specificity-determing positions (SDPs) analyses which involves the sharing of same kind of insect vector of geminiviruses. Based on the topocuvirus sequences, the clustering of sequences was done where the vector is the treehopper, Micrutalismalleifera. For the CP, the prediction of a set of highest scored amino acid was done which is helpful to identify the differences in the specificity of virus transmission. The vector of ToALCV could be a treehopper which is predicted in this study but there is a requirement of evaluation should be processed to confirm this and is demonstrated in this paper.

A begomovirus is caused the disease of *Papaya leaf curl virus* (PaLCuV) which is presented by Varun, S. Saxena et.al [7] and it is transmitted through whitefly (*Bemisiatabaci*) naturally. The papaya leaf curl disease is included the vital symptoms like stunted plant growth, inware or outward curling of plant leaves, and vein thickening with small distorted fruits or no fruits. For the production of crops, a major threat is the virus of *Papaya leaf curl* which has the ability to provide a rapid adoption of new plant hosts in their extension of host ranges and a risk is evolved in the production of papaya. In order to restrict this virus spread, the management of whitefly is the best method. To identify the begomoviruses at early phases of infection, various diagnostic methods specifically molecular techniques have been improved for controlling the spreading of begomovirus further. At later stage, there are no reports are available to avoid the infection of begomoviral. The information is provided in this chapter which involves various aspects such as phylogenetic and host range analysis of virus incorporated with the disease of papaya leaf curl, vector responsible for transmission or spread of disease, casual pathogen, and different approaches of resistance for management of the disease in a possible manner.

An algorithm is proposed and evaluated by G. Saleem, M. Akhtar et.al [8] based on a dataset of self-collected leaf images with the number of 625 and an available standard dataset of "Flavia" of 1600 leaf images publicly. Different types of classifiers are tested such as decision tree, k-nearest neighbour (KNN), multi-support vector machines (SVM), and naïve Bayes based on proposed algorithm. The final results are claimed by the best performing KNN and the proposed algorithm is revealed that it shows the precision of 97.6% and recall of 98.8% if the testing is done on the dataset of 'Flavia'. On the self-collected dataset, the proposed algorithm is given the results of recall and precision measure values such as 97.3% and 96.1% respectively. If the techniques of efficient segmentation method are augmented on raw leaf images, the results are confirmed that the proposed approach can be shown that it is an accurate recognition method of plant type significantly in practical cases. To make a classification on the datasets, a Convolutional Neural Network (CNN) based technique, AlexNet is compared which is contradictory to the approach of handcrafted feature-based and the robustness is outperformed later if the dataset of training is small.

By using mobile captured symptoms of images of Cotton Leaf Spot, the technical strategies is expressed by P. Revathi et.al [9] and the diseases are categorized based on neural network in this work. To achieve the intelligent farming, the training of a classifier is made that involves selective fungicide application, early identification of diseases in the groves, etc. With the use of techniques of Image Edge detection Segmentation, the proposed work is evaluated in which the processing of captured images is done for enrichment. To retrieve the target regions or disease spots, the feature image segmentation of R, G, and B is performed. For the

disease spots, the image features like shape, boundary, texture, and color are retrieved to identify the diseases and recommend the controlled pests.

The severe problems are included in the plant leaves which is characterised by the author Rahman et.al [10] and recognized that those issues are reducing the plants' lifespan usually. Owing to the three kinds of diseases like bacterial, viral, or fungal, diseases of leaves are caused effectively. The crop production is decreased with the diseased leaves that will lead to the negative impact on the agricultural economy. The effective method is needed to identify the diseases in plant in early phases as the agriculture field is playing a significant role in the economy. To recognize the diseased plants in fields, the traditional methods are utilized but these techniques are tedious and time consuming. To detect the healthy and unhealthy plant leaves, the machine learning approaches has been presented with a comparative analysis in this paper. Three different kinds of plant leaves are chosen for the purpose of experimental study that includes citrus, cabbage, and sorghum. The color based features like pixels, descriptors like Histogram of Oriented Gradients (HOG), and statistical features such as min, max standard deviation, and mean have been utilized to make a classification of healthy and unhealthy plant leaves.

For retrieving the soybean diseased leaves, a system of Content Based Image Retrieval (CBIR) is developed by the author Jayamala Kumar Patil et.al [11] and is presented in this research paper. The leaf features like color, texture, and shape have been used. Based on HSV color histogram, the features of color are retrieved. In the form of matching key points, the shape features are provided by Scale Invariant Feature Transform (SIFT). The texture features are utilized widely for Gabor filter and Local Binary Pattern (LBP). By merging Gabor filter and LBP, novel texture feature is proposed which is named as Local Gray Gabor Pattern (LGGP). For detection of three types of diseases in soybean leaves, all these features' performances are tested based on the retrieval precision. For improvement of performance, the shape, color, and texture features are merged. The precision of SIFT retrieval is increased when LGGP is incorporated with colour histogram.

With a technique of hyperspectral imaging, the possibility of disease of discriminating tomato yellow leaf curl is investigated by the author Jinzhu Lu et.al [12]. For both healthy and infected leaves in a tomato plant, hyperspectral images are gathered by the system of hyperspectral imaging. To choose band ratios and sensitive wavelengths, the analysis of both leaf area and background's data was analysed within the range of 500-1000 nm that involves the parameters such as first derivate reflectance spectra, reflectance spectra, and absolute reflectance difference spectra. For the segmentation of background, choosing of 853 nm was done to create a mask image. As a set of sensitive wavelengths, 720 nm from the reflectance spectra, four wavelengths with lower values (690, 840 nm) and higher values (586, 720 nm) in the absolute difference spectra, four peaks (560, 575, 712, and 729 nm) from the first derivative spectra were chosen. Based on four used vegetation indices (VIs), the comparison of Four band ratio images (560/575, 712/729, 586/690, and 720/840 nm) was done. By utilizing the grey level co-occurrence matrix (GLCM), the features of 24 texture were retrieved. Based on the curve analysis of receiver operator characteristic (ROC), each feature's performance was processed. With the use of Yondon's index, each feature's best threshold values were computed.

