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To Measure The Effectiveness Of Image Classification Using Support Vector Machine And Extreme Learning Machine

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ABSTRACT

In agricultural field, the most popular research area is disease identification and classification. The plant disease identification using the image analysis method reduces farmers relying on growers to safeguard farm goods. Recognition and Categorization of Rice crop Leaf Disease detection using a Novel Technique is presented in this paper. The designedmodelcomprises four major phases: pre-processing, segmentation, feature engineering and leaf disease cauterization. Primarily, the input imagesdimension is cropped and resized into 300×450 pixels to decrease the memory usage and computation power of the image. The black color in the RGB designindicates the pixel value and the imagebackground (non-diseased portion) was eliminated. The K-means clustering algorithm segments the disease-affected leaf disease parts. Color (standard deviation and mean) and texture features (energy, correlation, contrast, and homogeneity) are extracted. The Support Vector Machine (SVM) based Extreme Learning Machine (ELM) model classifies the paddy leaves into two classes that is either healthy or unhealthy. The implementation process is handled in Google Colab. The proposed method demonstrated superior results compared to other state-of-art techniques.

Keywords: *Leaf disease, K-means clustering, Support Vector Machine and Extreme Learning Machine.*

1. INTRODUCTION

Digital Image Processing [1] uses image processing techniques to process digital images in a computer. Image generation, enhancement, and restoration are the three divisions of image processing. Image generators produce numerous sensor models to figure out images from more than one extended channel. Before processing data or information to increase the image quality from a certain procedure. Slicing, histogram equalization, and contrast stretching are some of the methods of image enhancement [2]. The basic factors of image processing are image enhancement, restoration, acquisition, segmentation, compression, color image processing, and multi-resolution processing. The image of visual representation is enhanced by increasing the features.

Further, the restoration process was utilized to determine the original picture from the noisy image. Typically in image processing, there are three distinct levels as low, intermediate, and high. It is used in recognizing the image, handwriting analysis, and medical diagnosis finds various images from different patterns. The image of the features is identified to detect various parameters. In feature extraction [3], computing devices are processed from a large set of data to minimize the data group from dimensionality reduction. It increases the inference speed and training reduces the proportions of data to remove unnecessary data. In this process, the most relevant and important image attributes are tracked from the available data and selecting the feature from the original subset. It is a reduction process that decreases the class from an initial subset and has a large number of parameters. The feature vectors [4] are derived from a group of parameters to represent an object to classify and allow the parameters in the features. It identifies the image from the patterns by the features such as regions, points, edges, and corners.

The features are selected by the followings methods like filter, embedded, and wrapper methods. It increases the accuracy and decreases the training rate and over fitting. The images are classified by a set of rules to process the data is termed image classification [5]. For analyzing the images the classification is used to evaluate the size and color of the object. The types of classification to analyze the image are supervised unsupervised and object-based image analysis. The data is predicted to determine the related individual classes. Binary encoded classification requires two classes of the image from the number of pixels to be classified. Classification and regression are the two types of supervised classification [6] to determine the new data from the unknown features. The training samples are not used for the basic divisions to process the image dataset.

The classes determine the pixel groups, which evaluates the characteristics of sample classes. Image fragmentationwas deployed to classify the objects from the classification image pixels. The spectral information determines the classification of pixels to the original pixels. To classify the object's size, shape, and spectral properties is to assess the object-based categorization model. The pixel-based image categorizationdesignsare classified for each pixel. In image analysis, the feature engineeringis used to recognize the characters of pixels. Image analysis [7] is the process of remodeling the size, data, and information taken from the images before preprocessing.

