

¹ Suresh D²Dr.SreeKala T

Exploring Spectral Patterns of Tomato Phytophthora Infections using the VMRNMAF Deep Learning Framework



Abstract: Identifying and mitigating diseases affecting tomato crops pose significant challenges for researchers and agricultural producers alike. Effective disease detection is crucial for optimizing yields and implementing targeted treatments. This study presents a comprehensive framework, Vector Machine Recurrent Neural with Manual Activation Function (VMRNMAF), for early prediction of Phytophthora infestans and other common tomato diseases. Leveraging image preprocessing techniques and feature identification processes, VMRNMAF accurately distinguishes between healthy and infected tomato segments. By integrating Recurrent Neural Networks (RNNs) and manual activation functions in image segmentation, this framework enhances disease identification accuracy. Throughout deep learning methodologies, VMRNMAF streamlines the identification of bacterial, viral infections, offering a promising solution for improving tomato crop management practices. Experimental results demonstrate the efficacy of VMRNMAF in accurately identifying diseased areas within tomato crops, underscoring its potential for enhancing agricultural sustainability and productivity.

Keywords: Tomato, Leaf Mold, Phytophthora, SVM, RNN

I. INTRODUCTION

India, as a prominent agricultural nation, plays a significant role in global tomato product supply. With a vast expanse of land dedicated to farming, both for domestic consumption and export, India's agricultural output contributes substantially to international markets. Despite not being native to certain regions, Indian produce enjoys high demand worldwide. However, ensuring both quality and quantity remains pivotal for augmenting revenue streams and enhancing the livelihoods of agricultural producers.

Crop productivity faces multifaceted challenges influenced by various environmental factors. Among these challenges, early identification of disease outbreaks significantly impacts crop health and yield. However, discerning the types of infections affecting plant surfaces during initial growth stages poses a daunting task for farmers and agricultural experts. Therefore, effective control measures are imperative to contain the spread of both known and unknown diseases across agricultural produce.

Despite the availability of diverse scientific and clinical methodologies for disease detection, achieving accurate infection analysis presents practical hurdles. Early disease detection holds immense potential in addressing issues related to crop growth and productivity. Leveraging image processing and analysis techniques, particularly within the subset of deep learning in machine learning, offers a promising avenue for swiftly and accurately identifying infected areas within tomato crops.

Every human use Tomatoes on a daily basis to fill up various vitamin deficiencies that may occur in the body. Tomatoes are mostly consumed as food because of their high nutritional value, capacity to help people lose weight, build a strong digestive system, work as antioxidants, and even improve the heart. Products like jam, pancakes, pudding, ketchups and natural food coloring are regarded as byproducts of tomato crop since they heavily rely on the healthy growth and absence of illness infections of the tomato crop. The pro-vitamin, carbohydrate, and protein are a few commonly accessible tomato resources with medical benefits.

Tomato crop cultivation is particularly challenging for farmers since it must please many different types of individuals. Natural disasters like wind and heavy rain primarily affect how well tomato crop grow and make it exceedingly challenging for farmers to overcome hurdles to economic loss. In order to produce healthy tomato crop,

¹Research Scholar, Department of Computer Science, School of Computing Sciences, Vels Institute of Science, Technology and Advanced Studies (VISTAS), Chennai, Tamil Nadu, 600117- India. Mail id : dsureshsuse@gmail.com

²Associate Professor, Department of Computer Science, School of Computing Sciences, Vels Institute of Science, Technology and Advanced Studies (VISTAS), Chennai, Tamil Nadu, 600117- India. Mail id : sreekalatm@gmail.com

the farmers' planned tomato harvests are plagued by a number of bacterial infections. Many farmers feel that the effort being done by agro scientists to examine the different forms of tomato crop diseases are insufficient because the process can lead to a cure in the final stage. As a standard technique for identifying the sort of disease assaults on tomato crop, which are thought to be caused by a time-overlapping process, enormous lab tests and comparisons are carried out.

The ability to diagnose diseases that have affected tomato crops is becoming more and more technologically advanced every day. Even if technology has advanced for identifying the specific illness that attacked the tomato crop, there should be a time-saving technology to address the many issues that arise in the agricultural industry. The advancement of technology ought to provide farmers with the right cure at the right time and with extremely precise disease type prediction. One of the data mining approaches used to uncover problems that develop in a variety of industries, including business, marine, medicine, computer vision, satellite mapping, electronics, and agricultural, is image processing. Typically, image processing is viewed as a solution to a number of significant issues in digital photography. Image processing techniques are used to identify the tomato crop affected by the disease and provide growers with a suitable remedy.

