

Contents lists available at ScienceDirect



Journal of King Saud University – Computer and Information Sciences

journal homepage: www.sciencedirect.com

Machine vision based papaya disease recognition

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ARTICLE INFO

Article history:

Received 22 March 2018

Revised 7 June 2018

Accepted 13 June 2018

Available online xxxx

Keywords:

Papaya disease

Agro-medical expert system

Machine vision

k-means clustering

Support vector machine

ABSTRACT

Over the years little research has been performed for vision-based papaya disease recognition system in order to help distant farmers, most of whom require proper support for cultivation. Due to advancement of vision-based technology we find a good solution to this problem. Papaya disease recognition mainly involves two challenging problems: one is disease detection and another is disease classification. Considering this scenario, here we present an online machine vision-based agro-medical expert system that processes an image captured through mobile or handheld device and determines the diseases in order to help distant farmers to address the problem. Some experiments are performed to show the utility of the proposed expert system. First, we propose a set of features from the view point of distinguishing attributes. K-means clustering algorithm is used in order to segment out the disease-attacked region from the captured image and then required features are extracted to classify the diseases with the help of support vector machine. More than 90% classification accuracy has been achieved, which appears to be good as well as promising by comparing performances obtained with recently reported relevant works.

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1. Introduction

Bangladesh is a developing as well as densely populated country, where the prominent portion of the population depends on agriculture. It is agriculture that has managed employment for the astonishing 47% of the total population of the country (Agriculture in Bangladesh, xxxx). It is easily recognizable that it also has a remarkable contribution towards the GDP comprising 16% on the whole (Agriculture in Bangladesh, xxxx). After satisfying the local demand, Bangladesh has been exporting the agricultural commodities. To uphold this status, it is important that the

quality of the agricultural product must be maintained with proper care. In Bangladesh, the rate of literacy is only 64.6% (List of countries by literacy rate, 2018) and most of the farmers are illiterate. They have hardly any training on farming with advanced technology. Again, there are few problems that come into play. One of them is transportation problem and for this they cannot reach the agriculture centers easily. Even if they need any suggestion, they cannot reach the proper place for help. Another problem is the ignorance of the farmers towards the advanced technology due to the lack of education. They are comfortable with the ancient agricultural tools and mechanisms. If they are provided with proper support for producing better and disease-free crops then it will be highly beneficial for them. The reader should keep this in mind that in this paper, we are proposing an online machine vision based agro-medical expert system which works on the image captured through mobile or handheld device and determines the contamination of the product by diseases. Among many agricultural products, we have chosen papaya, an immensely popular and enormously cultivated fruit cum vegetables in Bangladesh. It is not only cultivated in firm land but also in yard by amateur gardeners as shown in Fig. 1. During the cultivation period, papaya is attacked by many diseases causing considerable

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Peer review under responsibility of King Saud University.



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<https://doi.org/10.1016/j.jksuci.2018.06.006>

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Please cite this article in press as: Habib, M.T., et al. Machine vision based papaya disease recognition. Journal of King Saud University – Computer and Information Sciences (2018), <https://doi.org/10.1016/j.jksuci.2018.06.006>



Fig. 1. Cultivation of papaya in Bangladesh: (a) Extensive papaya cultivation by professional farmer (b) On-yard papaya cultivation by amateur gardener.

damage. Consequently, the farmers face a huge economic loss. It is reported that about 39.9% of post-harvest losses of papayas were estimated in Bangladesh, for which fungal diseases were one of the major reasons (Hamim et al., 2014). It is also discovered in (Hamim et al., 2014) by a survey on ripe papaya in Mymensingh region that anthracnose is the most detrimental fungal disease of ripe papaya.

In this paper, we perform an in-depth exploratory research on papaya disease recognition following machine vision based approach. We propose an agro-medical expert system that can process papaya image and recognize the contamination of any disease in it. A feature set has been proposed for recognizing the diseases. Image processing techniques are used to extract the features from images. Then support vector machine (SVM) is used for successful classification of the diseases. The system is supposed to work almost in real time.

The rest of the paper is organized as follows. Section 2 describes the architecture of the proposed agro-medical expert system. Section 3 describes the current state of a solution to address the problem of automated fruit fault inspection. Section 4 explains the diseases as well as the features. Feature extraction mechanism is also presented in this section. Section 5 describes the entire methodology of our system. Section 6, shows the results and discussions. Finally, summary, limitations and future scope are presented in Section 7.

2. Literature review

The problem of machine vision-based disease or fault recognition can be decomposed into two domains, namely fault detection and fault classification. Some researchers confine their works on fault detection only, whereas some encompass the area of both fault detection and classification. However, very few attempts have been made for machine vision-based fruit disease recognition, specially focused on papaya. Dubey and Jalal (2014), Barbedo (2013) and Raut and Ingole (2017), in their review works, delved into not only state-of-the-art approaches for automated fruit and vegetable classification and fruit and leaf disease recognition but also the performances obtained by deploying these approaches. The notable thing is that none of these review works have not provide any research advancement on papaya diseases.

Chopaade and Bhagyashri (2016) performed an image processing based poor work in order to address disease detection only. They have not followed a vision-based approach, and that is why no features are presented and no classifier is used. They have only performed histogram-based segmentation for detecting fruit leaf (including papaya) disease. Hence their work cannot be considered as a successful vision-based application.