The following steps of preprocessing are to read the image, resize the image, segment, and remove noise. The training and testing are the two datasets to identify the input dataset. Normalization, threshold, resize, and binarizing of the dataset. It improves human analyses, visual interpretations are clearly identified, faster, cost-efficient, less noise, and it allows the high variance of images. The research's major contributions is listed below,

- To minimize the computation power and memory requirement, crop and resize the input image dimension into 300×450 pixels in pre-processing.
- The k-means clustering model segment the leaf disease affected parts.
- The texture (energy, correlation, contrast and homogeneity) and color(standard deviation and mean) features are effectively tracked.
- The leaf disease classes are classified via SVM and ELM classifiers.

The remaining portion of the research is described as: Section 2 views the recent research articles related works followed by the designed methodology is discussed in section 3. Section 4 discusses the intensive result analysis and the research conclusion in section 5.

2. LITERATURE SURVEY:

Krishnamurthy et al. [8] introduced an innovative algorithm for the detection of rice diseases using the deep convolutional neural network (DCNN) of InceptionResNetV2based on a transfer learningplatform. Generally, the diseases in the rice crop are categorized asbacterial blight, leaf blasts, and Brown spots. Further, the designed model alters the weights of the feature engineering to classify the healthy leaves from the diseased leaves. 15 epochs are modified to form a healthy class for different parameters to attain better performance. The modified accuracy is high. Thus, various plant and rice diseases will be explored.

Manavalan et al. [9] reviewedvarious computational algorithms to track the disease leaves from normal grain leaves. This method involves preprocessing, image fragmentation, feature engineering, selection, and categorization to predict the leaf diseases. The images of leaves such as wheat, rice, millet, and soybeans are used to analyze diseases. By the classification models, numerous healthy leaves are identified which increases the accuracy. Hence, different agricultural problems are solved to reduce complexity.

Tripathy et al. [10] designed a smart green-IoT architecture basedMyGreenalgorithm for providing sustainable agricultural productivity. This method utilized rose plant database for identification and testing, deploying the trivial farming approaches. In the treatment phase, the diseased plants are treated with pesticides, fertilizers, and other kind of minerals. This model employs data analysis mechanism for accumulating input data, assigning optimal resources and for controlling the computational time efficiently. The result analysis demonstrated increased accuracy, improved system learning rate, and enhanced crop productivity and decreases the computational overload and costs.

Savarimuthu et al. [11] reported an integrated system for the identification of plant diseases deploying an optimized deep learning (DL)-based EfficientDet-D2 framework.The diseases of plants are detected by EfficientDet-D2to optimize the parameters. To predict the abnormal plants, this methodology utilized a plant disease database consisting 3038 images. These images are trained and tested in the system. Furthermore, the outcomes are calculated and verified with the state-of-art designs regarding time, accuracy, etc. Thus, real-time observations are identified in large-scale cultivations.

Verma et al. [12] described a DL approach employing simple and effective recurrent neural system with the long-short term memory infrastructure.In the beginning stage, the attributes present in the video images are augmented as entropy, standard deviation, fuzzy, etc. These features are modified datasets with optional learning abilities. The rice crop of infected and disinfected plants produces 99.99% accuracy. The performance enhances the accuracy, filtered video, and noise rate. Hence, the spatial frequency features are explored in other plants.

Geetharamani et al. [13]suggested a disease detection framework for tracking the infected plant in agricultural sector. This method utilizes the DCNN to categorize the infected plants.The disease categorization involves two main stages: image collection and filtering. The designed model was tested with 38 different databases comprising both normal and infected plant leaf images.The database size and classes enhance the images from different image qualities. The method increases reliability, consistency, and accuracy. However, the training process is examined without classifying images.

Cap et al. [14] introduced aninnovative disease prediction approachemploying LeafGAN-based image-to-image transformationframework.This design uses a fragmentation scheme named label-free, which separate the infected portion from the healthy region. Subsequently, the training image data are dividedto eliminate the overfitting issue. The images are cogent and natural to give the best result of identifying the infected and healthy plants. The output evaluation defines that it increases the reliability, accuracy, etc., but depends on the image quality.