It is extremely difficult for farmers and agricultural officials to determine the specific disease that has affected the Tomato crop. The effects of fungus and bacteria are to blame for the frequent attacks on tomato crops. Farmers will be satisfied with removing numerous ecumenical hurdles if they are identified early and given a suitable remedy. The procedure has the potential to boost tomato crop yields. Utilising pre-processing methods, the Tomato crop images are gathered from several agricultural farms and examined. Before resizing the collected images, eliminate any extraneous elements that were discovered on the collected tomato crop images. For improved image processing simulations during testing and training, the resizing procedure is carried out.

The feature extraction step, which comes after the pre-processing stage, collects the necessary characteristics from bacterially infected portions present on the surface of the tomato crop. The features taken from the pre-processed tomato crop leaf are segmented using both the recurrent approach and the Rectified Linear Unit strategy. Recurrent Neural Network (RNN), Rectified Linear Unit (RLU) is used in the feature extraction process for classification. The process used for feature extraction makes it very easy to separate the greatest characteristics from the overall features. The images of tomato crop were gathered from the database "Plant Village," which contains 50,000 images of different plants with various diseases. The proposed Convolution Recurrent Neural Network (CRNN) is a hybrid machine learning algorithm; it is used for identifying the disease infected parts of the plantain leaves. This proposed VMRNMAF Framework basically follows a deep neural networking algorithm for user InterVision in simulating the results.

II. LITERATURE REVIEW

Tomatoes (*Solanum Lycopersicon*) stand as the second most significant vegetable crop globally, trailing only potatoes [1]. Thus, employing advanced yet cost-effective techniques become imperative for safeguarding tomato crops and their yields. Traditional methods like Enzyme-linked immunosorbent assay (ELISA) with transmission electron microscopy (TEM) persist in the detection and identification for viral particles and fungi, offering swift and accurate results [2][3]. However, reliance on these methods presents hurdles such as the need for expensive laboratory infrastructure and skilled technicians [4–6]. Consequently, there is a growing impetus for innovative technologies accessible to both researchers and commercial farmers, with a focus on automating plant disease diagnosis to streamline costs, resource utilization, and environmental impact.

A primary objective in plant management is the prompt detection and measurement of diseases within plant populations to facilitate timely intervention. While experienced tomato growers may visually identify some diseases, others necessitate laboratory testing, which is often time-consuming and unsuitable for routine use. Rapid disease identification is crucial to stop diseases from spreading within greenhouses, highlighting the criticality of time-sensitive interventions. Additionally, the cost and complexity of laboratory-based diagnosis underscore the need for on-site, automated detection methods empowering growers with greater control.

Two promising avenues for rapid and non-destructive plant testing and diagnosis involve image processing of leaf surfaces and analysis of Plants release volatile organic compounds, or VOCs. and pathogens [7],[8], [9-11]. These methods furnish data to software facilitating knowledge-driven decision-making for growers to implement intervention and control measures effectively. VOCs, naturally released by plants, exhibit diverse profiles in

response to various stresses, serving as both direct anti-infection agents and signals for defensive responses [12][13][14][15]. Monitoring changes in plant VOC profiles in different environmental conditions offers a non-destructive approach to assess plant health [16]. While Analysis using Gas Chromatography-Mass Spectrometry (GC-MS) has been used to detect and measure plant VOCs, its labour-intensive processes and high cost limit its practicality, especially in commercial plant-growing settings [17][18][19]. Overcoming these challenges requires the development of more accessible and efficient VOC analysis technologies suitable for early pest and disease detection in agricultural environments. Thus, advancing techniques for automated, on-site detection and diagnosis remains a critical frontier in enhancing crop protection and productivity.

