

Proceedings of the
SECOND INTERNATIONAL CONFERENCE
ON
**RECENT TRENDS IN MULTI-DISCIPLINARY
RESEARCH AND INNOVATION**
ICRTMRI' 25

19th September 2025

in Association with



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AVP (Autonomous)
COLLEGE OF ARTS AND SCIENCE



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96	ICRTMRI/25/ T2/96	A COMPARATIVE ANALYSIS ON DESCRIPTIVE MEASURES - CENTRAL TENDANCY	S. RIFANA, S. POOJASRI, Dr. V INDUMATHI	749
97	ICRTMRI/25/ T2/97	IOT-ENABLED SMART MEDICINE REMINDER AND REMOTE MONITORING SYSTEM FOR ENHANCED MEDICATION ADHERENCE IN ELDERLY AND CHRONICALLY ILL PATIENTS	GURUSHANKAR. P. J	757
98	ICRTMRI/25/ T2/98	EXTREMAL THRESHOLDS FOR CYCLES WITH DIAGONAL CONNECTIVITY IN DENSE GRAPHS	P.KIRUTHIKA, Dr. M.LALITHA	760
99	ICRTMRI/25/ T2/99	ARTIFICIAL INTELLIGENCE AND BLOCK CHAIN TECHNOLOGY IN CRYPTO CURRENCY MARKET-AN INDIAN PERSPECTIVE -AN INVESTIGATIVE ANALYSIS	Dr. R. SENTHIL KUMAR VISHNUPRIYA P,	768
100	ICRTMRI/25/ T2/100	FAKE JOB POST DETECTION USING MACHINE LEARNING	LAVANYA. U, C. DURGA DEVI	771
101	ICRTMRI/25/ T2/101	AWS BIG DATA PROCESSING DIFFICULTIES AND ANALYTICS USING CLOUD COMP. SYSTEMS	Dr.F.LEENA VINMALAR, Dr. ANANDHARAJ .K	777
102	ICRTMRI/25/ T2/102	ARCHITECTURE AND FRAMEWORK APPROACHES FOR SECURING VEHICULAR AD-HOC NETWORKS	PRABHAHARAN. A, Dr. P. V. RAVINDRA NATH	782
103	ICRTMRI/25/ T2/103	AN AUTOMATIC SOCIAL ENGAGEMENT MEASUREMENT DURING HUMAN ROBOT INTERACTION CONCEPT IN ARTIFICIAL INTELLIGENCE	Dr.T.SHANMUGA VADIVU	786
104	ICRTMRI/25/ T2/104	IDENTIFICATION AND CLASSIFICATION OF MAIZE PLANT DISEASES: PERSPECTIVE TO BACTERIAL FORAGING OPTIMIZATION	Dr. P. JAYAPRIYA	792
105	ICRTMRI/25/ T2/105	HEART DISEASE PREDICTION USING MACHINE LEARNING ALGORITHMS	Mr. M. MADHAN GIRI	798
106	ICRTMRI/25/ T2/106	EXPLORING EFFECTIVE EDGE AND PERFECT DOMINATING SETS IN INTERVAL-VALUED FUZZY GRAPHS OVER SEMIGROUPS	K. SANGEETHA, Dr. P. SOLAIRANI	803
107	ICRTMRI/25/ T2/107	TRUSTWORTHY IOT FORENSICS: A BLOCKCHAIN-ENABLED, AI- ASSISTED, EDGE-BASED FRAMEWORK	Dr. S. CHITHRA DEVI, PRAKUL.S, VINOLIN GRACE. V	807

IDENTIFICATION AND CLASSIFICATION OF MAIZE PLANT DISEASES: PERSPECTIVE TO BACTERIAL FORAGING OPTIMIZATION

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Abstract

Maize is one of the largest food crops after rice and wheat in all over the world. It has become a vital part in the agriculture to automatically monitor and diagnosis the plant disease in new era. In this paper, a unique maize plant disease identification system has been modelled using the optimization of recurrent neural network through bacterial foraging technique. Further it can be employed to moderate the search space of the classifier and provides better initial information for recognition network. Initially pre-processing and region growing based segmentation has been approved to identify and determine the neighbour pixel of seed points toward combining it in particular region. It is to increase the efficiency of the network by searching and grouping of seed points having common attributes to generate the optimal features for classification. Obtained segmented region has been processed using Recurrent Neural Network to capture sequential patterns based on longitudinal data to produce recurrent structures. Finally different classes of the plant disease have been classified and identified with new classic techniques. Experimental analysis using plant village dataset on the proposed model explains the performance measure in rudiments of dice coefficient, similarity and specificity towards disease identification.

