Automation of disease detection and classification in Brinjal plant based on optimization technique

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***Abstract*— This paper aims at detecting and classifying diseases found in Brinjal leaves using a computer vision based technique. Instead of manual diagnosis of plant diseases, the automatic disease detection can be achieved with the help of computer vision based technique. In this work, a novel ICA-SVM model has been proposed, that hybridized the imperialist competitive algorithm (ICA) and SVM to improve the accuracy of the disease image classification. This optimization mechanism involves kernel parameter in the SVM training phase which significantly influences the classification accuracy. The proposed method provides an effective and robust tool for segmentation in brinjal leaves for disease diagnosis. Moreover, the combinations of color features are extracted for classifying diseases. The ICA-SVM yielded an overall accuracy of 99.80% on 500 Brinjal leaves selected from five diseases against 91.40%, 94.30% and 97.40% for K-NN, RBFNN and SVM classifiers respectively.**

Keywords*— *Computer Vision; Color features; Image Classification; Support Vector Machine; Imperialist Competitive Algorithm

I. INTRODUCTION

Agriculture plays a crucial role in Indian economy with more than 70 percent people depending on agriculture for their livelihood. Agriculture sector contributes 17 percent of the total GDP and provides employment to over 60 percent of world population. Horticulture is the branch of plant agriculture dealing with garden crops, fruits and vegetables. Agriculture provides huge foreign exchange to several nations around the world. In India vegetables are grown in an area of 9.575 million hectares with the productivity of 17.7million/ hectares which contributes 14 percent of world production of vegetables.

Brinjal or Eggplant (Solanum Melongena L) is one of the most popular and principle vegetable crops grown in India. World production of Brinjal is estimated to be about 14.6 million tonnes. In India Brinjal is cultivated in 3.2 lakh hectares with the total production of about 5.0 million tonnes.

Brinjal is susceptible to several fruit diseases both under field as well as in storage condition. This crop is severely attacked by several bacterial, fungal and viral diseases such as Pseudomonas Solanacearum, Cercospora Solani, Alternoria Melongenea, Tobacco Mosaic Virus and Pythium Aphanidermatum. If the plant is affected by any disease, it should be identified and diagnosed without any delay. Most of the plant deficiencies can be identified by monitoring the leaves in their early stage. Farmers need to monitor the plant at regular time interval for identifying the disease, but it is inconvenient to manage a large crop field by the naked eye. Automatic disease recognition and diagnosis of the crop deficiency in the early stage is achieved by using image processing technique, so that the agricultural production and yield get increased. Researchers from the field of image processing and machine learning based on computer vision proposed numerous techniques for the detection and recognition of Brinjal diseases. Hussam et al. (Ali, 2017) presented a novel technique for detection and classification of citrus diseases using DeltaE color difference algorithm for the detection of infected part of the leaf image. The technique uses three types of features such as color, HOG and texture features for classification of the citrus diseases. The result shows significant improvement in terms of performance and accuracy. Deng et al. (Deng, 2016) proposed a new technique for citrus detection based on Huang Long Bing (HLB) and cost SVM for classification. The technique exploits color, texture, and HOG features for feature extraction and implemented PCA technique for the reduction of extracted features. SVM classifier achieved 91.93% accuracy with low cost and minimum computational time, as compared to other classification technique. Malik et al. (Malik et al., 2016) suggested an automating detection and segmentation for identifying disease in citrus fruits. Also, this technique includes preprocessing, shadow reduction, object separation, Kmeans clustering, and blob detection. Gomez et al. (Gómez Sanchis, 2008) proposed a new effective technique to improve the opposing effect created by the shape of spherical objects at image acquisition process. Kumar et al. (Kumar et al., 2015) presented a technique for sorting and color-based grading for defecting defects in citrus fruits based on Gray Level Co-Occurrence Matrix (GLCM) parameters to classify the fruits into different groups.

Pydipati et al. (Pydipati et al., 2005) proposed a technique for classification based on machine learning of the citrus diseases. The technique exploits color co-occurrence algorithm which include 39 texture feature sets for classification. These features are classified and compared by two neural network method based on Back Propagation and Radial Basis Neural Network. The results show the improved performance in accuracy of 95%. Georgina et al. (Stegmayer, 2013) introduced a new approach for automatic detection and classification of citrus diseases based on feature selection. The selected features are classified by comparing multiple classification methods such as CART, Naive Bayes and NN using Multi Perceptron Learning and attained 88% accuracy.