1. PROPOSED VMRNMAF DEEP LEARNING FRAMEWORK

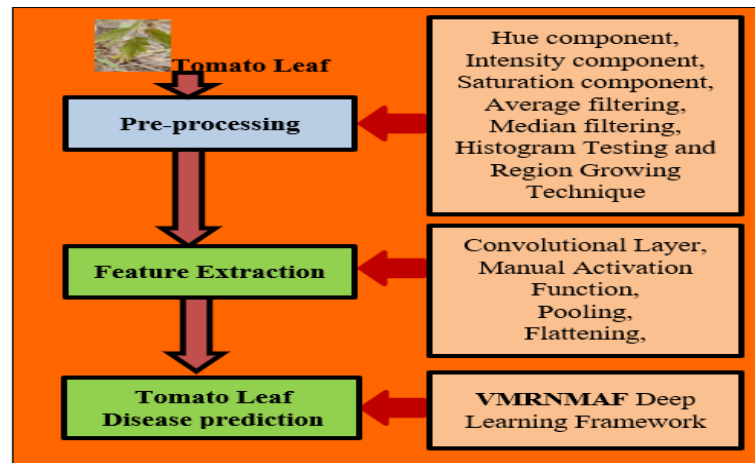


Figure 1. Framework of proposed VMRNMAF

The proposed model outlines a comprehensive approach for accurately identifying disease-infected segments within harvested tomato crops. The research begins by collecting data, wherein images of tomato crop components are sourced from the Plant Village database, comprising 50,000 images showcasing various plants afflicted by diverse illnesses. The primary objective is to pinpoint disease-affected areas within the tomato crop, prompting meticulous examination of the gathered data to isolate images depicting diseased tomato crops. Subsequent sections delve into a detailed discussion of the strategies and techniques employed throughout this research endeavor.

Pre-processing collected Tomato crop part initiating the image processing phase with the collection of images of diseased tomato crops from farmers and agricultural officials is pivotal for scientists to accurately identify the disease and prescribe optimal treatment solutions. These images may contain solely the affected portions of the tomato crop or entire images showcasing the infected areas themselves.

To enhance image processing efficacy, RGB images undergo initial conversion to grayscale as part of the formatting and pre-processing stage. While alternative models such as HSV, CMYK, HIS, and L^*a^*b are also utilized for analysis, RGB images collected typically offer optimal solutions for identification processes. HSV and HIS color models, mimicking human perception, are employed to standardize the captured images. In the HSV model, hue, saturation, and intensity are initially gathered.

Pre-processing plays a pivotal role in eliminating irrelevant components from damaged areas of the tomato crop. Central to the study is the separation of irrelevant or diseased segments from the infected sections. To facilitate easy identification during the analysis stage, images are downscaled to 512 x 512. Several significant image processing filtering techniques are applied during the filtering process for resized images. Techniques such as Median filtering and Wiener filtering are initially employed, followed by low-pass and high-pass Gaussian filtering techniques.

III. FEATURE EXTRACTION

In many research endeavors, the feature extraction process is often treated as an optional step. However, by carefully defining essential features for the analysis stage, researchers can significantly enhance the likelihood of accurately retrieving results. When selecting features, particular attention must be paid to critical criteria such as layer types. Increasing the number of parameters used in the suggested disease detection technique may indeed heighten the

probability of its efficacy. However, this could potentially lead to longer execution times and introduce complexities in analyzing results.

While discrepancies in categorization between different networks may not directly impact the ultimate purpose of the proposed model, they can contribute to improved accuracy and reduced implementation complexity. To attain the most precise features for the identification process, it's essential to integrate the detected object from the image with other extracted data using a proposed model or framework. This integration ensures a comprehensive approach to feature selection, fostering more accurate disease identification and analysis outcomes.

IV. USING CONVOLUTIONAL NEURAL NETWORKS (CNNs) TO FEATURE EXTRACTION

In a neural network, neurons are organized into layers interconnected through a specific structure. By assigning labels to pre-processed images, these neural layouts play a crucial role in transforming them into essential attributes for disease detection. Among automated models, the multilayer neural network stands out for its utilization of deep learning to extract features effectively, making it a successful approach for analyzing structured layers. Convolutional neural networks (CNNs), in particular, excel with minimal pre-processing of images and are skilled at simplifying the outcome. When carrying out the procedure of identifying and categorizing diseases, CNNs prove invaluable in accurately retrieving precise features essential for identifying and categorizing diseases.