Samajpati and Degadwala (2016) proposed a hybrid approach for apple fruit disease detection and classification. By hybrid, they have meant fusion of features. They have presented two types of features, namely color-based and texture-based features, which are composed of thirteen features in total. Three types of infections of apple fruits were considered in their cluttered work. It is not clear in their cluttered work that whether the diseased part of apple image has been segmented out using *k*-means clustering techniques and then used color and texture features together to classify the disease through random forest classifiers or these two steps happens in reverse order. For classification, they have used seventy (70) images in training data set and ten (10) images per class in test data set. Since they have used different fusion of features, their results of accuracies obtained ranges from 60%–100%. They have not performed any analysis of performance results obtained rather than just showing the varying accuracy. Batule et al. (2016) have performed a very much uninformed and vague work. Although they have proposed a method to detect the leaf disease by using noise removal technique and *k*-means clustering segmentation, almost all details are missing in their paper. They have also left the classification task undone by just telling that their work can be extended with SVMs in order to classify diseases. In fact, they have neither presented a feature set nor used SVMs for classification. Kurniawati et al. (2009) have tried to follow a vision-based approach for recognizing three paddy diseases only. They have separately used two thresholding segmentation techniques, namely local entropy and Otsu, in order to extract features. They have worked with two types, namely shape and color, features consisting of five (5) features in total. That means their span of research work is quite low. Although they have claimed to use rule-based classifier, no detailed information is provided in this regard. That is why the accuracies obtained by their approach (94.7% for local entropy and 61.2% for Otsu) do not manifest anything robust. Rozario et al. (2016) have worked with an image processing based approach. That means they have focused their work on only detecting faults of fruits and vegetables, namely apple, banana, tomato and potato. They have not performed no classification work. Naikwadi and Amoda (2013) applied a questionable and weakly informed vision-based approach for recognizing plant leaf diseases. They have failed to provide the information of not only number of plants but also accuracy obtained. They have claimed to use only thirty-two (32) image samples. They have claimed to use ten (10) color and texture features with neural network processing technique for the recognition of five plant leaf diseases, but most of the relevant information is missing in their paper. Although Kumar and Suhas (2016) have claimed to apply vision-based approach for recognizing different fruit diseases,

their work has become questionable and inadequately informed due to missing of many important details. They have claimed to use ten (10) different fruits, but the number of diseases dealt by them has not been reported. They have claimed to use a dataset of two hundred and forty-three (243) images, but they have not mentioned the number of features they used for classification. In essence, they have made their presentation of work cluttered. Missing of information of important details has weakened their obtained classification accuracy of about 87.47%.

Considering the research works described above, we can conclude that none has performed any in-depth research work on papaya disease recognition. Moreover, most of the works involving fruit or vegetables or leaf disease recognition are poor and not up to the mark. So, it is the clear research gap between current state of the works and up to the mark work.

3. System architecture

The architecture of online machine vision-based agro-medical expert system for recognizing the papaya disease is shown in Fig. 2. It originates with the hypothesis that someone, i.e. a farmer or a user captures an image of a disease affected papaya using a mobile phone or handheld device, where the proposed mobile app is already installed. Then he/she will send the image to our proposed expert system by using the app. After receiving the image through Internet at front-end software, it is sent to the back-end server, where our agro-medical expert system installed. The system will give its feedback based on the input image. The feedback will be dispatched as an SMS to the user's handheld device through the front-end software.

4. Research methodology

Fig. 3 shows a solution framework to the problem of machine vision-based papaya disease recognition. It commences with a color image of faulty papaya. The image data are collected locally as well as from Internet. First, the image is converted into a fixed-sized image by using bicubic interpolation (Bicubic interpolation, xxxx). Suppose the intensity values I and the derivatives p_x , p_y and p_{xy} are known at the four corners $(0, 0)$, $(0, 1)$, $(1, 0)$ and $(1, 1)$ of the unit square. Then the interpolated intensity surface can be written using (0).

$$p(x, y) = \sum_{i=0}^3 \sum_{j=0}^3 a_{ij} x^i y^j, \quad (1)$$

where a_{ij} are coefficients.

Then the contrast of the image is enhanced using histogram equalization technique. Suppose C is the number of columns in pixels, i.e. width, R is the number of rows in pixels, i.e. height, n_k is the number of pixels that have color intensity r_k , and L is the total number of possible color intensity levels in the image; then the processed or color-mapped image is obtained by mapping each pixel with color intensity r_k into a corresponding pixel with color intensity s_k using (1).

$$s_k = T(r_k) = \frac{L-1}{CR} \sum_{j=0}^k n_j, \quad (2)$$

where $k = 0, 1, \dots, L-1$.

Then the histogram-equalized image is converted from RGB color space to $L^*a^*b^*$ color space. This conversion takes place because Aqil Burney and Tariq (2006) reported that k -means clustering significantly segments images much better in $L^*a^*b^*$ color space as compared to RGB color space. First, transformation takes place from RGB color space to CIE (International Commission on Illumination) XYZ color space as written in (3) as per (Color Conversion Algorithms, xxxx).

$$\begin{bmatrix} X \\ Y \\ Z \end{bmatrix} = \begin{bmatrix} 3.240479 & -1.537150 & -0.498535 \\ -0.969256 & 1.875992 & 0.041556 \\ 0.055648 & -0.204043 & 1.057311 \end{bmatrix} \begin{bmatrix} R \\ G \\ B \end{bmatrix}. \quad (3)$$

In order for transforming XYZ color space into $L^*a^*b^*$ color space, we assume that X_n , Y_n and Z_n are the tristimulus values of the reference white. We assume more that

$$f(t) = \begin{cases} t^{\frac{1}{3}} & \text{if } t > 0.008856 \\ 7.787t + \frac{16}{116} & \text{if } t \leq 0.008856 \end{cases}. \quad (4)$$

Then we can write, as per (Color Conversion Algorithms, xxxx), the equations for L^* , a^* and b^* as:

$$L^* = \begin{cases} 116 \left(\frac{Y}{Y_n} \right)^{\frac{1}{3}} - 16 & \text{if } \frac{Y}{Y_n} > 0.008856 \\ 903.3 \frac{Y}{Y_n} & \text{if } \frac{Y}{Y_n} \leq 0.008856 \end{cases}. \quad (5)$$

$$a^* = 500 \left(f \left(\frac{X}{X_n} \right) - f \left(\frac{Y}{Y_n} \right) \right). \quad (6)$$

$$b^* = 200 \left(f \left(\frac{Y}{Y_n} \right) - f \left(\frac{Z}{Z_n} \right) \right). \quad (7)$$