Keywords- Maize Leaf Disease, Recurrent Neural Network, Linear Discriminant Analysis, Bacterial Foraging.

1. INTRODUCTION

Maize is a noteworthy food crop in the plant area and total output gives largest outcome in the world crop industry after rice and wheat. However, these crops have been affected with diseases due to changes of cultivation system on basis of climatic changes and pathogen changes [1]. Common plant disease used here are classified into eight types are Curvularia leaf spot, dwarf mosaic, gray leaf spot, northern leaf blight, brown spot, round spot, rust, and southern leaf blight [2]. In order to identify those diseases, automated image processing technique has been proposed to assist farmer for early identification of disease. Various literature reviews on employing machine learning and deep learning architectures has been identified [3]. Those architectures manifested with plant appearance and its visual symptoms. Meanwhile, those automation techniques affect the identification of the maize disease images due to many external factors such as illumination and shadows affects [4].

Besides, there is clear variation in the corresponding virus and diseases in various growth stages for maize, which leads to the complication on identification significantly. Hence effective image pre-processing [5], feature extraction [6] and segmentation [7] must be carried out to obtain the best recognition accuracy from large number of input images in the timely and accurate manner. It expands the scope of the automation process in the field of precision agriculture. In this, a novel deep learning based maize plant disease identification system has been modelled using the optimization of recurrent neural network through bacterial foraging technique on identifying both fungal and viral based disease of the maize plant [8].

Recurrent Neural Network has high recognition accuracy among other deep learning architecture. Initially pre-processing has been employed to eliminate the illumination and shadow effects of the image. Region growing based segmentation has been applied for grouping of seed points having common attributes as features. Those features have employed

with bacterial foraging to reduce the search space of the classifier and provide better initial information for better identification accuracy. Recurrent Neural Network is to produce the recurrent structures to different diseases on the maize plant leaves.

II. RELATED WORK

Identification along with classification of maize plant disease is a challenging task to perform. Many researchers worked on reciprocally traditional and deep learning approaches for segmentation. S.Zhanget al. [9] Proposed a method that uses sparse representation classification for Recognition of Leaf image-based cucumber disease. C.Dechant et al. [10] used Deep Learning for automated identification of northern leaf blight-infected maize plants. D.Oppenheimetal. [11] used Convolution Neural Networks for Potato Disease Classification. Mingjie Lv et al.[12] proposed feature Enhancement and DMS-Robust Alexnet for Maize Leaf Disease Identification. Ronnie Concepcion et al. [13] proposed a Gaussian Quantum Particle Swarm optimization and Recurrent Neural Network for surface assessment of diseased maize cercospora leafspot. Affinity Propagation identifies the changes of the leaf spots along plant pathologies that represent features set. Sparse Principle component analysis extracts the sparse information and its interrelationship on the feature set which is represented in form of max pooled data [14]. Further Linear Convolution Neural Network has been employed to generate class labels for sparse information. Gray levels edge detection and edge detection techniques are used to determine some common maize diseases. Improved deep convolution neural network model is used for identification of maize leaf disease with long connection times and large numbers of model parameters. Three ensemble methods like snapshot ensemble, weighted ensemble and unweighted ensemble were compared and ensemble snapshot method showed the best performance on the PlantDoc dataset [15].

III. PROPOSED MODEL

Maize Plant Disease identification model can be performed using Recurrent Neural Network Model along with bacterial foraging on plant village dataset is used to segment the leaf diseases using Linear Discriminant Analysis (LDA) along with region growing segmentation as shown below. The proposed method uses fitness function that is trained with Bacteria Foraging Optimization to find affected regions of maize plant. This special linear function is used to increase or decrease the distance from the center point. This helps to handle the complexity of the affected regions that exist in maize plant leaf images. Then it is further improved by using region growing algorithm for grouping of analogous attributes that helps in feature extraction process.