Abayomi-Alli et al. [15] presented an image fragmentation scheme to identify the abnormalities in the cassava leaves.Here, the ImageNet dataset was employed to differentiate the diseases classes. Further, feature engineering was applied to track the middle-level attributes, which is utilized for disease categorization. Moreover, to manifest the classification efficiency of this model a low-quality image dataset was utilized. The data augmentation method is used for low-quality images to improve the classification. The exploration of multiple class prediction algorithms provides better performances.

Akram et al. [16] designed DCNN system to categorize diseases present in the fruits. The feature engineering was performed upon tracking and selecting the optimal image attributes using the GoogleNetandAlexNet techniques. Finally, the classification was made using the softmax function in an iterative manner (image-by-image analysis). This method offers high system accuracy of 99.3%.

3. PROPOSED SVM-ELM CLASSIFIER MODEL:

Figure 1 describes the workflowdiagram of the designedmodel. Initially, the input images are accumulated following the image pre-processing algorithm. The leaf diseases are segmented via K-means clustering (KMC) algorithm. Further, the meaningful attributes of the image are tracked and then the disease categorization was performed using the designed SVM-assisted ELM model.

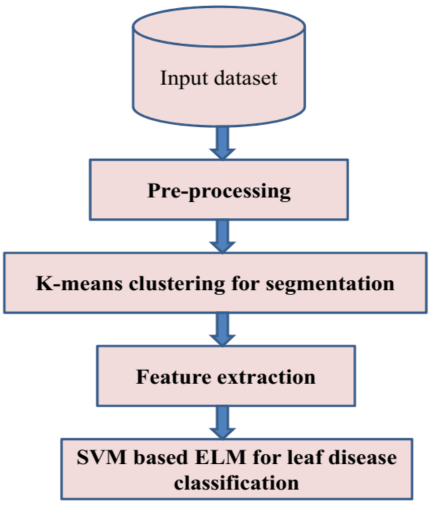

Figure 1: The overall proposed flow diagram

1.1 Pre-processing:

Crop and resize the input image dimension into 300×450 pixels. This makes the system to reduce the memory and power demands for an image during pre-processing [17]. To mitigate the image background, a hue was applied depending on fusion. The HSV is a conversion of the RGB image model. Due to its whiteness, the S value was assumed from the HSV design. The images are transformed into binary images based on the threshold value of images [18]. The background was removed by considering the pixel value as 0 in the fusion process. In the RGB model, the black color indicates the pixel value. Remove the image background without the diseased part.

3.2 Leaf segmentation using KMC:

The leaf fragmentationis carried out with the utilization of the KMCapproach. In clustering, the affected region of the leaf is extracted and distinguished as not affected and affected area [19]. This approach is mainly applied on the background removed HSV models of the leaf images. The hue component indicates the accurate color of the leaf without the inclusion of darkness and contrast information. Meanwhile, the commonly occurred randomness issues can be surmounted by the histogram analysis and therein estimates the centroid of the figure. After clustering the unnecessary green portion is removed. The histogram is generated from the hue elements of the background ignored image. The counts and hue values are derived from the generated histogram. Then the very important threshold value is set based on the histogram and diseased image portion and thus distinguishes the affected and non-affected leaf portion [20]. The hue values of normal and affected portions are saved in two individual arrays.

The centroid of the clusters is selected based on the maximized hue values of the affected and non-affected portion of the leaf. The classification accuracy can be affected by the green pixels and hence it is ineluctable to remove the unwanted green portion. The removal of the green color can be performed by setting the minimum and maximum values as 0.047 and 0.126 respectively [21]. This has been obtained with the color model that the green color lies in the range of 17.3 to 45 degrees and mapping has been performed. Based on these values the mask is generated to remove the unwanted green color. The process of segmentation of rice leaves into normal and disease-affected portions is illustrated in figure 2.