Then the image is segmented into a number of regions using k -means clustering technique. Thus, faulty parts are differentiated from fault-free parts. From the faulty part then two types of feature

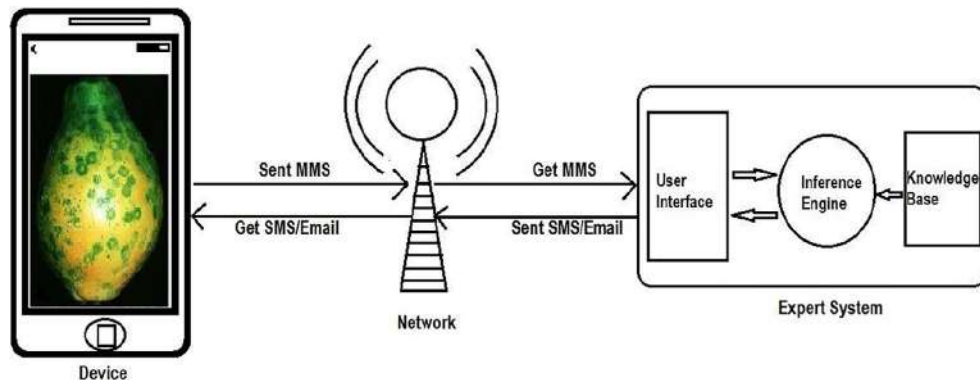


Fig. 2. The architecture of online machine vision-based agro-medical expert system.

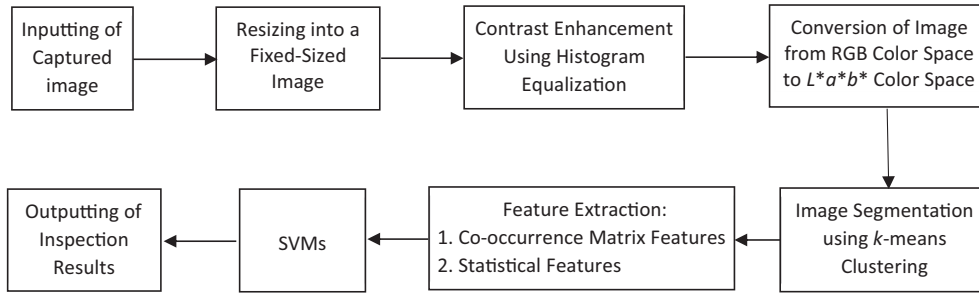


Fig. 3. Approach for solving the problem of machine vision-based papaya disease recognition.

vectors are formed, namely co-occurrence and statistical. We are going to describe these features in detail in the next section, i.e. Section 5.

We employ these feature vectors to SVMs. SVM can be considered as the extended form of linear classifier. There are plenty of application domains, in which SVM is proved to produce high accuracy and usually outperforms all other classifiers. It is originally designed for binary classification problems, but our problem is multiclass. In order to deal with our multiclass problem, we use a number of SVMs with the one-against-rest (1-*r*) approaches (Tan et al., 2006). After the SVMs are trained using training data set, we measure performance using test data set. In performance analysis, accuracy is not a rigorous metric for the real performance of a classifier, because it may not be well suited for evaluating classification models derived from imbalanced data sets, i.e. the numbers of observations in different classes vary widely. So, not only accuracy but also some other metrics are also required to keenly assess the performance of a classifier as described in Tan et al. (2006) and Han et al. (2012). A confusion matrix for a binary, i.e. 2-class problem reports the number of false positives (FPs), false negatives (FNs), true positives (TPs), and true negatives (TNs). In the case of multiclass, i.e. more than 2-class problems, the resulting confusion matrix will be of dimension $n \times n$ ($n > 2$). It is observed that the matrix contains n rows, n columns and $n \times n$ entries in total. From this matrix, it is not possible to directly calculate the number of FPs, FNs, TPs, and TNs. According to this approach, the values of FPs, FNs, TPs, and TNs for class i are calculated as (Confusion Matrix, xxxx):

$$TP_i = a_{ii}. \quad (8)$$

$$FP_i = \sum_{j=1, j \neq i}^n a_{ji}. \quad (9)$$

$$FN_i = \sum_{j=1, j \neq i}^n a_{ij}. \quad (10)$$

$$TN_i = \sum_{j=1, j \neq i}^n \sum_{k=1, k \neq i}^n a_{jk}. \quad (11)$$

Proceeding with this approach, the final confusion matrix, which is of dimension 2×2 , contains the average values of the n confusion matrices for all classes.

By using a confusion matrix, accuracy, sensitivity, specificity, precision, false positive rate (FPR), and false negative rate (FNR) of the recognition system are calculated. After our SVMs are trained, performance is measured in terms of these metrics using test data set. Thus, the SVMs become ready to classify papaya images as faulty and fault-free. Based on the confusion matrix accuracy, sensitivity, specificity, precision, FPR, and FNR are estimated in percentage as:

$$Accuracy = \frac{TP + TN}{TP + FN + FP + TN} \times 100\%. \quad (12)$$

$$Sensitivity = \frac{TP}{TP + FN} \times 100\%. \quad (13)$$

$$Specificity = \frac{TN}{FP + TN} \times 100\%. \quad (14)$$

$$Precision = \frac{TP}{TP + FP} \times 100\%. \quad (15)$$

$$FPR = \frac{FP}{FP + TN} \times 100\%. \quad (16)$$

$$FNR = \frac{FN}{FN + TP} \times 100\%. \quad (17)$$

We use holdout method (Tan et al., 2006; Han et al., 2012) in order to evaluate the performance of our classifier in terms of the evaluation metrics shown in equations (12)–(17). Then we apply receiver operating characteristic (ROC) curves for comparing the relative performances of three classifiers we use in total.