Figure 1



Figure 2



Figure 3

Figures 1, 2, 3 shows the sample images of maize plants affected with common rust, Northern leaf Blight and healthy leaf images. Figure 4 represents the architecture of the proposed model

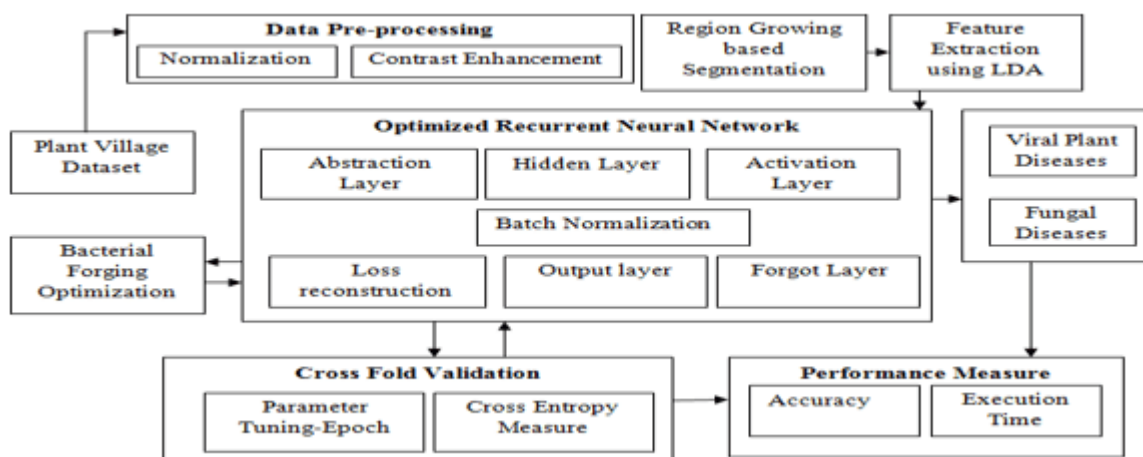


Figure4: Architecture of proposed model

3.1 Image Pre-processing

Image Pre-processing is used to enhance the pixel properties of the images using image normalization and contrast enhancement techniques. Further several computing parameters have been adjusted for subsequent processing of the dataset. Normalization of the image is carried out using histogram stretching. Further to reduce the noise and blur of the image, Contrast enhancement is employed in parallel along with image thresholding techniques to enhance the image details for further processing.

3.2 Region Growing based Segmentation

In this segmentation, seed representing distinct image regions of the maize plant has been initialized and allowed to increase until it reaches the entire image. A segmentation rule represents the growth mechanism, and a rule verifies the homogeneity of the feature regions after each growth process has been constructed.

3.3 Linear Discriminant Analysis (LDA)

Linear Discriminant Analysis is employed to extract a dominant feature vector using fisher criterion function on the specified projection in particular direction. The projection of feature extraction in particular direction obtains the homogeneous samples in the original data set as close as possible and the heterogeneous samples are separated as far as possible. LDA algorithm is employed to obtain the good transformation vector. The optimal feature vector is gathered on reduction of the feature space through employment of scatter matrix. Given M plant village dataset and images of size $N \times N$, first calculates the mean vector for the image. Linear discriminant analysis has been used to generate the optimal set of features through image normalization on pair wise similarities of the correlated features obtained from processing of the scatter matrix variance of the disease point of the image and dimensionality reduction on computing the linear fusion of diseases features on two or more vectors.

3.4 Recurrent Neural Network

Recurrent Neural Network (RNN) is used to identify the classes of the plant that belongs to any particular disease type. This can be used to find spatial and temporal sequence of the segmented region. This architecture has been composed for different disease processing states such as input state, cell state as well as input gate, forget gate and output gate. This produces classes of diseases in direct acyclic graph structure. Each layer of the recurrent network contains seed region that helps to segment image pixels. Table I represents the parameterized component of RNN. It follows a chain like structure for incorporating the spatial and temporal features for extraction of seed region in the image.

Generally, it has been found that above parameterized components are used for Recurrent Neural Network to carry out initialization of weight and for training the network to identify affected regions of maize plant image.

3.4.1 Abstraction Layer

In this RNN layer, Network Abstraction is carried out to extract high level features of disease regions of the plant. Features are presented in structure of vectors. Vector is processed in the activation function. It produces new state from old state with few parameters function using epoch functions. Feature selection is developed by combining the input vector in addition to the output of the LSTM input gate on feature vector on calculation of feature weight matrix and feature bias vector.

3.4.2 Hidden Layer

In this layer, the state usually contains the hidden vectors H helps for the feature extraction which is obtained from the abstract layer. The forget gate of RNN Model is used to find out the information to be stored in the cell state. And those seeded region has to be forgotten in future. The RNN forget gate incorporates the sigmoid function as its activation function. This is processed by the input gate, which is to determine $mf(t)$ as it as determination process to remove the features.