In addition to the identification of leaves, the grape leaf diseases' classification is proposed by N.Krithika et.al [13]. With the help of grape images, the leaf skeletons are detected primarily. These skeletons of leaves are helped to determine the directions and positions of leaves easily. For extracting the skeletons' images, the Tangential Direction (TD) based segmentation technique is developed. The generation of a color channels and the histograms of H is done and the pixel values are observed to differentiate the tissues of healthy and diseased types in leaves when the leaf images of grape plants are classified. To identify the

diseases in plant leaves, the features are extracted and classified based on the algorithm of KNN classification.

By using the movement of monopartite begomovirus, *Tomato yellow leaf curl virus* (TYLCV), the proteins of capsid protein (CP), V1, and C4 functional properties are investigated by R Van et.al [14]. The proteins and GFP fusion proteins' transient expression are also expressed by utilizing the microinjection of *Escherichia coli*. The nucleus and nucleolus are localized to the TYLCV CP and termed as a nuclear shuttle which is used to facilitate the DNA import and export. The functional homolog of the bipartite begomovirus BV1 is served by CP. Around the nucleus, the localization of TYLCV V1 is done at the cell periphery and colocalization with the endoplasmic reticulum is developed. The localization of C4 with the cell periphery was done. As similar as the bipartite begomovirus BC1, the localization patterns' were done together which is known to provoke the movement of cell-to-cell. To move and provoke the trafficking of macromolecular, a limited capacity was included in V1 and C4 alone or in combination through the epidermal plasmodesmata or mesophyll which is in contrast to BC1. At three phases of development, the experiments like *in situ* PCR and immunolocalization were conducted for tomato plants. However, the tissues of leaf, steam, shoot apical, and floral phloem cells were excluded from the infection of TYLCV.

The tomato yellow leaf curl virus (TYLCV)'s genomic DNA molecule is presented by the author S. Fukuta, et.al [15]. By using the loop-mediated isothermal amplification (LAMP), the amplification of a whitefly-transmitted geminivirus was done from the TYLCV-infected tomato (Lycopersiconesculentum)'s DNA extracts. For amplification of TYLCV DNA from individual whiteflies (Bemisiatabaci)'s total DNA extracts, the procedure was implemented that had been fed on the infected plants of TYLCV. To synthesize a large amount of DNA, LAMP method is having an ability which is one of the main characteristics. A white precipitate of magnesium pyrophosphate is produced from a large amount of by-product, pyrophosphate ion in the reaction mixture. Without using gel electrophoresis, easy identification of amplification of TYLCV genomic DNA is allowed with the presence or absence of the white precipitate.

An approach is proposed by Usama Mokhtar et.al [16] that includes four different stages such as pre-processing, feature extraction, image segmentation, and classification. The segmentation is done at each input image and created the descriptor for each segment. To detect a subset of optimal features, some measurements of geometric are incorporated. For classification, an algorithm of support vector machine (SVM) with different kernel functions is utilized. For both the phases of training and testing, total 200 infected tomato leaf images' datasets with TYLCV and TSWV were exploited. To determine the presented approach's performance, a technique of N-fold cross-validation is utilized. The proposed classification technique's experimental results have been obtained that the accuracy values of 90% and 92% on an average with the quadratic kernel function.

3. PROPOSED METHOD

The figure 2 shows the block diagram of proposed method. The block diagram contains input image, pre-processing, Active Contour, Fourier descriptor and 1DCNN blocks. The input image is resized by the pre-processing. After the pre-processed image is segmented by Active contour. The segmented image is binarized using image binarization technique. So, the image contains only black and white pixel information. The Fourier descriptor will generate number of features for the image, these features are trained and classified by using 1DCNN network.

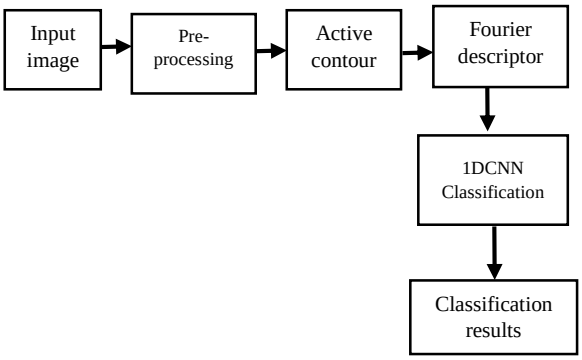


Figure.2. proposed method block diagram

3.1 Pre-processing: The basic pre-processing methods used in our experiment. Pre-processing is an improvement of the image data that suppresses unwanted distortions or enhances some image features important for further processing. And here using the image is resized to next process requirement.

3.2. Active contour model

From an initial state to a position where the minimization of an energy is moved in an active contour with the internal forces' influence. The features are pulled from image forces towards like edges and lines. Owing to the way of contours move into the position, these three curves are known as snakes by minimized energy. In the computer vision fields, the popular type of active contours is included image segmentation, 3D reconstruction, edge extraction, and motion tracking. The models of active contour and the proposed theory are conversed in detail in the below subsections.