Min et al. (Zhang and Meng, 2011) suggested a new technique for automatic detection of citrus canker by the combination of global and local features from the leaf. To extract features, an improved Ada-Boost method was used and classification was done by means of NN, SVM, and KNN. Yachun.W, Zhanliang. C., Hongda. W, 2008) suggested a novel technique for grading plant diseases using computer vision system. This technique used Otsu method to extract the leaf image and then Sobel operator is used to detect edges of the diseased spot. At last, a plant disease is classified based on different types of diseases. Camargo et al., (Smith, 2009) introduced an automatic preprocessing and SVM classifier to identify disease symptoms of cotton diseases. Phadikar et al. (Sil. J., Das. A, 2012) proposed a novel technique to classify the leaf brown spot and the leaf blast diseases of rice plant. This system is used to identify the disease using the Bayes and SVM classifiers. Guo et al. (Wang. B, 2010) developed a novel approach by Genetic Algorithm and rough set for the feature selection. Then SVM (Support Vector Machines) was applied to classify the disease based on the selected feature set.

II. Proposed Methodology

The proposed methodology for disease detection on plant leaves comprises of five distinct stages: Image acquisition, Image Preprocessing, Segmentation, Feature Extraction and Classification as shown in Fig A.1.

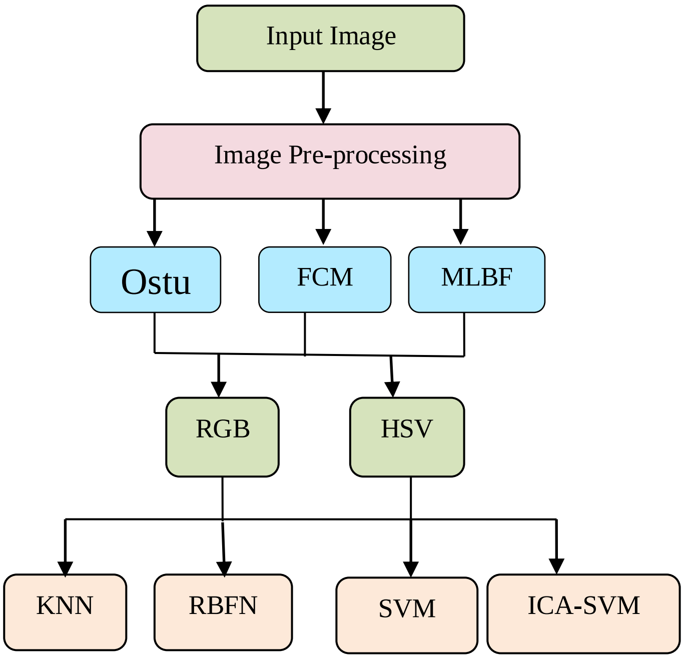

Fig A.1. Flow diagram of leaf disease detection

A. *Image Acquisition*

In the first step, the Brinjal leaf images are captured directly from the agricultural field using digital camera to increase the sample dataset. Physically the images are captured from an open farm. In this research, five types of Brinjal leaf diseases such as Pseudomonas solanacearum, Cercospora Solani, Alternoria Melongenea, Tobacco Mosaic virus and Pythium Aphanidermatum have been tested, in order to produce an automated model for detecting Brinjal leaf diseases with advanced computer vision based software. Pseudomonas Solanacearum is caused by bacteria during the time of flowering, characterized by foliage, dropping and slight yellowing of leaves and vascular discoloration. Alternaria Melongena A. Solani is characteristic by spot on the leaf with concentric rings which turns yellow and drops off prematurely. The lesion area of the leaf appears 1-2mm black or brown in color and leads to expand and develop another new lesion. Tobacco Mosaic Virus is caused by a viral infection. The important symptoms for this disease are yellowish spots on the leaf with irregular pattern. In Cercospora Solani newly infected leaves have small spots (Lesions) and as lesion grow, they appear as brown spots surround by a yellow green margin on each spots. Pythium Aphanidermatumis caused by viral disease which characterized light yellow in color in the early stage and the size of the leaf get reduced.