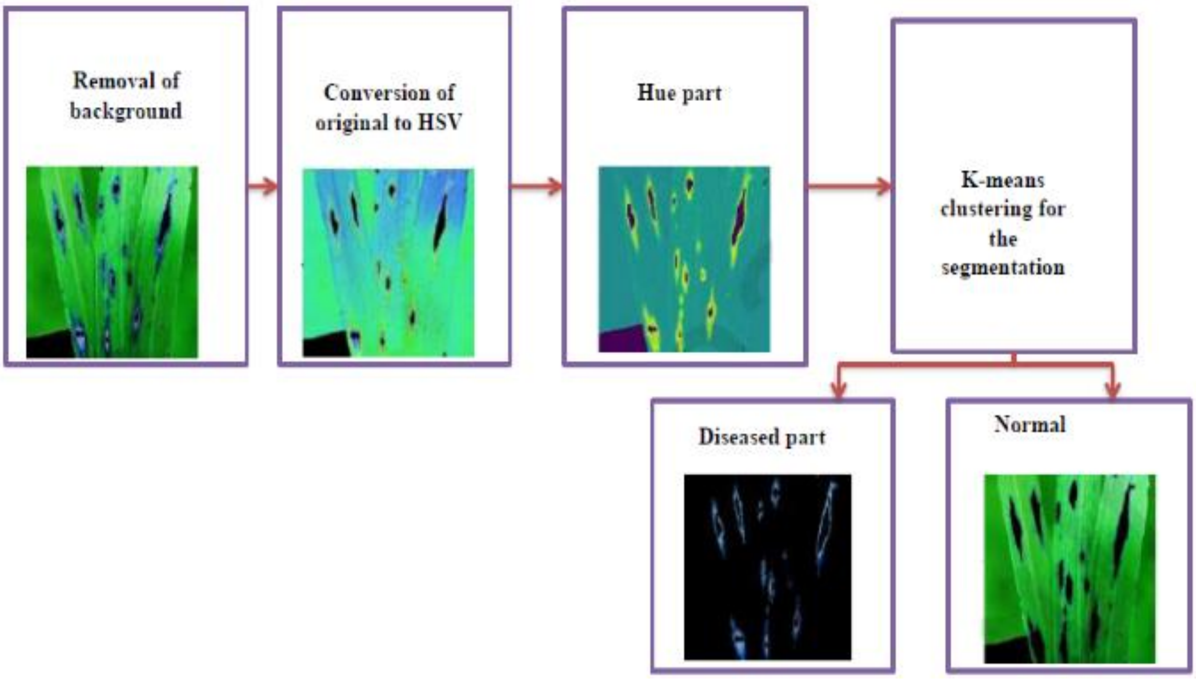

Fig 2: Segmented image based on K-means clustering from hue part

1.2 Feature extraction:

Both color (standard deviation and mean) and texture (similarity, divergence, energy, and interconnection) features are extracted.

(i) ***<u>Texture attributes:</u>***

The GLCM captures the image textures via spatial correlation between the pairs of gray value intensity. From GLCMs, the attributesincluding contrast, energy, correlation and homogeneity are extracted [22]. These features are formulated as follows;

$$CR_z = \sum_{y=0}^{m} R_{zy} \left(z - y\right)^2 \qquad (1)$$

$$HOM_z = \sum_{y=0}^{m} \frac{R_{zy}}{1 + \left(z - y\right)^2} \qquad (2)$$

$$ENY_z = \sum_{y=0}^{m} \left(R_{zy}\right)^2 \qquad (3)$$

$$CON_z = \sum_{y=0}^{m} R_{zy} \frac{\left(z - N\right)\left(y - N\right)}{S_z} \qquad (4)$$

From the above equations, the energy, correlation, contrast and homogeneity are ENY_z , CR_z, CON_z and HOM_z. The standard deviation, mean and pixel values are S_z, N_z and R_{zy} .

(ii) ***<u>Color features:</u>***

- For the disease portion, extract the R, G and B elements. Evaluate standard deviation and mean values [23].
- Estimate the mean values and extract the H, S and V components from HSV model.
- Calculate the mean value and extract the L, A and B components from te LAB color model.