A curve is represented the snake here curve is v(s) = [x(s), y(s)] s ∈ [0, 1], where s represents curve's length. The snake energy is defined as:

$$E_{snake} = \int_0^1 E_{int}\big(v(s)\big)ds + \int_0^1 E_{ext}\big(v(s)\big)ds \quad (1)$$

The terms of $E_{int}\big(v(s)\big)$is represented the internal energy of the snake and $E_{ext}\big(v(s)\big)$is represented the external energy of the snake. For controlling the snake's deformability, the internal energy is utilized which is written as follows:

$$E_{int}\big(v(s)\big) = \frac{1}{2}(\propto (s)|v_s(s)|^2 + \beta(s)|v_{ss}(s)|^2 \quad (2)$$

Where $v_s$is the first spatial derivative which represents the behaviour of membrane-like or elasticity whereas the second term v_{ss} is the second spatial derivative which represents thin-plate or rigidity behaviour. The weighing parameters are known as the coefficients$\alpha \ \ and \ \beta$ which control the contour's elasticity and rigidity respectively. From the energy of an image, the derivation of external energy function is done. If the edges of the images are of interest, the energy definition can be described as follows:

$$E_{ext}\big(v(s)\big) = -|\nabla(G_\sigma(x,y) * I(x,y))|^2 \quad (3)$$

Where $G_\sigma(x,y)$ is a Gaussian funtion with standard deviation σ, ∇ is the gradient operator and * represents convolution while I(x,y) is the image intensity function. For removing the noise, this convolution is used by smoothening the images. By substituting (2) and (3) in (1), the snake's whole expression is given below:

$$E_{snake} = \int_s (1/2(\alpha(s)\,|v_s(s)|^2 + \beta(s)|v_{ss}(s)|^2) - (\nabla G_\sigma(x,y) * I(x,y))^2 ds \quad (4)$$

A snake minimizing (4) must satisfy the following Euler equation:

$$\alpha v_{ss} - \beta v_{ssss} - \nabla E_{ext} = 0 \quad (5)$$

By reducing the value of E_{snake}, the final contour is retrieved by the solution of the above equation. The consideration of equilibrium function as the force equilibrium function could be done and it is defined as mentioned below:

$$F_{int} + F_{ext} = 0 \quad (6)$$

As the pulling of snake by external force towards the edges of desired images, the stretching and bending is discourages by the internal force. The final contour $(F_{int} - F_{ext})$ is deformed if evolving the original contour. The internal and external forces are identical for every point and opposite directions are performed by providing a stable state. The deficiencies have included in the snake active contour. Two major disadvantages of the snake active contour are initial curve's sensitivity and detection of nonconvex objects' failure.

The Active Contour system is especially designed for detecting the shape of the leaf images for plant disease applications. The environment where these disease structures are found plant such as segmented. These become the unwanted background information that hinders the performance of the active contour in tracking the object outline accurately. In addition, angiogram images also contribute various obstructions that reduce the performance of the active contour such as color, noise, low contrast and poor quality images. Therefore, the Active Contour System developed in this paper aims at optimizing the performance of object tracking by introducing various image processing techniques.

An active contour is essentially a curve made up of various energies. The curve deforms dynamically to mould to the shape of a targeted object. There are various methods for implementing an algorithm to achieve object outlining. Traditionally, the active contour algorithm requires an initial user approximation surrounding the interested object and then deforms this curve by minimizing the energies contained to achieve the object outline matching as shown in Figure.3.

Two categories are divided in the energies of active contour. The relationship between external and internal energy is discussed. By focusing on the contour's intrinsic properties, the functions of internal energy like curvature and elasticity are retrieved while relating the image properties such as brightness and contrast to the functions of external energy.

$$E_{snake} + E_{internal} + E_{external} \qquad (7)$$

These energy functions are subjected to the different weighting for monitoring the contour's various properties which are crucial for an object outline's good match. These weightings have the effect of controlling the rate at which the contour minimizes and most importantly stop the contour from further shrinking once the outline of the object is tracked. This is known as the final approximation of the contour. Energies contained in the contour, are minimized due to simulated forces acting upon it. The minimal state has been reached by the contour and the object outline's final approximation is the curve's outcome if all forces are included at equilibrium. Figure 3 is the example of active contour, the object outline matching the leaf.

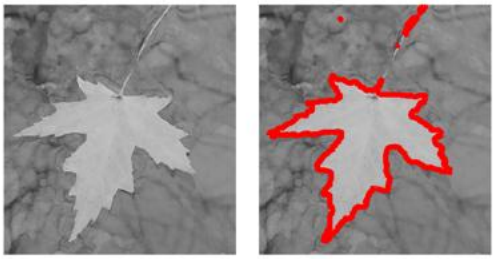


Figure.3. the object outline matching the leaf.

3.3. Fourier Descriptors

Consider a region boundary having K points $(x_0, y_0), (x_1, y_1), \ldots\ldots\ldots, (x_{k-1}, y_{k-1})$ encountered while traversing the boundary in the counter-clockwise direction with (x_0, y_0) being any arbitrary point. We can represent the x and y coordinates of each pair as a discrete signal $x(k) = x_k \; and \; y(k) = y_k \; where \; k = 0,1, \ldots\ldots, K-1$. Thus the boundary sequence be represent as $s(k) = [x(k), y(k)]$. If we treat the sequence as a complex number such that,

$s(k) = x(k) + jy(k)$ and compute the K point DFT of the signal then the resulting complex coefficients acquired are called the *Fourier descriptor* of the boundary. i.e. $a(u)$ where

$$a(u) = \sum_{k=0}^{K-1} s(k) e^{\frac{-2\pi i}{K} uK} \quad (8)$$

The original boundary shape can be retried from the FD coefficients by simple taking the inverse DFT of the same.