B. Image Preprocessing

Most of the collected images have more than one leaf in a single image. So the leaves are cropped automatically and extracted as an individual leaf image and set white background to make the images more visibly. Then the images are resized to a standard dimension of 256 * 256 pixels and stored in jpeg format. To make the image more effective, color space transformation is applied by reducing distortions.

C. YCbCr Color Transformation

The YCbCr is a non-linear RGB image, represented by luma from a weighted sum of RGB values. It is commonly used in color space. Because this type of representation makes it easy to reduce the redundant color information. This YCbCr color space transformation makes more simple and explicit separation of luminance and chrominance components. In this color space, luminance information is stored as a single component (Y), and chrominance information is stored as two color-difference components (Cb and Cr) where Cb represents the difference between the blue components. Cr represents the difference between the red components. Using the following formulas RGB image is transformed into YCbCr color model.

$$Y = 0.299 * R + 0.567 * G + 0.114 * B \tag{1}$$

$$Cb = 0.168 * R - 0.331 * G + 0.500 * B \tag{2}$$

$$Cr = 0.500 * R - 0.418 * G - 0.081 * B \tag{3}$$

D. Multi scale lesion based Fuzzy segmentation

The images captured from the field can be categorized into extensive and non extensive cases based on the specific layout condition between the lesions and the surrounding regions. In case of extensive, the lesion leaf has a uniform color and is located at the centre of the leaf but not connected to the boundary. But in non-extensive cases, the lesion area is connected to the image boundaries either on one side or both sides of the leaf. The lesion boundaries can be separated from the collected leaf by using the

$$B_{xy} = \frac{\left|\{A | A \in I, A \in B_s\}\right|}{\sqrt{A | A \in I|}} \tag{4}$$

Where A is the leaf image and B_s is the set of image boundary located within the leaf image (I).

Then partition the image into N clusters ($A = A_1, A_2, A_3 .....A_N$) Where N is the total number of image cluster from the lesion boundary by using multi scale lesion based fuzzy clustering by improving objective function which helps to capture the structural information from the leaf. The area of each cluster A can be defined as

$$Area(A) = \sum_{i=1}^{N} exp \frac{\left\| d_g^{\,2}(A, A_i) \right\|^2}{2\sigma_k^2}$$

$$= \sum_{i=1}^{N} B(A, A_i) \tag{5}$$

$$A_S(A) = \sum_{i=1}^{N} B(A, A_i) * \delta(A_i \in B_S) \tag{6}$$

Where $d_g(A, A_i)$ is the geodesic distance between any two clusters and σ_k is a Gaussian kernel parameter. and δ is one for segments on image boundary and δ is zero for otherwise.

$$d_g(A,A_i)=min\sum_{i=1}^{N-1}d(A_i,A_{i=1}) \tag{7}$$

Then the clustered image can be grouped into segmented region by using the formula

$$S_{xy}=\frac{A_s(A)}{\sqrt{Area(A)}} \tag{8}$$

The probability for the segmented region can be computed by,

$$p(\frac{I}{\phi_m})=\prod_{x(z)}\frac{Y_a(x_z)}{Y_a} \tag{9}$$

where, each pixel z is denoted by color histogram. $Y_a(x_z)$ indicates the infected part of the leaf (x_z) and Y_a is the total number of pixel in the leaf .

The probability density functions as a mixture of Gaussian model

$$p(\frac{A}{\phi_m})=\sum_{m=1}^{k}\alpha_m p\left(\frac{I}{\phi_m}\right) \tag{10}$$

Where k is the mixing probabilities of α_m component. Gaussian mixture component can be represent as

$$\phi_m=[\mu_m,V_m] \tag{11}$$

Where μ_m represents the mean and V_m represents the covariance.

$$\mu_m=\frac{\sum_{i=1}^{N}E_k^iA^i}{\sum_{i=1}^{N}E_k^i}$$

$$V_m=\frac{\sum_{i=1}^{N}E_k^i(A^i-\mu_k)(A^i-\mu_k)^T}{\sum_{i=1}^{N}E_k^i}$$

At every iteration process in the clusters, Gaussian mixture is estimated with the help of EM algorithm. The EM algorithm has comprises of two steps. In the E step, weight is assets by summing to one for each cluster. A^i, i=1,2,….,N where A^i has three components, corresponding to the L,A and B color channels .