The below formula calculates the standard deviation and mean values.

$$Sd = \sqrt{\frac{1}{m} \sum_{Y=1}^{m} \left(R_{yz} - N_z\right)^2} \qquad (1)$$

$$N_z = \frac{1}{m} \sum_{y=1}^{m} R_{yz} \qquad (2)$$

The pixel value is R_{yz} and the total number of pixels is *m*. Perform normalization in which the texture and color features are extracted effectively. Employ min-max model for normalization process.

3.4. Classification:

After the feature extraction, the SVM-based ELM modelcategorizes the infected region of the diseased leaf. The explanation for the leaf disease categorization using the SVM-ELM model is detailed below,

(i) ***<u>Support vector machine (SVM):</u>***

Based on the statistical learning, one of the commonly used machines learning techniques is support vector machine (SVM) [24]. From the given dataset, compute M-dimensional hyper plane and label the training dataset instances as $\{(y, z)\}, j = 1,2,...,M$. In the training dataset y_j , the instance class is Z_j . In the high dimensional space, the hyper plane is separated via maximum margin via the major issue of SVMs [25]. The sum of a distance among the hyper plane points closer to the dimensional space points are computed via SVM. The following equation computes the largest margin boundary function.

$$Minimization U(\varphi) = \frac{1}{2} \sum_{j=1}^{M} \sum_{k=1}^{M} z_j z_k \varphi_j \varphi_k f\left(y_j, y_k\right) - \sum_{j=1}^{M} \varphi_j \qquad (3)$$

Subjected to,

$$\forall j : 0 \leq \varphi_j \leq D \quad and \qquad \sum_{j=1}^{M} \varphi_j z_j = 0$$

From the above equations, the soft margin parameter is *D* (as $D > 0$) and the vector of *M* variables are φ.

The SVM kernel function is represented as $f(y_j, y_z)$. The data instances into various classes are separated via an SVM set of kernel functions. Various kernel functions are expressed as below:

- Sigmoid kernel: $f(y_j, y_z) = \tanh(\chi y_j^T \cdot y_k + R)$ in which the kernel parameters are χ, e and R.
- The radial basis function kernel as $f(y_j, y_z) = \exp\left(-\chi \|y_j - y_k\|^2\right), \ \chi > 0$
- The polynomial kernel is $f(y_j, y_z) = (\chi y_j^T \cdot y_k + R)^D, \ R > 0$
- The linear polynomial is $f(y_j, y_z) = y_j^T \cdot y_k$

(ii) Extreme learning machine (ELM):

Through ELM model, the non-linear activation function at *M* hidden nodes function with *M* different interpretations was learned. Moreover, the ELMs hidden units does not require any tuning process, as it follows the traditional training approach of the feed-forward neural system [26]. Furthermore, the metrics of the hidden units are selected randomly in the ELM and it reduces the training error by allocating weights of the output-hidden unit randomly. Systematicallyevaluate the output weights. Where, $\chi_j = [\chi_{j1}, \chi_{j2}, .., \chi_{jn}]^T \in \Re^n$ and $y_j = [y_{j1}, y_{j2}, .., y_{jn}]^T \in \Re^n$ isfor M arbitrary distinct instances $\{(y_j, \chi_j) : j = 1,2,..., M\}$. The following derivation designs the activation function, *f*-hidden neurons, *n*-outputs and *m*-inputs [27].

$$\sum_{j=1}^{k} \gamma_j h(V_j^T y_k + a_j) = 0, \quad k = 1,2,..., M \tag{4}$$

The input neurons, which interconnects the weight vector from the *j*[th] hidden neurons is represented as $\alpha_j = [\alpha_{j1}, \alpha_{j2}, ..., \alpha_{jn}]^T$ and $V_j = [V_{j1}, V_{j2}, ..., V_{jm}]^T$ in which a_j indicates the threshold of the hidden neuron. Based on zero error with *M*-instances, the ELM with the hidden neuron is $K = M$.