The Basic Concept of Fourier Descriptors

Fourier descriptors have two main purposes in practice: One is to extract a compact shape descriptor for matching and retrieval the other is to efficiently record and compress the boundaries. The Fourier descriptor algorithm consists of two stages: *shape signature* and *discrete Fourier transform* (DFT). The 2-D boundary is mapped into a 1-D sequence in the first stage i.e. known as the shape signature. In the second stage, it applies the DFT on the 1-D signature which lead to the coefficients of a set of DFT frequency for representation of a boundary. The coefficients of low frequency are only kept for describing and recording the boundary with efficiency.

In general, the second stage is seen as a fixed operation, so previous work of Fourier descriptors primarily focuses on how to design the shape signatures process. the cumulative angular function in addition to the boundary; the complex coordinate, denoted as the *conventional Fourier descriptor*. Amid of several existing signature shapes, the comparative analyses are given by In Zhang *et al.* based on the matching performance. An important characteristic of shape signatures is the *reversibility*: If the shape signature is not reversible from the 1-D sequence to the 2-D boundary, it is not available for boundary reconstruction.

There is also some work aiming to explore the RST-invariant properties and to design the matching metric for accurate image retrieval. A special Fourier descriptor algorithm that performs the 2-D Fourier transform on the whole image rather than performs the 1-D Fourier transform on the boundary sequence.

Fourier Descriptors for Non-closed Segments

The Fourier descriptors mentioned above are mainly used for closed boundaries. However, for non-closed segments, which occur in character recognition and edge recording frequently, their performances may degrade due to the non-adjacent end points. That is, the non-adjacent end points lead to discontinuity of a signal at the two ends of the 1-D signature, resulting in significant high-frequency coefficients that cannot be directly eliminated for contour recording.

To solve this problem, the shape signature process should be designed to produce a signature with similar end point values. Computed the sequential point difference along a contour as the shape signature. The method does reduce the high-frequency components in the shape signature and preserve the exact end point locations, but in case of digital images, the process of equal length sampling is not applicable. The Fourier descriptor is applied when the segment of non-closed is present at the two ends. The author is claimed that the distortion feature is only displayed at the extended area, the extended length is undefined, and the end points of original values would be stored after compression. By making changes to the function of cumulative angular, the generalized Fourier descriptor has been derived. Here, he mentioned that the function is not valid for deriving the boundary compression and it has a slow convergence speed.

Another method to solve the non-closed segment problem is to perform the discrete cosine transform (DCT) rather than the DFT on the shape signature. Namely, the shape signature is first extended into the even-symmetric form, which indeed has same end point values; the DFT is then applied to get the frequency coefficients for contour recording. Although this method is efficient and could alleviate the distortions after compression, the end point locations are not guaranteed to be preserved.

3.4 1D Convolutional Neural Networks

In the previous section, the traditional method of deep CNNs is designed to deal with the 2D data of images and videos exclusively. That is the reason; the method is termed as "2D CNNs" most often. Recently, a new method of 1D Convolutional Neural Networks (1D CNNs) is implemented alternatively with the added modifications to the 2D CNNs. For certain applications of 1D CNNs, these studies have proved that the proposed methods are advantageous. For dealing with 1D signals, the method is preferred to their 2D counterparts owing to the below-mentioned causes:

- Simple array operations are required for BP and FP in 1D CNNs instead of matrix operations. Hence, 1D CNNs' computational complexity is lower when compared to the 2D CNNs.
- The challenging tasks are learned with the involvement of 1D signals relatively with the shallow architectures of 1D CNNs based on recent studies that means small number of neurons and hidden layers are investigated. In order to handle such type of tasks, deeper architectures are needed in 2D CNNs usually. To make a training and implementation, the networks with shallow architectures are easier to use obviously.
- A special hardware setup is required to train the methods of deep 2D CNNs. For example, GPU farms or cloud computing. To train the compact 1D CNNs with neurons (e.g. < 50) and hidden layers (e.g. 2 or less), any type of CPU implementation is feasible and reliable for a standard computer.
- For low-cost and real-time applications specifically on mobile or hand-held devices, compact 1D CNNs are suited perfectly owing to their low computational requirements.

A superior performance is demonstrated by 1D CNNs on the applications where high signal variations and a limited labelled data are acquired from various sources like civil, aerospace or mechanical structures, power engines or motors, high-power circuitry, patient ECG, etc. in the above-mentioned studies. In 1D CNNs, two different types of layers are mentioned which illustrated in Figure 5) These are called as "CNN-layers" in which both sub-sampling (pooling) and 1D convolution are occurred 2) second layers are named as Fully-connected layers which are similar to the Multi-layer Perceptron (MLP)'s layers hence these are termed as "MLP-layers". By considering the below-mentioned hyper-parameters, a 1D-CNN is configured:

1) Number of hidden CNN and MLP layers/neurons (as shown in figure 4, hidden MLP and CNN layers with the number 2 and 3 respectively in the sample 1D CNN).
2) Filter (kernel) size in each CNN layer (in the sample of all hidden CNN layers, filter size is 41 as shown in the figure 4).
3) Subsampling factor in each CNN layer (here, the subsampling factor is 4 based on the sample 1D CNN as illustrated in figure 4)
4) The functions of activation and pooling are selected.