$$E_k^i=\frac{\alpha_k p\left(\frac{A^i}{\hat{\phi}_m}\right)}{\sum_{m=1}^{k}\alpha_m p\left(\frac{A^i}{\hat{\phi}_m}\right)} \tag{12}$$

Where $\overline{\varphi_m}$ denotes the estimated parameters for the m^{th} component obtained by the iteration process.

$$\alpha_m = \frac{1}{N}\sum_{i=1}^{N} E_k^i \tag{13}$$

E. Color Feature Extraction

The color features are taken from the histogram of the segmented image. The histogram is a representation of numeric data which is distributed. In feature extraction, the histogram is calculated for every channel. In addition, the feature set is formed by concatenating features in a single array

F. RGB Histogram Featurs and HSV Histogram Features

Leaf image from the plants has 3 channels, RGB images, in which the individual channel contains different information. In the red channel, more information can be obtained where as in blue channel less information is obtained. The histogram is a statistical distribution of images as the sum of frequencies of intensity levels. The HSV feature gives the illumination invariance caused due to different lighting conditions. For the HSV histogram features, RGB image is transformed to HSV color space. In addition, the histogram features are formed by concatenating the individual channels. The RGB and HSV histogram features are given in eq. and eq. respectively.

$$(R,G,B) = [\sum_{I=0}^{M} f_r \sum_{I=0}^{M} f_b \sum_{I=0}^{M} f_g] \tag{14}$$

Where M represents the total number of gray levels, f_r, f_b and f_g represents the frequency value of I^{th} gray level of R, B and G channels of the image.

$$(H,S,V) = [\sum_{I=0}^{M} f_h \sum_{I=0}^{M} f_s \sum_{I=0}^{M} f_v] \tag{15}$$

Where M represents the total number of gray levels, f_h, f_s and f_v represents the frequency value of I^{th} gray level of H, S and V channels of the image. The combined set of {RGB, HSV} is formed by hybrid the HSV histogram features followed by RGB histogram for getting improved performance.

G. Imperialist Competitive Algorithm

Imperialist Competitive Algorithm is an evolutionary algorithm based on human phenomena. ICA starts with an initial population of two categories: The best countries are selected as imperialist and the rest are from the colonies. The fact that the imperialist completion is ruled for obtaining the most powerful emprise which tends to increase their power, while the poorest one tends to collapse. This phenomenon decrease the imperialistic countries during the run time and the colonies of the defeated imperialist will leave and move to another empire.

Step 1: Initialization of the empires

In an N dimensional, a country is an L*N array. This array is defined as follows

$$Country = (f_1, f_2 .... f_n) \tag{16}$$

Initially population is created randomly with uniform distribution and is divided into imperialists and determined from the countries with the highest cost. The cost of the countries is defined by

$$cost = c_{ij} = f(x_1, x_2 ... x_N) \tag{17}$$

The colonies can be distributed among the imperialists with respect to the power of each imperialists .The normalized cost for the imperialists can be defined by

$$c_{nor} = c_n - max_i(c_{ij}) \tag{18}$$

Where c_n is the cost of n^{th} imperialist and c_{nor} is the normalized cost. Finally, the normalized power for each imperialist is defined by

$$P_{nor} = \frac{|c_{nor}|}{\sum_{i=1}^{I_q} c_{ij}} \tag{19}$$

Where I_q is the total quantity of imperialists. The initial number of population of an empire can be determine from the normalized power of an imperialists and is defined by

$$N.c_{nor} = round(P_{nor}.N_l) \tag{20}$$

Where $N.c_{nor}$ is the initial number of colonies (infected leaves in the data set) and N_l represent the quantity of colonies (the lesion area in the data set).