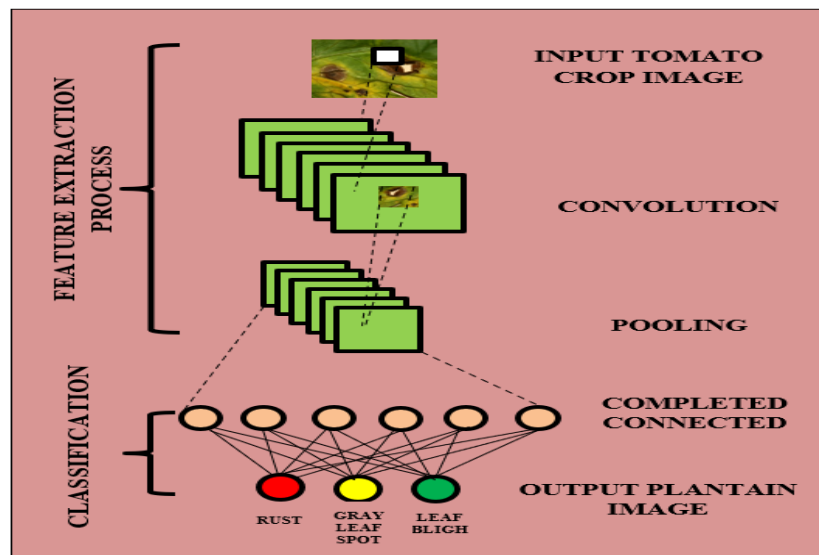


Figure 2. Recurrent Neural Network in Tomato crop parts classification

The Convolutional Neural Network (CNN) comprises three primary components: convolution, pooling, and fully connected layers, as illustrated in Figure 2, providing clear representations of their functionalities. In the context of gathered images of tomato crop parts, the initial two layers serve as pivotal agents for processing and extracting features during the feature extraction procedure. The final layer offers a comprehensive depiction of numerous tomato crop image segmentations essential for the categorization process.

When utilized effectively, Convolutional Neural Networks furnish an automated system for extracting requisite features from raw tomato crop images. Rectified Linear Units (ReLUs) serve as activation functions in the final connected layer, playing a significant role in learning high-level features crucial for classifying the gathered images into predefined categories. Additionally, the ReLU divides the automatic feature extraction and classification processes into two distinct components, enhancing the efficiency and accuracy of the overall system.

V. CONVOLUTION LAYER

Convolutional neural networks employ diverse layering schemes to process various components. At the heart of every CNN architecture lies the convolution layer, a pivotal element in its processing pipeline. This layer conducts multiple operations on the input functions iteratively, aiming to enhance overall performance. In the context of processing images of tomato crop parts, the convolutional processes are instrumental in mapping features from these pictures. The fundamental approach in convolution layering involves extracting characteristics from input images of tomato crop parts, thereby converting them into spatial information within the data. When selecting convolution

kernels for training, careful consideration of CNN input is essential, as the weighting provided in the layering process significantly impacts network performance and efficiency.

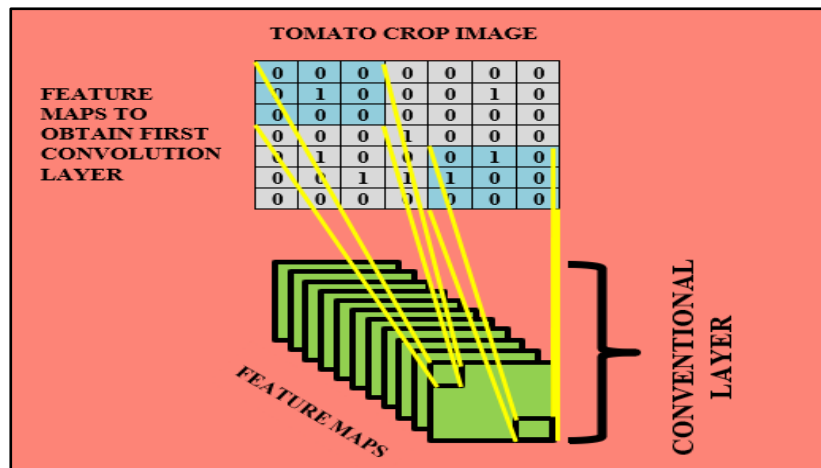


Figure 3. Convolution layer in prediction process

VI. ACTIVATION FUNCTION

Following the mapping in the convolution layer, the subsequent step involves activating the extracted features essential for further processing. Researchers commonly employ various activation algorithms to refine the organized layers. Among these methods, Rectified Linear Unit (ReLU) stands out as a prominent choice in contemporary research, particularly for narrowing down convolution layers to precisely identify afflicted areas, such as those in tomato crop sections. Leveraging ReLU in 3 x 3 convolution layers can notably enhance the accuracy of disease identification procedures.

These distinctive activation functions play a crucial role in training deep learning neural networks, enabling non-linearity and effectiveness with unsupervised pre-processed input. While the sigmoid function is also prevalent in activation function usage across various research studies, ReLU offers advantages in mapping convolution layers, yielding highly accurate simulations with minimal computational resources.

The utilization of ReLU, as observed in mapping sick tomato crop areas, extends beyond specific applications, demonstrating effectiveness in processing diverse and complex datasets while enabling rapid computation and time savings.