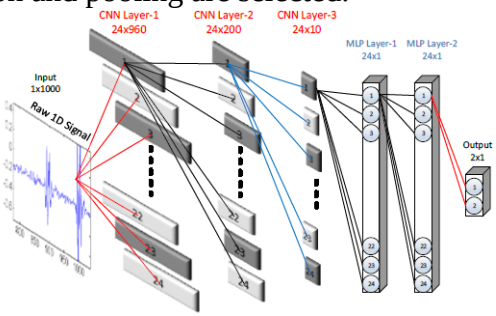


Figure.4. A sample 1D CNN configuration with 3 CNN and 2 MLP layers.

The input layer is considered as a passive layer as mentioned in the traditional 2D CNNs. However, the raw 1D signal is received and a MLP layer is considered as an output layer with

the number of classes are equal to the number of neurons. In figure 4, the 1D CNNs' consecutive three layers are illustrated. The sub-sampling factor and sizes of ID filter kernels are 2 and 3 respectively in which a sequence of convolutions are performed through the activation function f, the sum of which is passed, kth neuron in the hidden CNN layer, l, based on the sub-sampling operation. Between 1D and 2D CNNs, the main dissimilarity is that 2D matrices are replaced by 1D arrays for retrieving the both feature and kernels maps. The raw 1D data is processed by CNN layers in the next step and such features of "learn to extract" are utilized to perform the classification task with the use of MLP-layers. The operations of both classification and extractions are merged as one process which can be utilized to improve the performance of classification. 1D CNNs has a major advantage of a low computational complexity as the operation is included a sequence of 1D convolutions with the two 1D arrays' linear weighted sums simply. During the operations of Forward and Back-Propagation, such type of a linear operation can be implemented in parallel effectively.

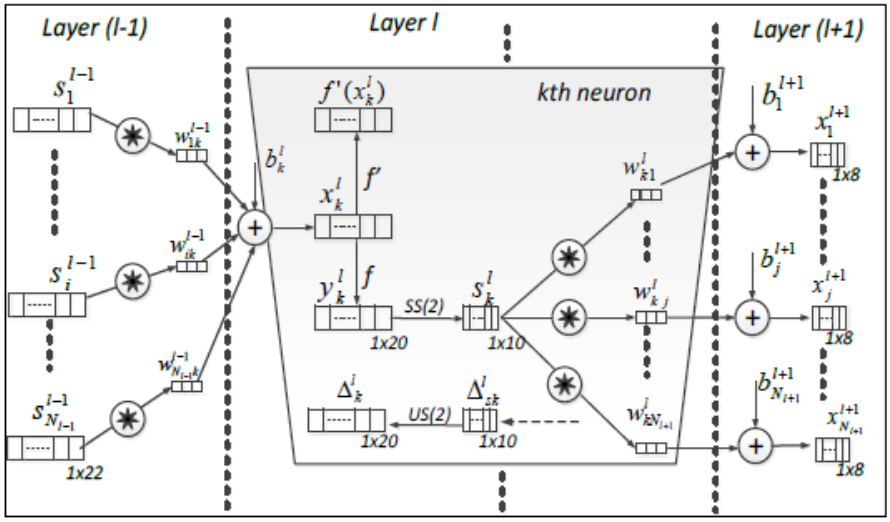


Figure.5. Three consecutive hidden CNN layers of a 1D CNN.

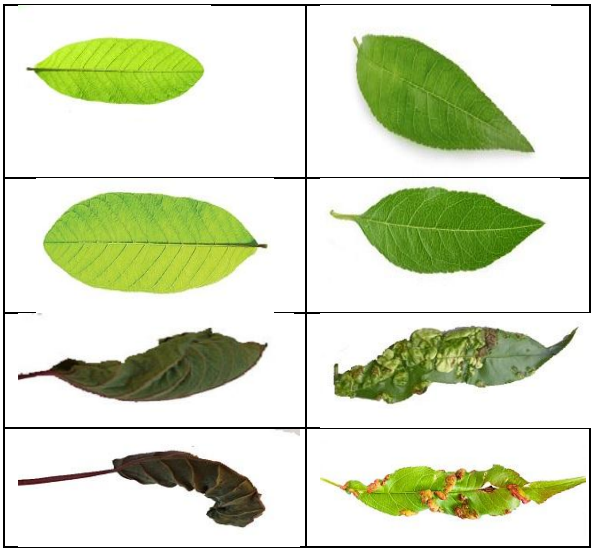
As the topology of CNN will have the ability to include the input layer dimensions' variations, an adaptive implementation is considered in a way that the output CNN layer's sub-sampling factor is tuned. In the next sub-section, the functions of Forward and Back-Propagation in CNN layers are mentioned in detail.

3. RESULTS

This segmentation and classification describe the study experimental findings. The experiment contains Peach and Guava leafs images with their curl disease. Primarily segmentation was done by Active contour. Then the segmented input given to the Fourier descriptor which gives the feature of leafs. These features trained by 1D CNN for classification. The input images are shows in the table 1.

Table 1: Different Guava and Peach leaf images

Input Guava leafs images	Input Peach leafs images



The figure 6 shows the Training process for peach leaf. The training process requires set of layers and options. Reach the computational architecture of the neural network. Constructing a collection of layers requires the input image unique size.

The training process includes generally two graphs which are accuracy and loss. If the training process reaches to maximum epoch, the training process will be completed. In both accuracy and loss graphs consists 3 lines. The thick line represents the training (smoothed). Thin line with dots represents the training and the dash line represents the validation.