Step 2: Movement of colonies towards the imperialist

Moving the colonies in a space domain towards its imperialist is called assimilation. The distance between the colonies and their imperialist is called assimilation coefficient the new position of the colony can be computed by

$$CP_{new+1} = CP_{new} + \gamma.\delta..d \tag{21}$$

Where is the colony's position, is the assimilation coefficient, δ is the random number which is normally distributed in the range of (0, 1) and d is the distance between colony and imperialist. After this movement, new position of a colony is determined will higher cost than the imperialist. So this colony will be considered as the new imperialist where as the old imperialist will be considered as a colony of the same

Step 3: Evaluation of the total cost of an empire

The cost of an empire (lesion area in the data set) is affected by the imperialist cost which may also affected by the colonies cost. The total cost of n[th] empire can be determined by

$$C_{total} = C(i) + \in .mean(cost(e)) \tag{22}$$

Where $\in$ is the positive and represent the cost of colonies.

Step 4: Realization of an imperialist completion

The imperialist competition is implemented by choosing the weakest colony which will lose their power partially and will be collapsed one by one. The normalized cost can be defined by

$$C_{nor} = T.cost_{nor} - max_i(C_{ij}) \tag{23}$$

$T.Cost_{nor}$ is represented by the total cost of empire

H. Optimization Based ICA-SVM Classification

ICA-SVM is optimization based classification technique is proposed for brinjal leaf classification. The aim of this system is to optimize the SVM classifier accuracy by automatically solving the SVM model selection by estimating the highest cost of the colony and radial basic kernel parameters which is a powerful tool in pattern recognition. The significant features of SVM are kernel based feature spaces. The main idea of SVM is hyper-plane separation, that can be separated linearly but cannot be mapped the predictors. If it is higher dimensional, then it can be separated linearly. Usually, the misclassification problem arises due to the selection of wrong kernel function. So that the best location can be decided for the decision plane for making the clear kernel function to create linear boundaries. To train the support vector classifier is defined as

$$S = \{(p_i, u_i) p_i \in (-1,1)\}_{i=1}^{n} \tag{24}$$

Where, p_i represents an input feature vector containing k attributes of training sample and q_i is the desired output. The main goal of the classification is splitting the data into five classes of diseases by means of hyper-plane. In order to obtain high performance, SVM classifier has extended the hyper-plane margin. If the two classes are linearly non-separable, then a non-linear transformation is needed from input space to feature space as given in Eq.(A.25).

$$\varphi(p) = p \in R^k \to R^m, k << m \tag{25}$$

In order to obtain linear separability in feature space, the hyper-plane can be

$$f(p)=\sum_{i=1}^{N}x_i\varphi(p_i)+b\geq 1.\forall_i : q_i=+1$$

$$f(p)=\sum_{i=1}^{N}x_i\varphi_i(p_i)+b\leq -1\forall_i : q_i=-1$$

The system is derived from the hyper-plane for optimization based on ICA. In ICA, algorithm starts with the leaf disease data set called countries. The highest cost is chosen as the imperialists and the rest form the colonies of the imperialists. To implement optimization based ICA-SVM classification, the RBF kernel function is used. Since the RBF kernel function can analyze based on the higher dimensional data. The RBF kernel and the colony which represent the leaf disease data set must be optimizing using ICA-SVM system.

$$KF(p_i,p_j)=\varphi(P_i).\varphi(P_j) \tag{26}$$

The hyper-plane can be defined by

$$f(p)=\sin n(\sum_{i=1}^{N}\gamma_i q_i KF(P_i,P_j))+b \tag{27}$$

Where $0\leq\gamma_i\leq\varepsilon$

III. Results and Discussion

For this research different types of Brinjal leaves, both healthy and unhealthy are collected from various farms in different locations over South India (Nagercoil, Valliyoor and Panakudi and Kerala (Neyyattinhara). The collected images consist of various diseases such as. Pseudomonas solanacearum, Cercospora Solani, Alternoria Melongenea, Tobacco mosaic virus and Pythium Aphanidermatum as shown in Fig A.2. The data set are divided into groups such as 80% for training and 20% for testing.

Fig A.2. Pseudomonas solanacearum, Cercospora Solani, Alternoria Melongenea, Tobacco mosaic virus and Pythium Aphanidermatum

Segmentation results of each algorithm are compared. As Ostu algorithm is severely affected by background noise and cannot separate the spots from the background. While the FCM algorithm is greatly improved over Ostu segmentation. Because this FCM algorithm can segment the spots and its noise resistance is trediblily higher than Ostu segmentation. But the Multiscale lesion based fuzzy segmentation effectively eliminates the effects of noise and background during image processing and also achieves more accurate segmentation on sharp edge spots. Compared to other two algorithms, the fuzzy lesion based segmentation achieved the best segmentation even in noisy spots as shown in Fig A.3.