5. Disease and feature description

5.1. Description of diseases

Disease analysis is a very important part of our approach, because it helps to properly understand the flaws due to diseases and gives clues to appropriate features. In this work, we have dealt with five diseases, which frequently occur all over Bangladesh, namely black spot, powdery mildew, brown spot, phytophthora blight, and anthracnose. The pictures of the attacks of all of the diseases are shown in Fig. 4.

5.2. Extraction of features

Based on the analysis of diseases, a feature set, which consists of statistical and gray-level co-occurrence matrix (GLCM) features, is selected for recognizing the diseases. Tarek Habib and Rokonuzzaman (2011) have shown the discriminatory quality of statistical features in the context of textile defect recognition. Since in this work, we are also in quest for defects, we have chosen some discriminatory statistical features presented in Tarek Habib and Rokonuzzaman (2011). These features are discussed here.

- Mean (μ): If there are N pixels in faulty regions, M pixels in fault-free regions, and gray-scale color intensity of a pixel in faulty regions is represented by GS , then

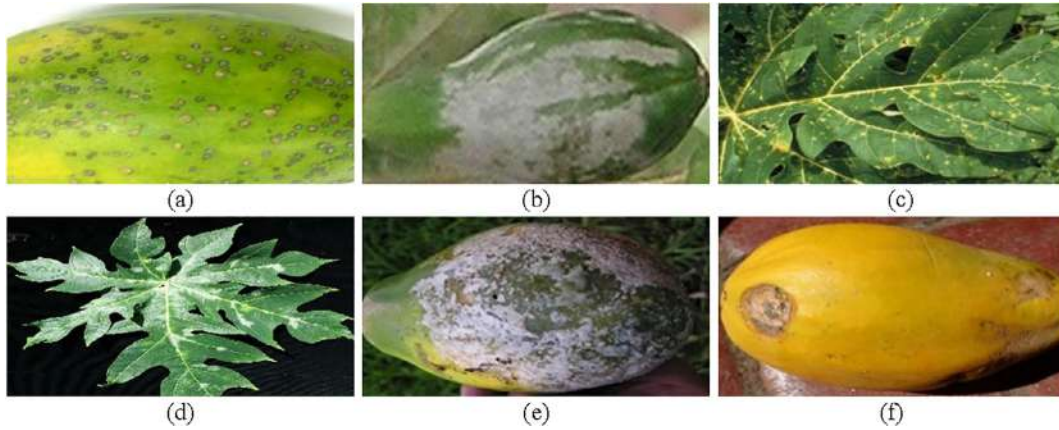


Fig. 4. Some diseases frequently occurred all over Bangladesh. (a) Black spot. (b) Powdery mildew (fruit). (c) Powdery mildew (leaf). (d) Brown spot. (e) Phytophthora blight. (f) Anthracnose.

$$\mu = \frac{\sum_{i=1}^N GS_i}{N} \quad (18)$$

- Standard deviation (σ): If there are N pixels in faulty regions, where GS and μ represent gray-scale color intensity of a pixel and mean gray-scale color intensity of all pixels respectively, then

$$\sigma = \sqrt{\frac{\sum_{i=1}^N (GS_i - \mu)^2}{N}} \quad (19)$$

- Variance (σ^2): If there are N pixels in faulty regions, where GS and μ represent gray-scale color intensity of a pixel and mean gray-scale color intensity of all pixels respectively, then

$$\sigma^2 = \frac{\sum_{i=1}^N (GS_i - \mu)^2}{N} \quad (20)$$

- Kurtosis (κ): If there are N pixels in faulty regions, where GS and μ represent gray-scale color intensity of a pixel and mean gray-scale color intensity of all pixels respectively, then

$$\kappa = \frac{\frac{1}{N} \sum_{i=1}^N (GS_i - \mu)^4}{\left(\frac{1}{N} \sum_{i=1}^N (GS_i - \mu)^2\right)^2} - 3 \quad (21)$$

- Skewness (γ): If the mean, mode, and standard deviation of gray-scale color intensity of all pixels in faulty regions are represented by μ , σ and Mo respectively, then

$$\gamma = \frac{\mu - Mo}{\sigma} \quad (22)$$

In addition to statistical features, a number of GLCM features is used, which are first proposed by Haralick et al. (1973). These features have been proved to be a useful method of extracting textural features from images, because they provide a measure of the variation in intensity at the pixel of interest by considering the relation between two pixels at a time. The features are discussed here.

Let us assume that $f(x, y)$ be a two-dimensional digital image of size $M \times N$ pixels with number of gray levels L . We more assume that (x_1, y_1) and (x_2, y_2) are two pixels in $f(x, y)$, the distance is d and the angle between the two and the ordinate is θ . Then a GLCM $P(i, j, d, \theta)$ becomes as per (Bicubic interpolation, xxxx):

$$P(i, j, d, \theta) = |\{(x_1, y_1), (x_2, y_2) \in M \times N : d, \theta, f(x_1, y_1) = i, f(x_2, y_2) = j\}| \quad (23)$$

In this work, five GLCM features have been used, namely contrast (C), correlation (ρ), energy (E), entropy (S) and

homogeneity (H). Eqs. (24)–(28) are formulas for calculating these five features:

$$\text{Contrast : } C = \sum_{i=0}^{L-1} \sum_{j=0}^{L-1} (i - j)^2 P(i, j). \quad (24)$$

$$\text{Correlation : } \rho = \frac{\sum_{i=0}^{L-1} \sum_{j=0}^{L-1} i j P(i, j) - \mu_x \mu_y}{\sigma_x \sigma_y}. \quad (25)$$

$$\text{Energy : } E = \sum_{i=0}^{L-1} \sum_{j=0}^{L-1} P(i, j)^2. \quad (26)$$

$$\text{Entropy : } S = - \sum_{i=0}^{L-1} \sum_{j=0}^{L-1} P(i, j) \log P(i, j) \quad (27)$$

$$\text{Homogeneity : } H = \sum_{i=0}^{L-1} \sum_{j=0}^{L-1} \frac{P(i, j)}{1 + (i - j)^2}, \quad (28)$$

where μ_x , μ_y , σ_x and σ_y are the sum of expected and variance values for the row and column matrix entries, respectively.