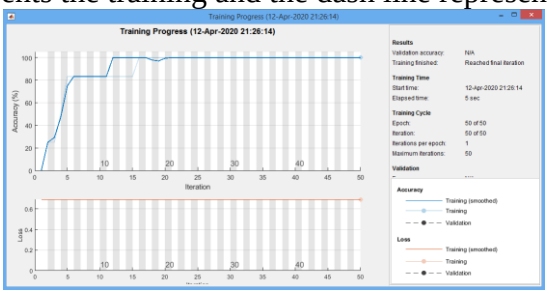


Figure. 6. training process for peach leaf

The figure 7 shows output for Active Contour. Active contour segmentation requires two inputs which are input image with mask. In the below subplot, first row show input image and mask. Second row shows the active contour segmentation with segmented output.

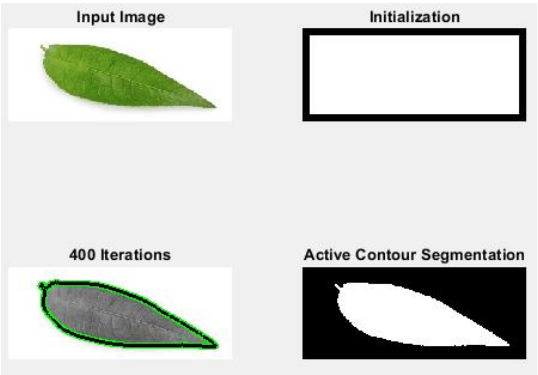


Figure.7. Active contour segmentation. a). Input image b). Mask c). Contour region d). Segmented output

The figure 8 shows the Fourier Descriptor results. The segmented output is given to the Fourier Descriptor input. The output features are show in the graph format.

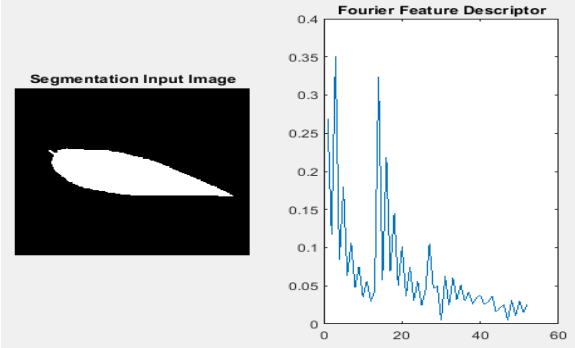


Figure. 8. Fourier feature Descriptor

The figure 9 shows the classification result. Here, the training features are saved into mat file. This file load into testing process, in the testing process also we follow the same steps like First segment the input image using active contour and find the feature values using the fourier descriptor, then this feature values give to the 1D CNN testing process along with trained network. In 1D CNN, the trained features compared with the test image features and gives the classification result.

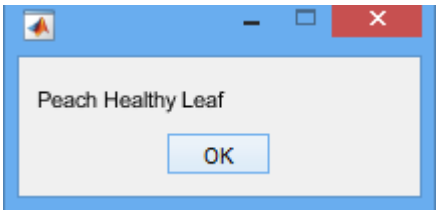


Figure.9. classification output

The figure 10 shows the output for Active Contour. In the below subplot, first row show input image and mask. Second row shows the active contour segmentation with segmented output.

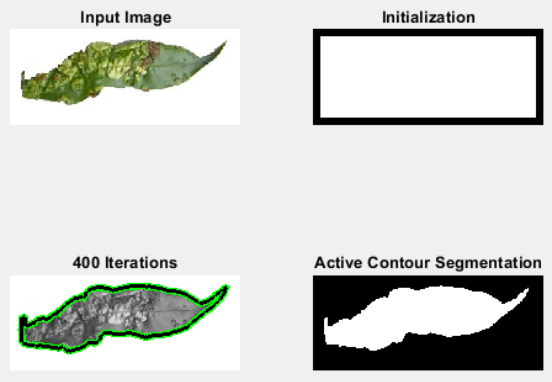


Figure. 10. Active contour segmentation

a). Input image b). Mask c). Contour region d). Segmented output

The figure 11 shows the Fourier Descriptor results. The segmented output is given to the Fourier Descriptor input. The output features are show in the graph format.

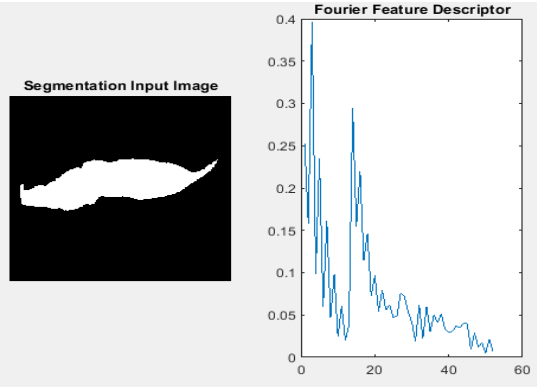


Figure. 11. Fourier feature Descriptor

The figure 12 shows the classification result. In 1D CNN, the trained features compared with the test image features and gives the classification result.

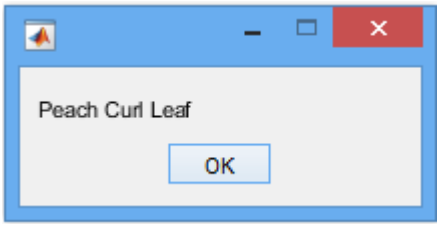


Figure. 12. Leaf classification results

The figure 13 shows the training process of the Guava leaf. The training process requires set of layers and options. Reach the computational architecture of the neural network. Constructing a collection of layers requires the input image unique size.