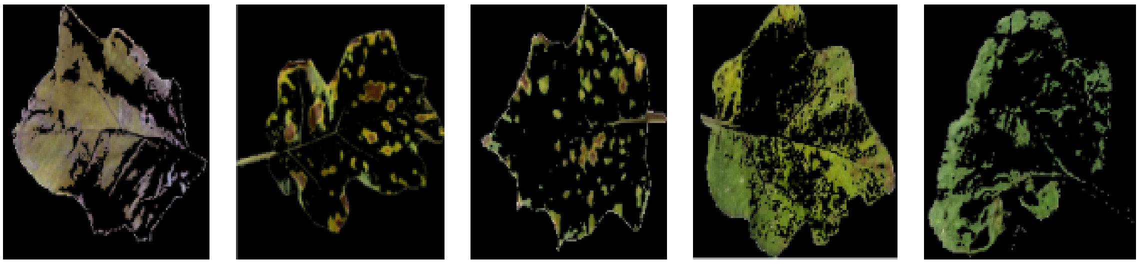

Fig A.3. Multiscale lesion based Fuzzy segmentation Aphanidermatum

The number of True Positive (TP) False Positive (FP) True Negative (TN) and False Negative (FN) are used in evaluating the performance of the segmented results. Sensitivity and specificity are widely used in diagnostic purpose for the identification of diseases. Sensitivity refers to the proportion of leaf with diseases, which has an infected part of leaf.

$$Sensitivity = \frac{TP}{TP + FN} * 100 \tag{28}$$

Specificity refers to the proportion of leaf without diseases, which has foliage in some part of leaf.

$$Specificity = \frac{TN}{TN + FP} * 100 \tag{29}$$

Accuracy is used as an overall measure and can be represent by

$$Accuracy = \frac{Sensitivity + Specificity}{2} * 100 \tag{30}$$

Table A.1. Performance evaluation for the segmented results.

Segmentation method	Sensitivity	Specificity	Accuracy
Ostu	0.3589	0.3879	54.36
FCM	0.4387	0.4298	66.43
Proposed	0.6692	0.6074	94.37

To classify different type of diseases using SVM method with the help of feature set for training and testing phase are compared with two other classification technique namely, K-nearest neighbor (K-NN) and the Radial Basis Function (RBF) Neural Network classifier. To improve further accuracy of the SVM classifier, optimization based ICA-SVM classification technique is applied based on the different feature set. Average accuracy is obtained from SVM classifier based on the RBF kernel and the results have better than those achieved by KNN and RBFN classifier. The proposed optimization based classification method aims to improve the SVM classification by evaluating the effectiveness of this methodological enhancement. For this purpose, the ICA –SVM classifier is applied to the available training data set. At convergence of the optimization process, the ICA-SVM classifier accuracy is evaluated on the test samples. For RGB histogram feature, its worst class accuracy was obtained, for blue histogram feature which is 90.10%, while green histogram feature has 91.60% and for best class accuracy for red histogram feature 98.30%. In the same way for HSV histogram, its worst class accuracy was obtained, for HSV feature which is 92.30%, while Saturation feature has 98.20% and for best class accuracy for Value features 98.40% as shown in Table A.2.

Table A.2. Accuracy results for different classifier using RGB and HSV histogram feature

Diseases	Feature sets	KNN	RBFNN	SVM	ICA-SVM
1 2 3 4 5	R	81.40%	87.60%	96.40%	98.30%
	G	78.60%	83.40%	90.70%	91.60%
	B	76.50%	81.60%	88.30%	90.10%
	RGB	73.90%	84.30%	94.40%	96.50%
1 2 3 4 5	H	87.30%	90.40%	94.10%	98.20%
	S	89.90%	94.20%	97.60%	98.10%
	V	88.50%	92.70%	96.30%	98.40%
	HSV	81.30%	84.30%	86.20%	92.30%

The capability of ICA-SVM classifier to reduce the gap between the worst and the best class accuracies while keeping overall accuracy at a high level. The performance of RGB, HSV for different classifier is compared on the basis of accuracy. Further, the combination of these features is useful in the detection and identification of the infected part of the leaves as shown in Table 3.