6. Experimental evaluation

We perform investigative experiment following our approach to machine vision-based papaya disease recognition as per Fig. 3. The starting point of our approach is to capture an image of papaya. One hundred and twenty-eight color images of faulty and fault-free papayas are gathered. The captured images are of different sizes. Images of different sizes are used in our experiment by considering the factor that different people will capture papaya images using their own devices and send to our proposed expert system as shown in Fig. 2.

First, the captured image is converted into an image of size 300×300 pixels. This size has been chosen by taking the size of handheld device into account. Then contrast stretching of the image takes place by using color intensity mapping based on (1). Then the color-mapped image is segmented into a number of regions using k -means clustering technique. This segmentation algorithm is chosen since its better performance than most other existing segmentation algorithms is reported in Rozario et al. (2016). Thus, faulty parts are separated from fault-free parts. The step-wise images are shown for all types of faults in Fig. 5. Table 1 and Fig. 6 show the performance results of k -means clustering segmentation on different faults

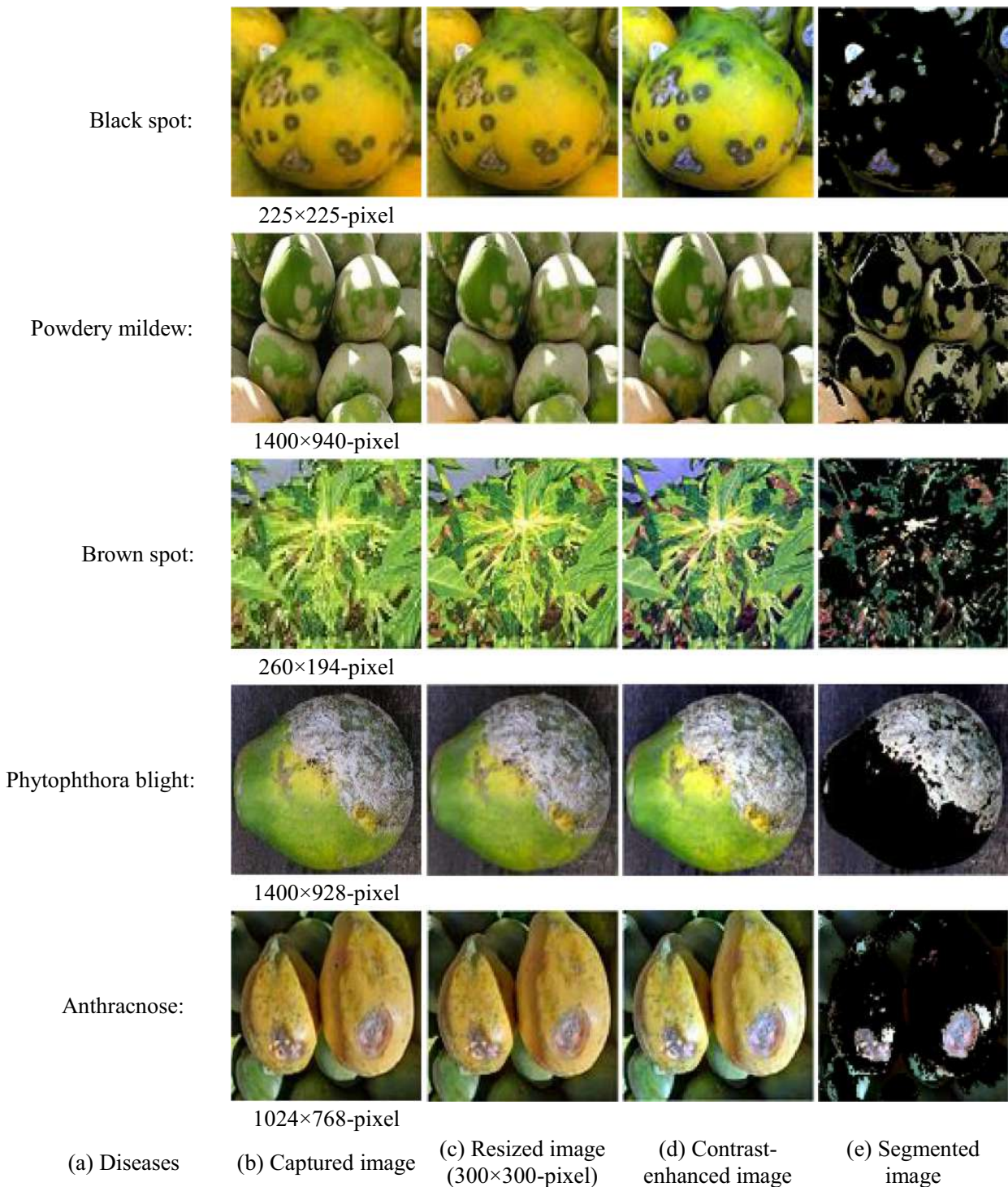


Fig. 5. (a) Diseases, (b) Captured image, (c) Resized image, (d) Contrast-enhanced image, (e) Disease-attacked segmented regions.

by comparing the k -means labeling with manually labeled ground truth images. We see from Table 1 that black spot and anthracnose are contracted and powdery mildew, brown spot and phytophthora blight are spread out with respect to ground truth image. Anthracnose is most localized and brown spot is least localized.

Good quality of segmentation is required since it affects the performance of subsequent steps. In order to assess the performance of k -means clustering segmentation, manually labeled

ground truth images are used. The performance results are given in Table 1. We used total 129 color images of papaya (with and without disease). Fig. 7 shows two test images where the values of all extracted features are shown. Between these two one is classified correctly and the other one is classified incorrectly.

We split the entire sample data set into two parts, namely training part and testing part. We use holdout method (Tan et al., 2006) for selecting the proportion of data reserved for

Table 1

k-means clustering segmented region under different diseases with respect to ground truth.