The training process includes generally two graphs which are accuracy and loss. If the training process reaches to maximum epoch, the training process will be completed. In both accuracy and loss graphs consists 3 lines. The thick line represents the training (smoothed). Thin line with dots represents the training and the dash line represents the validation.

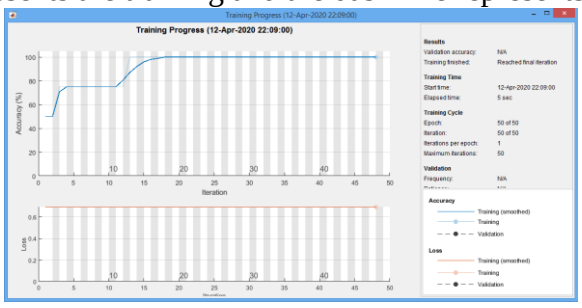


Figure. 13. the training process for Guava leaf

The figure 14 shows output for Active Contour. Active contour segmentation requires two inputs which are input image with mask. In the below subplot, first row show input image and mask. Second row shows the active contour segmentation with segmented output.

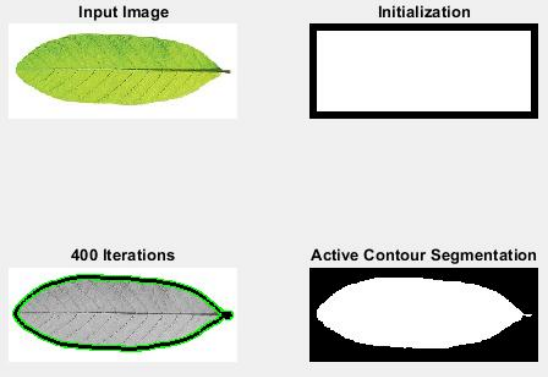


Figure. 14. Active contour segmentation
a). Input image b). Mask c). Contour region d). Segmented output

The figure 15 shows the Fourier feature Descriptor output for Guava leaf. the segmented output is given to the Fourier Descriptor input. The output features are show in the graph format.

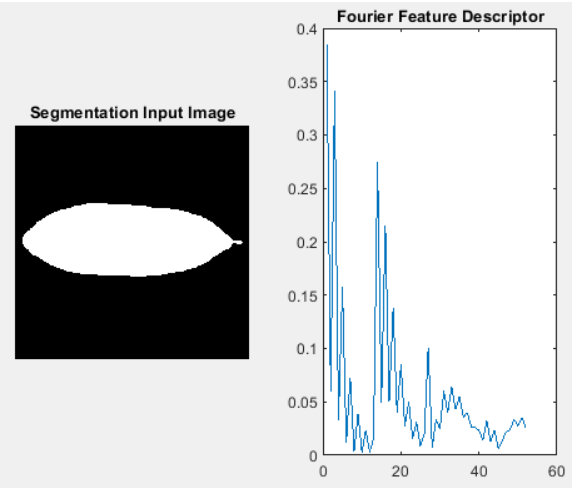


Figure. 15. the Fourier feature Descriptor

The figure 16 shows the classification result. In 1D CNN, the trained features compared with the features of text image and the classification result is given.

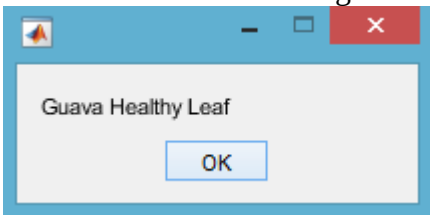


Figure.16. classification output

The figure 17 shows output for Active Contour. Active contour segmentation requires two inputs which are input image with mask. In the below subplot, first row show input image and mask. Second row shows the active contour segmentation with segmented output.

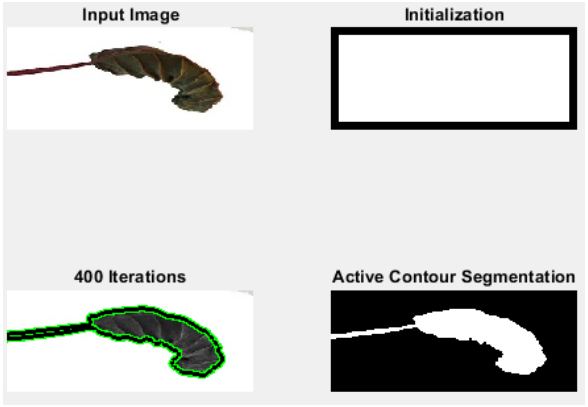


Figure. 17. Active contour segmentation for Guava leaf
a). Input image b). Mask c). Contour region d). Segmented output

The figure 18 shows the Fourier feature Descriptor output. The segmented output is given to the Fourier Descriptor input. The output features are show in the graph format.

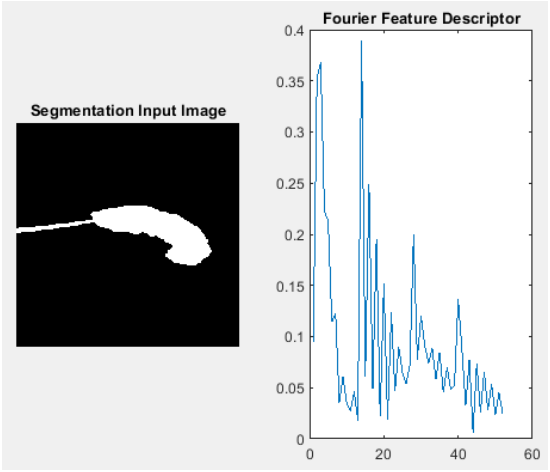


Figure. 18. the Fourier feature Descriptor output

The figure 19 shows the classification result. In 1D CNN, the trained features compared with the features of text image and the classification result is provided.