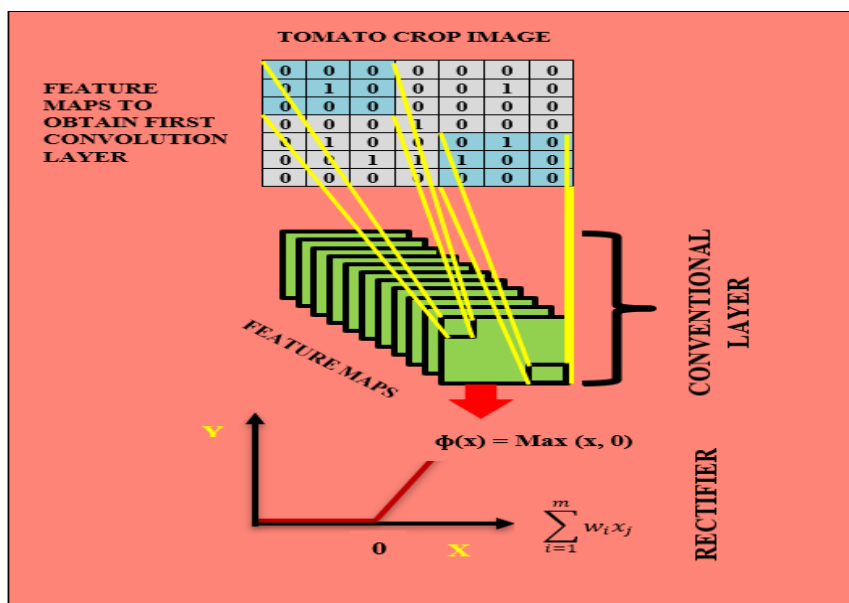


Figure 4. Rectifier liner unit in Activation Function

VII. POOLING

After the convolution layers, which refine the mapping of features, the next step in the processing pipeline is the pooling procedure. Here, the generated layers serve as input for another pooling operation, aimed at reducing processing time and enhancing feature processing accuracy. The pooling procedure plays a vital role in providing a clear depiction of objects, simplifying their identification, particularly when pinpointing the source of infection in tomato crops.

Pooling operations typically involve computing either the average or maximum pixel values from the images of tomato crop segments. Convolutional neural networks predominantly utilize the maximum pooling method to detect diseases. This procedure helps in reducing the dimensionality of mapped features and shrinking learning parameters, which proves beneficial in processing vast amounts of data efficiently.

In CNN processing, two primary pooling algorithms are utilized: average pooling and global pooling. Average pooling computes the average elements within defined regions post-convolution stacking. In contrast, global pooling condenses all channels to a single channel, simplifying the process by reducing three-dimensional channels (nh x nw x nc) to a 1 x 1 x nc feature mapping. This offers an alternative to feature mapping in the nh x nw dimensions.

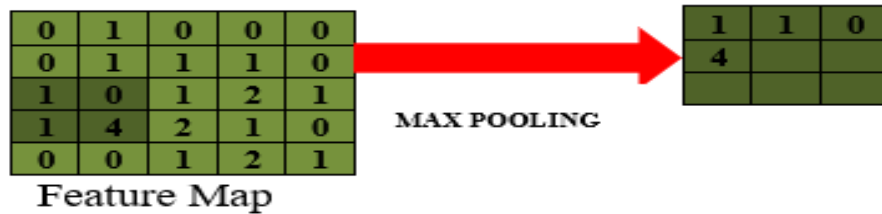


Figure 5. In feature mapping, maximum, average, and global pooling

VIII. FLATTENING

The convolution layer and pooling processes, as discussed earlier, play a crucial role in acquiring the necessary features through high precision mapping. To facilitate a straightforward evaluation process throughout the implementation of the neural network, the features accumulated in the pooling stage, there needs to be organized in a column-wise manner, as illustrated in Figure 7. Additionally, this technique flattens the pooling process outcomes. Further streamlining the evaluation process and enhancing efficiency.



Figure 6. Flattening values from pooled feature mapping.

IX. FULL CONNECTION

A fully connected layer operates as a feed-forward neural networking process, interpreting the mapped layers obtained previously. Neurons in the next layer are formed by connecting active neurons using linear rectifiers. To integrate this into a fully connected layering procedure, all layer dimensions must be converted into single-dimensional data. Figure 8 highlights a notable distinction between output layer connectivity and fully connected layers.

Before employing neural networking to predict infections in tomato crop parts, the region produced using the process of convolutional stacking and pooling undergoes conversion into one-dimensional data. This step prepares the data for further processing and analysis in the fully connected layer.