Fault Category	Ground Truth Region	Estimated Region w.r.t. Ground Truth	Deviated Region w.r.t. Ground Truth
Black spot	100%	89.76%	-10.24%
Powdery mildew	100%	123.09%	+23.09%
Brown spot	100%	159.33%	+59.33%
Phytophthora blight	100%	109.11%	+9.11%
Anthraco nose	100%	93.17%	-6.83%
Total	100%	114.89%	+22.46%

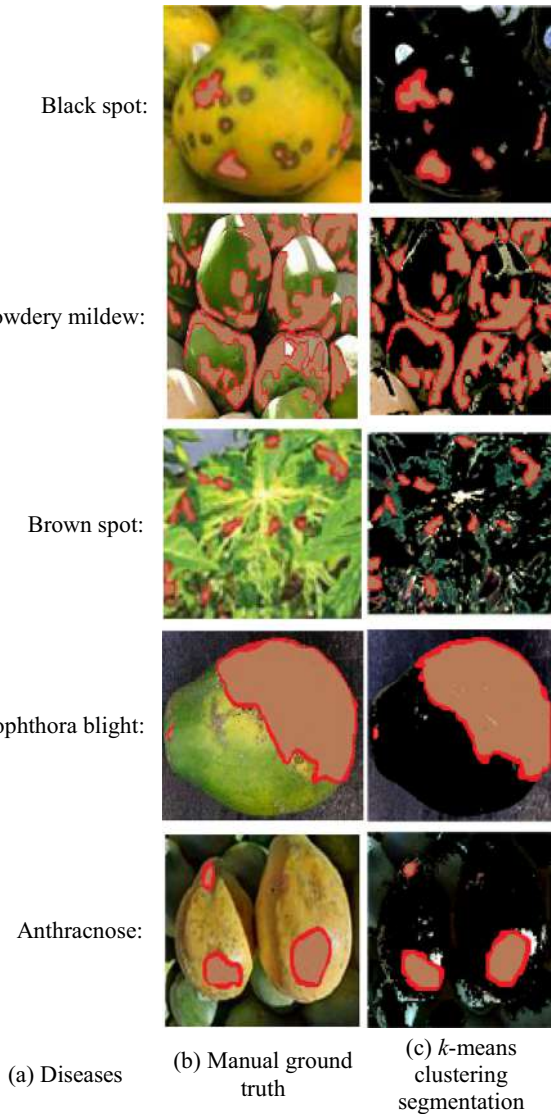


Fig. 6. (a) Diseases, (b) Manually determined ground truth of the attacked regions (c) Estimated attacked regions using *k*-means clustering.

training and for testing. We split the sample data set at the proportion of about two-thirds (84 color images) for training and about one-third (45 color images) for testing. In order to avoid model over fitting problem (that means to have low training error and low generalization error), we use a validation set. In accordance with this approach, we divide the original training data set into two smaller subsets. One

of the subsets is used for training, while the other one for validation. We fix two-thirds (56 images) of the training set for classifier building while the remaining one-third (28 images) is used for error estimation. We repeat holdout method five times in order to find the finally trained classifier. After each execution of holdout method, we find out the performance of the classifier using the test set. The five-times-found results are averaged in order to form multiclass confusion matrix and resulting six binary confusion matrices (Confusion Matrix, xxxx) as shown in Tables 2 and 3. Then analysis of results takes place.

Now comes the issue of using classifier. We use linear SVMs for nonseparable cases as our classifier. We have the training data $\{(\mathbf{x}_1, d_1), (\mathbf{x}_2, d_2), \dots, (\mathbf{x}_{84}, d_{84})\}$, where $\mathbf{x}_i = (\mu, \sigma, S, \sigma^2, \kappa, \gamma, C, \rho, E, H)$ is the input vector; $d_i = \pm 1$. Then the Lagrange multipliers $\{\alpha_1, \alpha_2, \dots, \alpha_{84}\}$ is calculated which maximize the objective function:

$$Q(\alpha) = \sum_{i=1}^{28} \alpha_i - \frac{1}{2} \sum_{i=1}^{28} \sum_{j=1}^{28} \alpha_i \alpha_j d_i d_j \mathbf{x}_i^T \mathbf{x}_j. \quad (29)$$

subject to the constraints

- (1) $\sum_{i=1}^{28} \alpha_i d_i = 0$
- (2) $0 \leq \alpha_i \leq C$ for $i = 1, 2, \dots, 28$

where C is a positive parameter working as an upper-bound value of α_i .

We use a high numeric value for C in our work. We set all parameters of SVMs through a training process. We have used four kernels, namely linear, polynomial, sigmoid and Gaussian. Since their accuracy varies over the range only ± 0.75 on our not so large data and linear kernel is the simplest among them and takes the least time to process, we use linear kernel finally. The summary of stepwise experiments performed is shown in Table 4.

In order to analyze the performances of the trained classifier, the final binary confusion matrix is formed as shown in Table 5. Then accuracy, sensitivity, specificity, precision, *FPR*, *FNR* are calculated from this matrix as shown in Table 6 and accuracy per class is shown in Table 7.

We see from Table 6 that accuracy is 95.2%; that means overall recognition rate is good enough. Sensitivity is 85.6%; that means the rate of recognizing fault-free samples is not so high; and that is why false negative rate is a bit high (14.4%), which is not good. Again, specificity is 97.12%; that means the rate of recognizing faulty samples is a bit high; and that is why false negative rate is a bit low (2.88%), which is good. Precision is 85.6%; that means fault-free sample recognition rate is not so high.

In the fashion described so far in this paper, we experimentally evaluate other two classifiers, namely decision tree and naïve Bayes, for making our assertion rigorous by dint of comparison, which is shown in Table 8. The detailed specifications of these two classifiers are given in Appendix A. We can see from Table 8 that SVMs outperforms the other two classifiers in terms of the six performance metrics, where the decision tree classifier stands in the middle by defeating the naïve Bayes classifier in terms of these six performance metrics.