$$\sum_{k=1}^{M} \|O_k - \chi_k\| = 0 \tag{5}$$

$$\sum_{k=1}^{M} \alpha_k h(M_k^T y_k + a_k) = \chi_k, \ \ k = 1,2,..., M \tag{6}$$

Rewritten the above equation and express as, $\chi\alpha = \lambda$

$$\lambda = \begin{bmatrix} h(M_1^T y_1 + a_1) & \cdots & h(M_K^T y_1 + a_K) \\ \vdots & \cdots & \vdots \\ h(M_1^T y_M + a_1) & \cdots & h(M_K^T y_M + a_K) \end{bmatrix} \tag{7}$$

$$\alpha = \begin{bmatrix} \alpha_1^T \\ \vdots \\ \alpha_K^T \end{bmatrix} \tag{8}$$

$$\lambda = \begin{bmatrix} \chi_1^T \\ \vdots \\ \chi_M^T \end{bmatrix} \tag{9}$$

Here, χ defines the result of the j^{th} column of hidden neuron. Moreover, the utilization of ELM training enables to determine the least squaresfunction of a linear model. The parameter λ^* indicates the inverse matrix of generalized Moore-Penrose and by using the certain non-linear kernel operation, the ELMs hidden layer feature mapping are determined. The most common and popular kernel function utilized in ELM is the Gaussian radial basis function kernel.

(iii) ***<u>SVM based ELM for leaf disease classification:</u>***

After the feature extraction, we have used SVM-ELM model for categorizing the leaf diseases. Then, theclassification resultsare validated and evaluated. From the dataset images, the SVM-based ELM model is trained via 10 % of training dataset. Typically, while training the designed framework with the entire dataset, it causes certain errors. Due to memory overflow, the system undergoes single point failure in which the most significant one are the training time of SVM is rather long [28].

A new small high-quality training databasewascreated and the size of the database was reduced. Based on the original training dataset, all the instances are represented with the high quality means the resulting dataset instances. To minimize the classifier's training time, a few instances with the new training datasets are reconstructed and five classes of leaf diseases are obtained from the extracted features [29]. The SVM-based ELM classifiers performance is retained. Finally, the paddy leaf was categorized either as healthy leaf or unhealthy leaf. Figure 3 describes the SVM-ELM-based leaf disease classification design.

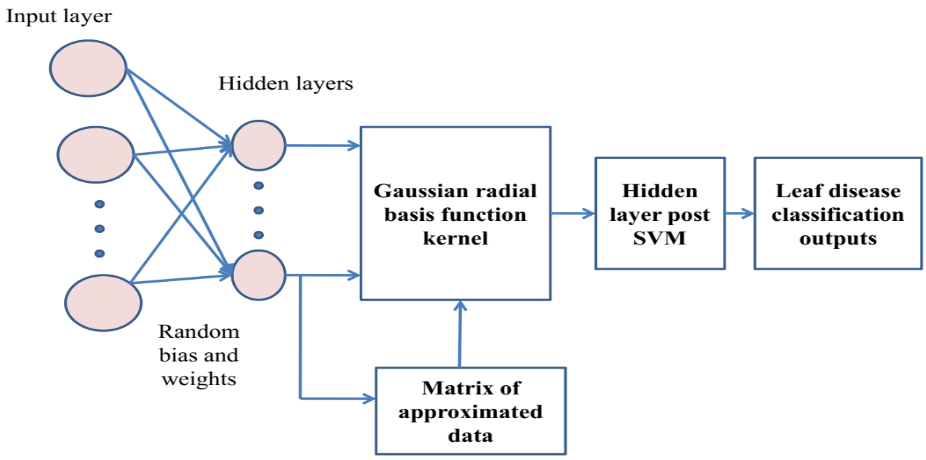

Figure 3: SVM based ELM design for leaf disease categorization

4. RESULT ANALYSIS:

This module provides an intensive analysis of the designed model results, dataset, comparative assessment, and experimental arrangement were examined.