Table A.3. Performance of trained classifier on test images using concatenating RGB and HSV histogram feature based on accuracy.

Diseases	Concatenating feature	KNN	RBFNN	SVM	ICA-SVM
1 2 3 4 5	RGB and HSV	91.40%	94.30%	97.40%	99.80%

According to Fig A.4. and Fig A.5. KNN reached the maximum number of iterations each time, while the running time is significantly longer than other algorithms. When using RKFN for classifying the types of diseases, running time and number iterations are greatly reduced as compared to KNN classifier. However, RKFN classifier still requires many iterations and extensive running time for classifying five different types of diseases. When using SVM classifier, running time was significantly better than previous two algorithms but still required much iteration. By using optimization based SVM classifier, the number of iterations is fewest the running time is shortest and producing better accuracy results.

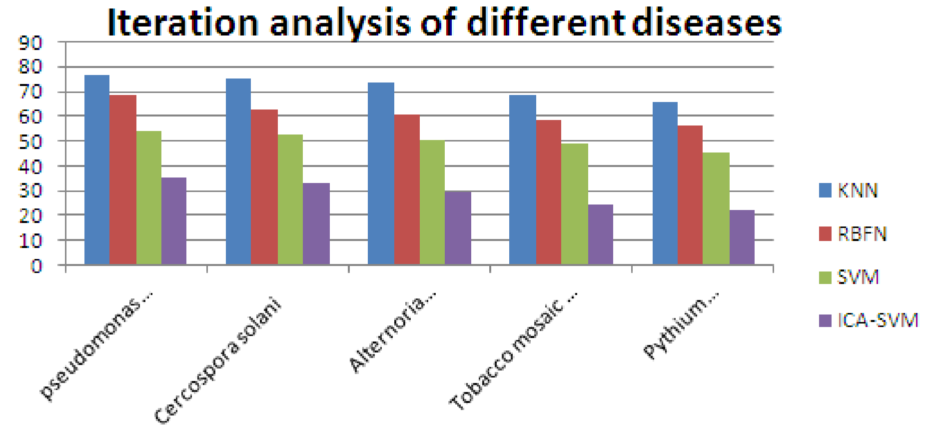

Fig A.4. Iteration analysis of different diseases

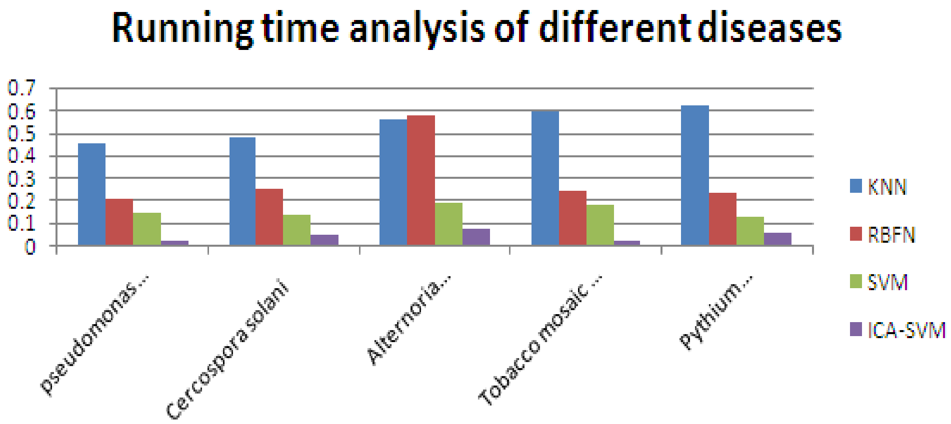

Fig A.5. Running time analysis of different diseases

IV. Conclusion

Accurate identification of disease image is important for both diagnosis and giving precaution to the farmers. Optimization based ICA-SVM classification technique is used for improving the SVM classification with the help of RBF kernel. These parameters proved to be excellent for leaf disease detection by concatenating the feature set which produce an accuracy of 99.80% which is better compared to other existing technologies. Besides, the feasibility of a real time implementation of the expert diagnosis system is made more accurately by increasing the capability of detecting and classifying different types of diseases.

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