3.4.3 Activation function

Activation function decides the learning rate of the proposed approach to manage and vary the weights of the input sequence from hidden layer by applying sigmoid function. RNN activation function is represented in many to one data structure to parse the sigmoid function. The activation function is customized to enhance the output layer. It is employed for analysing the disease features towards identifying disease class and to differentiate the feature on basis of distance measures.

3.4.4 Output Layer

The particular layer operates on the RNN model as output gate. The pathological information has been incorporated into the final output of the RNN layer on computation by LSTM output gate state. In this layer, future classes of the plant disease have been outputted by the activation function of the RNN with reference to $o(t)$ output gate function of LSTM, as it termed as final output $z(t)$. In this this research, output layer identifies the disease type as viral or fungal guidelines of the Global vegetation index.

RNN containing the hyperbolic tangent function filters the disease outcome of the plant on computing the activation function of the output layer to generate the subsequent results. It generates the RNN output in the range of $(-1, 1)$, which also provide assurance to the network without diverging the sequence of input pixel by the LSTM inputs gate.

3.4.5 Loss Layer

Loss layer of the model is to confirm the prediction accuracy of disease class results by fine tuning. Fine tuning of the feature is done to rectify parameter of multiple layers of recurrent neural network to confirm the model producing the minimum reconstruction error in classification of the feature from the hidden layer and sigmoid activation layer of seed region. Furthermore, cross entropy of the loss function has considered to control data smash up for acknowledged information. RNN network parameter is enhanced to identify the results of the plant disease type. Soft max and cross entropy approach on the seed region has considered to obtain accurate identification of the disease on eight diseases of the maize plant.

3.5 Bacterial Forging based optimization

Kevin Passino instigate Bacterial Foraging Optimization (BFO) algorithm in 2002. Cluster foraging behaviour of bacteria such as *M. Xanthus* and *E. coli* motivates the development of BFO. This algorithm is enthused by the chemotaxis performance of cybernetic bacteria that is in motion towards (in the direction of) or away (not in the direction of) from the specific signals. This performs by taking small steps often in searching for nutrients in the problem search space.

Basic process in BFO includes Chemotaxis, Swarming, Reproduction, Dispersal and Elimination. Feature space has been computed using bacterial foraging for identification of disease type on the maize plant on viral and fungal patterns. Initially Search space has been collected from output layer of the RNN model. The proposed model uses fitness function for training the RNN feature set as shown

IV. EXPERIMENTAL RESULTS

Experimental analysis is done through the plantvillage dataset. The model is simulated in Matlab (version 2018b). The processing of the image for training and validation are highly exigent. During processing, 60 percent of the data has been taken for training, 20 percent of the data has been utilized for validation and remaining 20 percentages of data has been employed for testing. 5-fold validation has been smeared to improve the performance of the segmentation and classification to identify disease region.

Alex net is used to utilize the iterations to achieve the high recognition accuracy for detection of disease regions based on viral, fungal and other category. The model provides the better results on identifying the lesion region with varied size and characteristics compared with existing methods. The concept of the proposed model is done with three quantitative measures Dice coefficient, sensitivity, and specificity for validating the segmentation performance region.

Dice similarity Coefficient

It is computed by considering the difference between the segmented result and ground truth data. In addition, it can be computed using true positive, false positive and false negative values of segmentation results. It is denoted as

$$\text{Dice Similarity Coefficient} = \frac{2TP}{2TP + FP + FN}$$

Sensitivity

It is the measure of percentage of True Positive which computes the skull correctly in terms of various features. It is given by

$$\text{Sensitivity} = \frac{TP}{TP + FN}$$

Specificity

It is the measure of percentage of True Negative which computes in terms of features of the data. It is given by

$$\text{Specificity} = \frac{TN}{TN + FP}$$

V. CONCLUSION

A design of novel framework named as Recurrent Neural Network along with optimization of bacterial foraging on the seed region of the image segment is implemented. The image segments has been obtained using the region growing segmentation and seed features are extracted on basis of spatial and temporal aspects through linear discriminant analysis. Plant disease diagnosis is carried using establishing recurrent structures using RNN on the seed features of the image. Recurrent structure is eligible to identify the disease type of the plant. Segmentation technique based on deep learning produces the higher accuracy and less mean squared error with less time consumption. It produces the better results on volumetric changes, imaging artifacts, anatomical variability, varying contrast properties, and poor registration of the diverse dataset on analyzing the modalities and pathologically altered tissues.

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