In order to make our assertion more rigorous, we make use of receiver operating characteristic (ROC) curves. ROC curves can be used as a visual tool for comparing the performance of a number of classifiers. Moreover, the area under the ROC curve (A_{ROC}) provides another approach for evaluating which classifier is better on average. If the model is perfect, then its A_{ROC} must equal 1. A classifier whose performance is better than that of another would

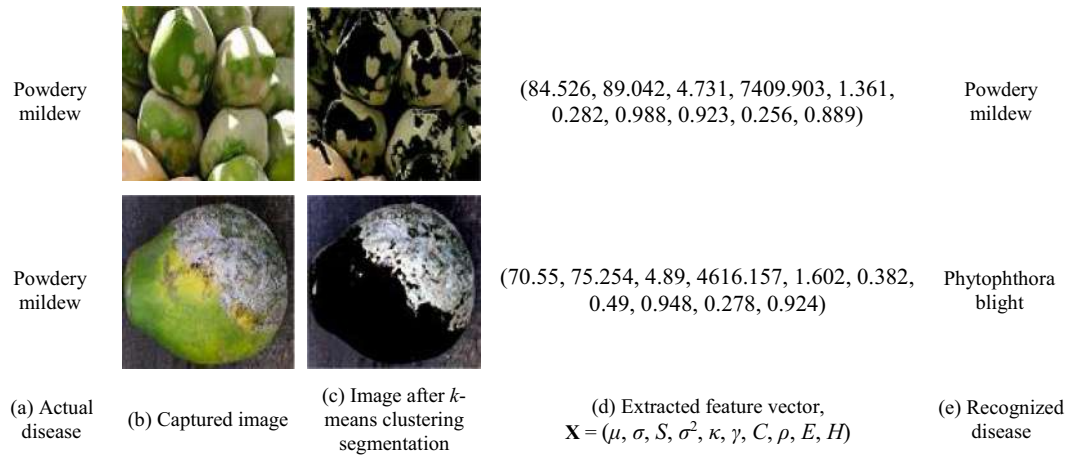


Fig. 7. The values of all features extracted from two faulty papaya images, where one is correctly classified and the other one is misclassified. (a) Actual disease, (b) Captured image, (c) Image after k -means clustering segmentation, (d) Extracted feature vector. (e) Recognized disease.

Table 2
The multiclass confusion matrix.

		Predicted Class					
		Black Spot	Brown Spot	Powdery Mildew	Phytophthora Blight	Anthracnose	Fault-free
Actual Class	Black spot	6.5	0	0	0	1	0
	Brown spot	0	7	0.5	0	0	0
	Powdery mildew	0	0	6	1.5	0	0
	Phytophthora blight	0.5	0	1	6	0	0
	Anthracnose	0.5	0.5	0	0	6.5	0
	Fault-free	0	0.5	0	0	0.5	6.5

Table 3
The binary confusion matrices for each class.

Class	Matrix				Class	Matrix			
Black spot			Predicted Class		Brown Spot			Predicted Class	
			+	–				+	–
	Actual Class	+	6.5	36.5		Actual Class	+	7	36.5
		–	1	1			–	1	0.5
Class	Matrix				Class	Matrix			
Powdery mildew			Predicted Class		Phytophthora blight			Predicted Class	
			+	–				+	–
	Actual Class	+	6	36		Actual Class	+	6	36
		–	1.5	1.5			–	1.5	1.5
Class	Matrix				Class	Matrix			
Anthracnose			Predicted Class		Fault-free			Predicted Class	
			+	–				+	–
	Actual Class	+	6.5	36		Actual Class	+	6.5	37.5
		–	1.5	1			–	0	1

Table 4
Summary of stepwise experiments performed.

Experiment Step	Method/Parameter Used
Resizing	Bicubic interpolation
Contrast enhancement	Histogram equalization
k -means clustering	$L^*a^*b^*$ color space
SVM classifier	Linear kernel, a high numeric for C

Table 5
The final confusion matrix contains the average values for all six classes.

		Predicted Class	
		+	–
Actual Class	+	6.42	1.08
	–	1.08	36.42

Table 6
Results of metric-wise performance of our SVM classifier.

Metric	Value
Accuracy	95.2%
Sensitivity	85.6%
Specificity	97.12%
Precision	85.6%
False positive rate	2.88%
False negative rate	14.4%

Table 7
Accuracy per disease class.

Disease Class	Value
Black spot	96.84%
Brown spot	94.71%
Powdery mildew	95.08%
Phytophthora blight	94.1%
Anthracnose	95.07%
Defect-free	95.24%

Table 8
Comparison of the three experimentally evaluated classifiers.

Classifier	Accuracy	Sensitivity	Specificity	Precision	False positive rate	False negative rate
SVMs	95.2%	85.6%	97.12%	85.6%	2.88%	14.4%
Decision tree	86.67%	60.0%	92.0%	60.0%	8.0%	40.0%
Naive Bayes	77.78%	33.33%	86.67%	33.33%	13.33%	66.67%

have a larger A_{ROC} . In this work, the ROC curves of all three classifiers is shown in Fig. 8 and their area under curves (AUCs) are shown in Table 9.

We can see from Fig. 8 that SVMs outperforms the other two classifiers, where the decision tree classifier stands in the middle by defeating the naïve Bayes classifier. This assertion is strengthened by Table 9 in terms of AUC values.