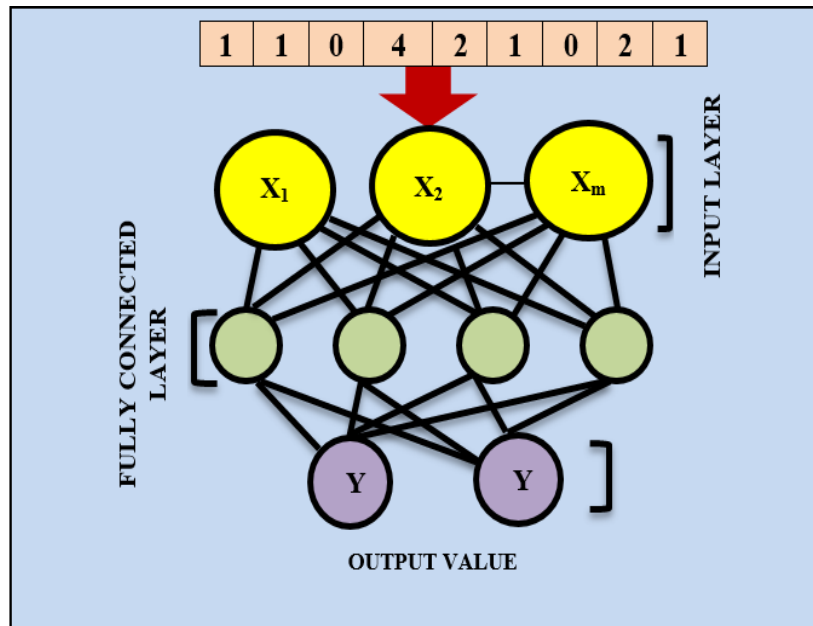


Figure 7. Converting input layers to fully connected layer

X. NEURAL NETWORK ALGORITHM IN IDENTIFICATION PROCESS

The final phase of this research endeavor focuses on applying machine learning techniques to analyze the categorized affected parts of the tomato crop. As a branch of machine learning, deep learning is particularly instrumental in this implementation process. The key distinction between deep learning and traditional machine learning algorithms lies in the utilization of human intervention for analysis and testing of the deep learning neural network algorithm.

Deep learning techniques are paramount for prediction and analysis due to their capability to streamline the feature engineering process, thereby mitigating practical challenges. Unlike traditional image classification techniques reliant on hand-engineered processes, deep learning leverages feature engineering tasks to multitask and expedite the extraction and identification processes while addressing various complex challenges. In contrast to relying solely on features located in previous steps, deep learning relies on learned variables, enhancing the adaptability and effectiveness of the overall analysis.

XI. PROPOSED VECTOR MACHINE RECURRENT NEURAL

The suggested VMRN is a hybrid model that combines recurrent neural networks and deep learning's vector machine. The main layers that are combined with the recurrent neural network technique are: the vector machine layer, the activation function, the pooling, the flattening, and the fully connected layers. Convolutional layers in various levels, including the convolution layer, activation functional layer, pooling layer, flattening layer, and complete connection layer, are used to process the collected tomato images. After the convolution layer's final fully connected layers, the generated regions are used for the RNN procedure. The Recurrent Neural Network's fundamental idea is to use the output gathered from the previous stage and provide it as input in the current step. The old Neural networking approach had problems predicting the next piece of information because the inputs and outputs were handled separately. With the aid of hidden layers, the issues are resolved, and RNN develops a fresh perspective for forecasting the required data. The RNN algorithm's hidden layer is regarded as its most crucial layer. Recurrent neural network methods have the ability to store previously performed computations and information, and they are able to perform the same task with zero error using the identical specifications for all and every input. The task can be completed using a hidden layer, which is mostly intended to store those temporary variables. In contrast to conventional neural network techniques, the process can be helpful in decreasing the complexity of parameter tuning.

The equation used for the calculating the current state in VMRN model is given as follows

$$h_t = f(h_{t-1}, X_t) \quad (1)$$

where: h_t - current state, h_{t-1} - previous state and x_t - input state.

The equation used to activation function for VMRN model is given bellow

The activation function's formula (tanh)

$$H_t = \tanh(W_{hh}h_{t-1} + W_{xh}X_t) \tag{2}$$

Where: w_{xh} -weight at the input neuron, w_{hh} -weight at the recurrent neuron.

The output obtained from the VMRN can be calculated with the equation

$$Y_t = W_{hy}h_t \tag{3}$$

location: Y_t -output, reason: weight at the output layer

In the VMRN model's training phase, back propagation and forward propagation are divided into two sections. The output values from convolutional layers are collected and calculated in the first stage of the VMRN forward propagation. The balance that was accumulated for updating the weights is sent through back propagation, which comes after the CNN training procedure.