4.1 Experimental arrangement

The presented framework was designed and executed in the MATLAB software operating on Windows 10 (64 bit) OS. The specifications of the implementation parameters includes:Intel(R) RAM with the speed of Core(TM) i7-3.4 GHz + GEFORCE GTX 1080 Ti GPU+16 gigabytes.

4.2 Dataset Explanation

In Asian nations, rice is often considered as the major crop; therefore, it is significant to safeguard the rice plant from variety of crop diseases. The disease in crops adversely affects the productivity and causes various losses to the agricultural workers. The outcomes of the designed model are analyzed using the database utilized in [30], which contains rice leaf images of 2340 jpg.The Leaves are classified as,

- Leaf Smut
- Bacterial Leaf Blight

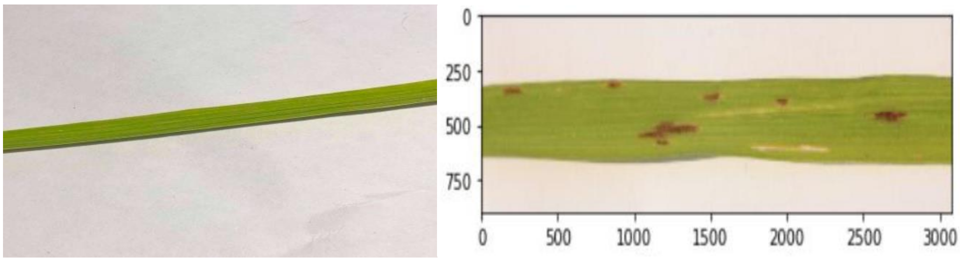

Fig 4: Sample images (a) Healthy leaf, (b) Unhealthy leaf

From the dataset we have used 70% for training and the enduringwas utilized for the validation. The accuracy and loss evaluation in the training and validation process were described in figure 5, and 6, in which the red line defines the loss/accuracy occurred during the training process, and the blue line represents the loss/accuracy occurred during the validation process.

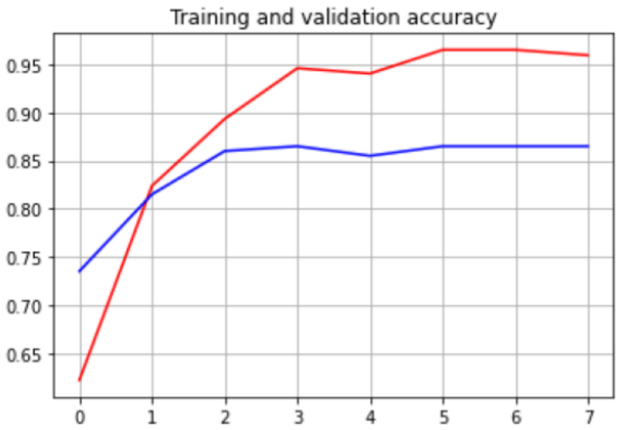

Fig 5: Analysis of accuracy in training and validation process

Fig 6: Training and validation loss analysis

4.3 Confusion matrix

The confusion matrix is defined as the summary of predicted outcomes over the classification issues. The corrected and uncorrected predictions of leaf diseases are concluded with count values and broken down by each disease classes. This is the key factor of the confusion matrix. In addition, it demonstrates that how well the designed model gets confused while detecting the leaf diseases. Figure 7 displays the confusion matrix of the designed model. Here, the confusion matrix was strategized for the three different classes available in the database.