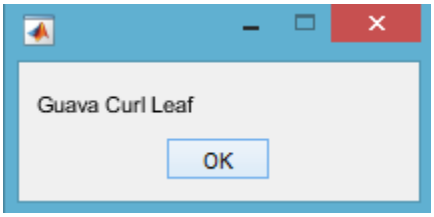
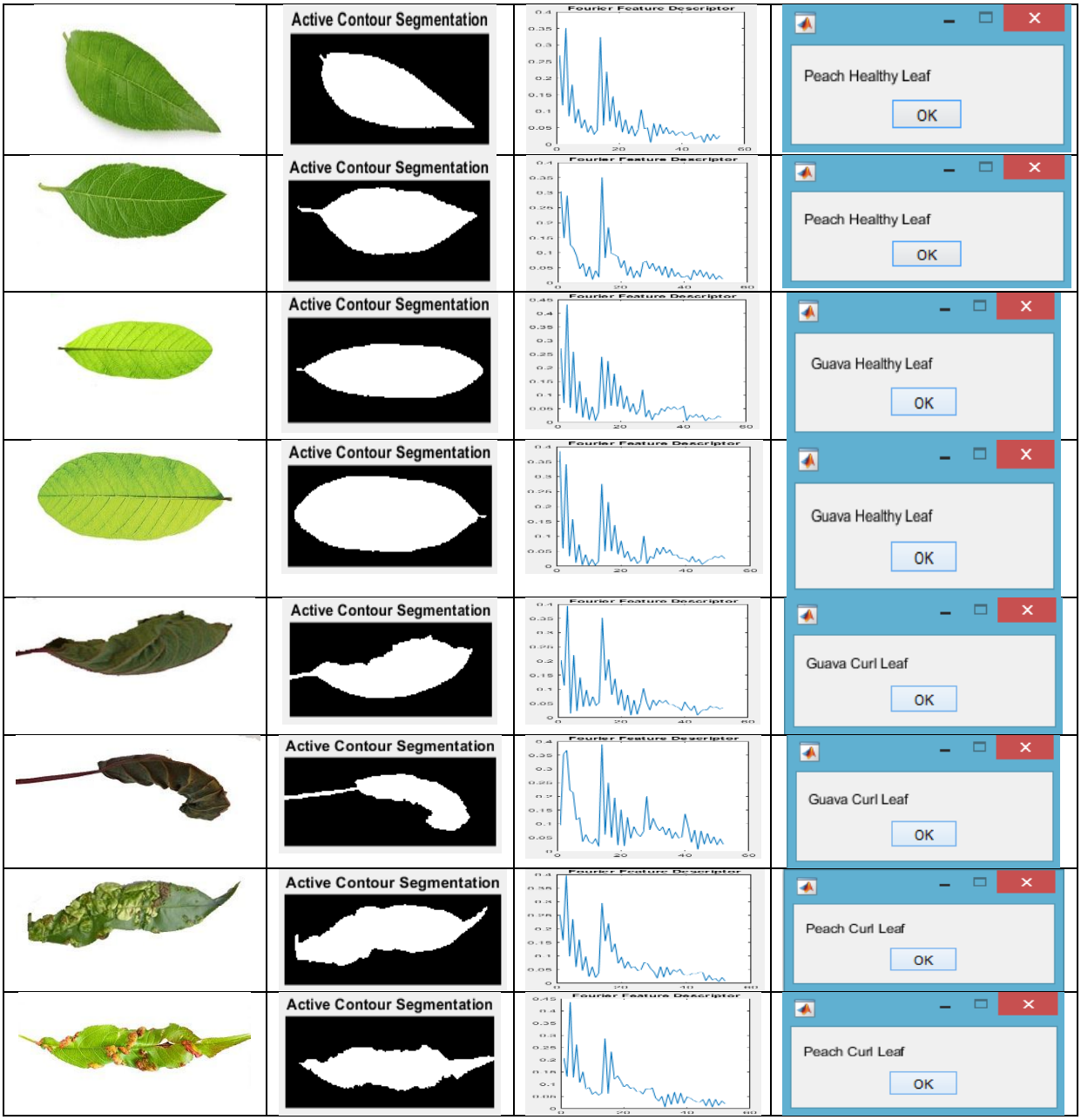


Figure.19. classification output for Guava leaf

The Table 2 shows the segmented output images, feature extraction graphs, and classification results.

Table 2. Segmented output images, feature extraction graphs, and classification results

Input Images	Active contour Segmentation	Fourier descriptor	Classification Results



5. CONCLUSION

For plant leaf curl disease detection, a survey on classification techniques of diseases is presented in this paper. In addition to this, an algorithm is also proposed based on an image segmentation method to classify the plant curl leaf diseases. The proposed algorithm is tested on some of the ten species of Guava and Peach. For identification, the related diseases were considered for these plants. The optimum results were achieved with the less computational efforts which are shown that the proposed algorithm is effective in identification and classification of curl leaf diseases. During initial or early phases, the plant diseases can be detected by using the proposed technique which is another major advantage. 1D CNN classifier is utilized to develop the recognition rate in the process of classification. The Active contour and Fourier descriptor can be used segmentation and feature extraction for these methods are gives the best results to curl leaf disease detection.

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