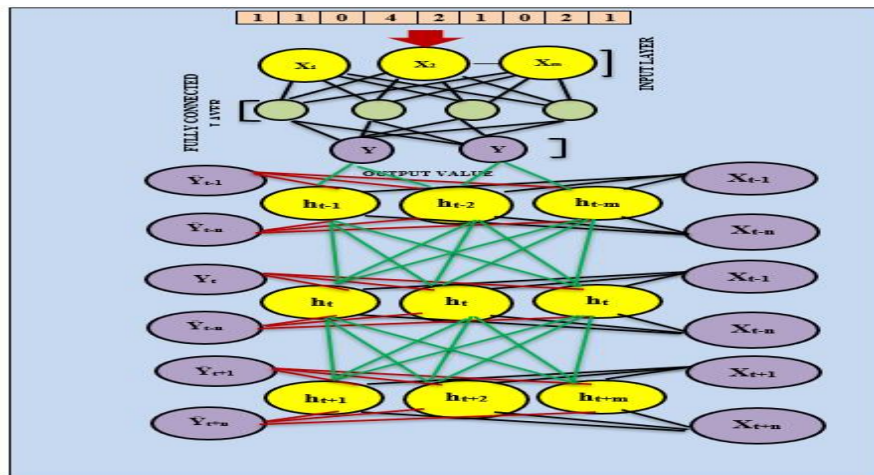


Figure 8. The Unfolded Convolutional and Recurrent Neural Network.

Given are a series of latent representations h_i ($i = 1, 2, \dots, m$), an order of predictions y_i ($i = 1, 2, \dots, m$), and a series of training samples x_i ($i = 1, 2, \dots, m$). Biases are represented by the vectors b_h and b_y . W_{hx} is the input-to-hidden weight matrix, W_{hh} is the hidden-to-hidden weight matrix, and W_{hy} is the hidden-to-output weight matrix [26]. The classification function g activates the SoftMax function, while the activation function e is a sigmoid. The terms "Algorithms 1 and 2" refer to the Forward Propagation Algorithm and the Weights Update Algorithm, respectively. For a single training pair (x_i, y_i) , the objective function for RNNs is written as $f() = L(y_i: y_i)$ [26], where L is a distance function that calculates how far The forecasts y_i are off from the actual labels y_i . Let k represent the Volume of current iterations and represent the learning rate. Suppose the set have a list of labels $y_i(i = 1, 2, \dots, m)$. The procedure followed in proposed VMRN model starts from stage 1 of algorithm 1 and incorporates the algorithm 2.

Initial Forward Propagation Algorithm Algorithm

Enter x_i (where $i = 1, 2, \dots, m$)

Output y_i 1: do 2 for i between 1 and m : $W_{hx}x_i + W_{hh}h_{i-1} + b_h = t_i$

3: $\text{sigmoid}(t_i) = h_i$

4: $s_i = W_{hy}h_i + b_y$

5: $\text{SoftMax}(s_i) = y_i$

6: conclude for

Update of Algorithm 2 Weights Algorithm

Enter h_{yi}, \hat{y}_{ii} (where $i = 1, 2, \dots, m$). $\theta = \{W_{hx}, W_{hh}, W_{yh}, b_h, b_y\}$ is initialized.

$\theta = \{W_{hx}, W_{hh}, W_{yh}, b_h, b_y\}$ is the output.

1: for i , do 2 for k down to 1. Determine the cross-entropy between the label and output values: $- \sum_j y_{ij} \log(\hat{y}_{ij}) + (1 - y_{ij}) \log(1 - \hat{y}_{ij}) = L(y_i; \hat{y}_i)$

3: Determine the partial derivative concerning θ_i : $\delta_i \leftarrow dL/d\theta_i$

4: Updated weight: $\theta_i \rightarrow \theta_i \eta + \delta_i$

5: conclude for

XII. RESULT AND DISCUSSION

In this study, the output values generated by the convolutional neural network (CNN) serve as input for the recurrent neural network (RNN) technique during both the training and testing phases. Through the convolutional approach, regions depicting healthy and diseased areas are translated into values and utilized in the recurrent process. Different regions of tomato crops are affected by different types of illnesses, such as Bacterial Wilt, Early Blight Disease, Late Blight Disease, Leaf Mold, Bacterial Spot, Tomato Pith Necrosis, Buckeye Rot, and Anthracnose; these can be effectively treated with convolutional neural network models.