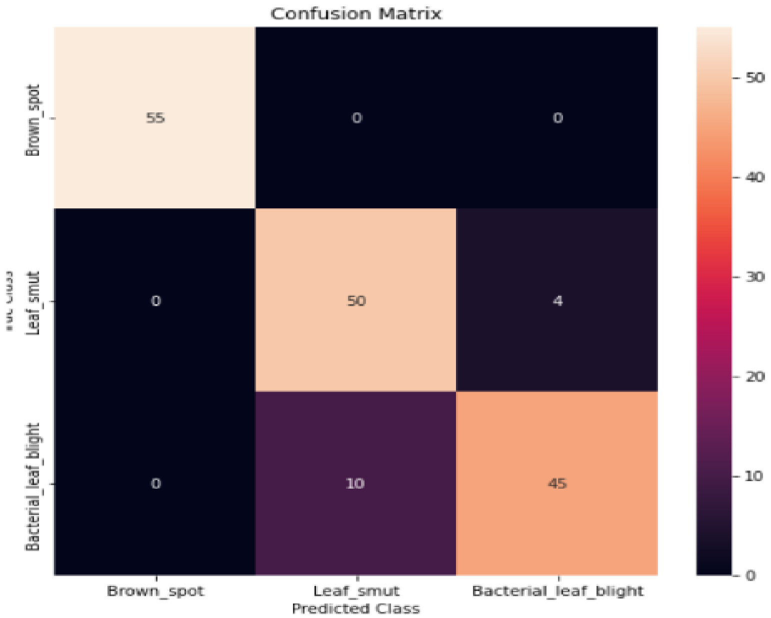

Fig 7: Confusion matrix of our proposed approach

4.4 Comparative study

This section shows the comprehensive comparative outcome evaluationof the designedframework with other approaches such as Deep convolution Neural Network (DCNN) [31], Fast Recurrent CNN (FRCNN) [32], Neural Network based Bayesian Optimization approach (NN-BO) [33], and Dense Convolution Neural Network based Multiclass plant disease (DCNN-MC) [34]. Here, it is compared with the constraintsincluding accuracy, specificity, sensitivity, and Precision. The outcomeconstraintsare defined below,

- **Accuracy (A):** It determines the output of the designed that how exactly it identifies different types of rice leaves are classified or predicted and is represented mathematically as,

$$A = \frac{T_P + T_N}{T_P + T_N + F_P + F_N} \qquad (10)$$

- **Specificity (SP):** It can be defined as how the leaves are classified as normal and disease affected area and can be formulated as,

$$SP = \frac{T_N}{T_N + F_P} \qquad (11)$$

- **Sensitivity (SN):** It is defined as the classification leaves from the dataset based on the disease types and can be formulated as,

$$SN = \frac{T_P}{T_P + F_N} \qquad (12)$$

- **Precision:** It is determined as the how positive values are classified precisely. It can be formulated as,

$$\Pr ecision = \frac{T_P}{T_P + F_P} \qquad (13)$$

Here, T_P denotes true-positives, T_N indicates true-negatives, F_N represents false-negatives and F_P defines false-positives.

5. CONCLUSION

This article presented a novel approach for leaf disease classification.To begin, the input image dimension is cropped and resized into pixels to reduce the image's computation power and memory requirement. The K-means clustering algorithm divides the diseased leaf disease into sections. Color characteristics (standard deviation and mean) and texture characteristics (energy, correlation, contrast, and homogeneity) are extracted. The SVM and ELM classifies paddy leaf disease classes such as Normal, Sheath rot, Brown spot, Bacterial blight, and Blast. Google Colabis used to implement the experimental parts. The proposed method performs superior classification results. The loss function is analyzed with respect to the probability value and attains our proposed method has less loss than the other approaches. The proposed approach achieves better sensitivity of about 96.99%.

Compliance with Ethical Standards

Conflict of interest

The authors declare that they have no conflict of interest.

Human and Animal Rights

This article does not contain any studies with human or animal subjects performed by any of the authors.

Informed Consent

Informed consent does not apply as this was a retrospective review with no identifying patient information.

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Consent for publication: Not applicable

Availability of data and material:

Data sharing is not applicable to this article as no new data were created or analyzed in this study.

Code availability: Not applicable

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