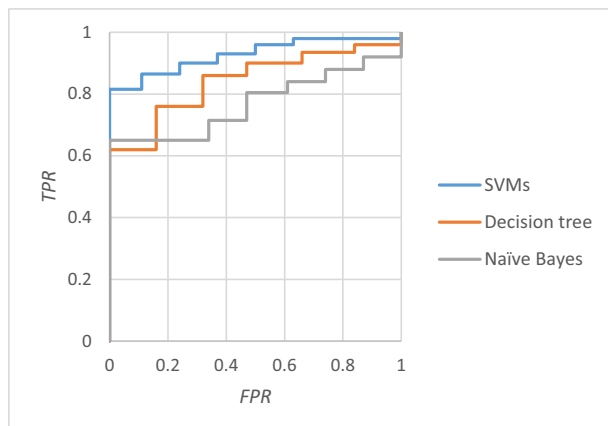


Fig. 8. The ROC curves of all three experimentally evaluated classifiers.

Table 9
AUC values of the three experimentally evaluated classifiers.

Classifier	AUC
SVMs	97.03%
Decision Tree	88.93%
Naive Bayes	80.89%

7. Comparative analysis of results

In order to evaluate the merits of our proposed agro-medical expert system in recognizing papaya diseases, we need to compare some recently published relevant research outcomes. The survey of the literature reveals that most of the research reports are limited to the demonstration of concepts of machine vision strategy for detection and classification of papaya diseases without the support of adequate numerical results and their comparison with similar works. Moreover, the absence of use of a common database of samples of papaya diseases makes it challenging to have a fair comparison of merits of different approaches. There have been observed some encouraging trends in papaya disease recognition research for past few years, but systematic and comparative performance evaluation based on practical assumptions is not sufficient. Despite such limitations, we have attempted to review the numerical results related to papaya disease detection and classification to assess comparative merits of our work. Table 10 shows an overview of all methods of different works including our works.

In the survey work (Dubey and Jalal, 2014), it is reported that the SVM classifier performs better as far as vision-based papaya disease recognition is concerned. The purpose of the work (Chopaade and Bhagyashri, 2016) is to recognize the leaf diseases affecting the fruit crops using image processing technique whereas the classifier and accuracy were not mentioned. In apple fruit disease recognition (Samajpati and Degadwala, 2016) process diseases are classified by using random forest classifier by taking 80 images as sample data size and the accuracy is fluctuated based on features. Image processing technique is implemented to detect (Batule et al., 2016) the leaf diseases and the diseases are classified using SVM but they have not mentioned any particular leaf as well as the efficiency of the proposed method. For developing a system for recognizing paddy leaf diseases (Kurniawati et al., 2009) two threshold methods have been applied on ninety-four paddy leaf images. The accuracy of two methods that used local entropy threshold is about 94.7% and Otsu threshold method is about 61.2% but no classification is employed in the proposed system. Paper (Rozario et al., 2016) introduced a computer vision-based approach to identify defected regions from several fruits (apple, banana) and vegetables (tomato, potato). This approach only detects the defected regions of fruits or vegetables but not for classification of the diseases. In paper (Naikwadi and Amoda, 2013) plant leaf disease is detected using histogram matching and the training process includes 32 samples from each class of leaves. Classification is implemented through a pre-trained neural network but accuracy was not mentioned.

With respect to the scenario discussed from the beginning of this section, our obtained accuracy of more than 90% turns out to be both good and promising enough. As we have mentioned before, due to the lack of uniformity in the image data set, i.e. captured images with different resolution, background texture and faults, performance evaluation and the nature of the intended application, it is not prudent to explicitly compare merits of our approach with other works.

Table 10

results of the Comparison of Our Work and Others' Works.

Method/WorkDone	Object (s) Dealt with	Problem Domain	Sample Size	Segmentation Algorithm	Classification Performed	Size of Feature Set	Classifier	Accuracy
This work	Papaya (Both fruit and leaf)	Recognition	126 images	<i>k</i> -means clustering	✓	10	SVM	90.15%
Chopaade and Bhagyashri, (2016)	Papaya, Mango, Banana (Leaf)	Detection	NM	Histogram based thresholding	×	NA	NA	NA
Samajpati and Degadwala (2016)	Apple (Fruit)	Recognition	80 images	<i>k</i> -means clustering	✓	13	Random forest classifier	60%–100%
Batule et al. (2016)	Leaf (NM)	Recognition	NM	<i>k</i> -means clustering	×	NA	NA	NA
Kurniawati et al. (2009)	Paddy (Leaf)	Recognition	94 images	Local entropy threshold Otsu method	✓	5	Rule-based classifier	94.7%
Rozario et al. (2016)	Apple, Banana, Potato, Tomato (Fruit)	Detection	63 images	<i>k</i> -means clustering Modified <i>k</i> -means clustering Otsu method	×	NA	NA	61.2% NM
Naikwadi and Amoda (2013)	Plant (Leaf)	Recognition	32 samples	<i>k</i> -means clustering	✓	10	Neural Network	NM
Kumar and Suhas (2016)	Fruit	Recognition	243 images	<i>k</i> -means clustering C-means clustering	✓	NM	<i>k</i> -nearest neighbor	87.47%

¹NM: Not Mentioned.²NA: Not Applicable.

8. Conclusion and future work

In this paper, we have presented a machine vision-based agro-medical expert system. Here, we have presented a two-feature set consisting of ten features in total to solve papaya disease recognition. Image processing techniques have been employed to extract the features. The classification of the papaya diseases has been accomplished with SVM and the relative merits of our work have been assessed by analyzing results of similar works thereafter. We achieved an accuracy of 90.15%, which is good as well as promising. There remains a potential future work with a very large data set of images to cover a wider range of papaya diseases.

Appendix A

(See)

Table A.1

Detailed specifications of the two classifiers decision tree and naïve Bayes.

Classifier	Specifications
Decision tree	Degree of impurity: Gini index Information gain: Entropy Minimum number of split = 2 Maximum depth of tree = ∞ [Nodes are expanded until all leaves are pure or until all leaves contain less than minimum number of split samples.]
Naïve Bayes	Gaussian distribution: Mean (μ) Variance (σ^2) Probability density function (f), where $f = \frac{1}{\sqrt{2\pi}\sigma} e^{-\frac{(x-\mu)^2}{2\sigma^2}}$

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