The initial convolutional stages of the model involve manual processing, followed by the systematic treatment of infections using recurrent neural networking algorithms. The process is evaluated using different neural networking algorithms and measurements. Among 50,000 photos depicting various disease-affected plant sections, 3,689 images of tomato crop components were identified as infected.

The accuracy of the proposed VMCRN model is evaluated based on true positive (TP), false positive (FP), true negative (TN), and false negative (FN) error rates during testing. These terms are defined as follows:

True Positive (TP): The number of anomaly records correctly detected as anomalous, same as those that were appropriately rejected. False Positive (FP): The number of typical records mistakenly labelled as anomalous, akin to "incorrectly rejected." True Negative (TN): The quantity of typical records is accurate. designated as normal, akin to those appropriately admitted. False Negative (FN): Number of deviant occurrences wrongly classified as normal, comparable to those incorrectly allowed.

$$AC = \frac{TP+TN}{TP+TN+FP+FN} \tag{4}$$

This metric provides an overall assessment of how well the VMCRN model performs in correctly classifying both normal and anomalous records during testing. A higher accuracy indicates better performance in distinguishing between normal and anomalous data instances.

Accuracy is calculated as the proportion of accurately classified records to the total amount of records.

$$TPR = TP \text{ divided by } TP+FN \tag{5}$$

False Positive Rate (FPR): divided by the total number of records, the percentage of records that are wrongly rejected is

Table 1. The percentage of accuracy confusion matrix

Actual Class / Expected Class	Anomaly	Normal
Anomaly	TP	FP
Normal	FP	TN

Regular records, as indicated by (6).

$$FPR = \frac{FP}{FP+TN} \tag{6}$$

Thus, the proposed VMRN is to obtain the accuracy and detecting the infected part of the tomato crop parts with lower false positive rate.

Table 2 : Accuracy of tomato crop data set training

Testing Data (%)	Data Trained (%)	Time (Seconds)	Accuracy
60	10	131	0.9896
50	20	103	0.9898
40	30	90	0.9899
20	40	103	0.9898
10	50	130	0.9890
60	10	266	0.9880
50	20	211	0.9889
40	30	191	0.9955
20	40	211	0.9970
10	50	261	0.9975

When considering alternative representations, the training approach used to select features from diseased portions of tomato crops is compared with training data (20%) and testing data (40%) to determine the best accuracy. This comparison aims to assess the effectiveness of feature selection and model training in accurately distinguishing between healthy and diseased crops. By splitting the data into training and testing sets, with a larger portion allocated for testing, the model's performance can be robustly evaluated. The goal is to achieve the highest accuracy on the testing data, indicating the model's ability to generalize well to unseen instances and effectively identify diseased portions of tomato crops. The time required completing a specific training and testing set is 100 minutes, and 211 minutes are required to complete a specific section. The acquired accuracy of 0.9970 is thought to be the most appropriate for further processing.

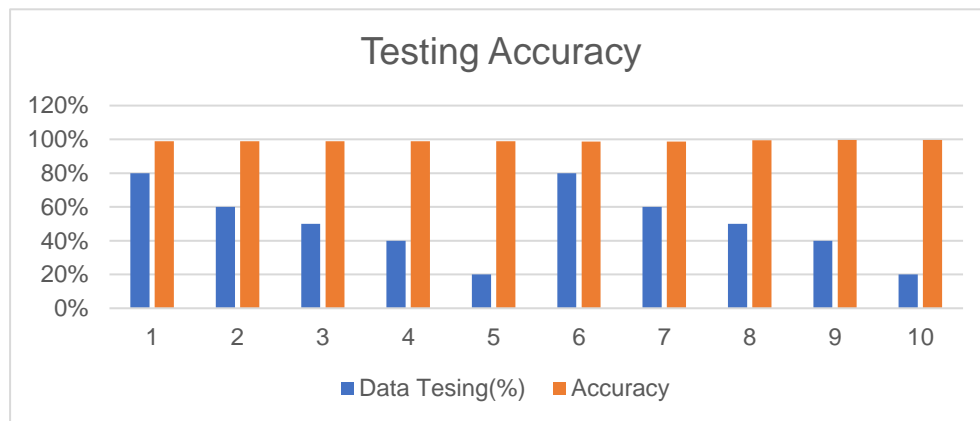


Figure 9. Data Testing Accuracy

The accuracy and execution time of the retrieved characteristics are calculated. Figure 10 depicts the data testing accuracy range, and table 2 shows that count 9 has the greatest accuracy level of 0.9970. The data examined represents a 20 percent sample of the 3, 689 tomato crop portions overall that were diseased.

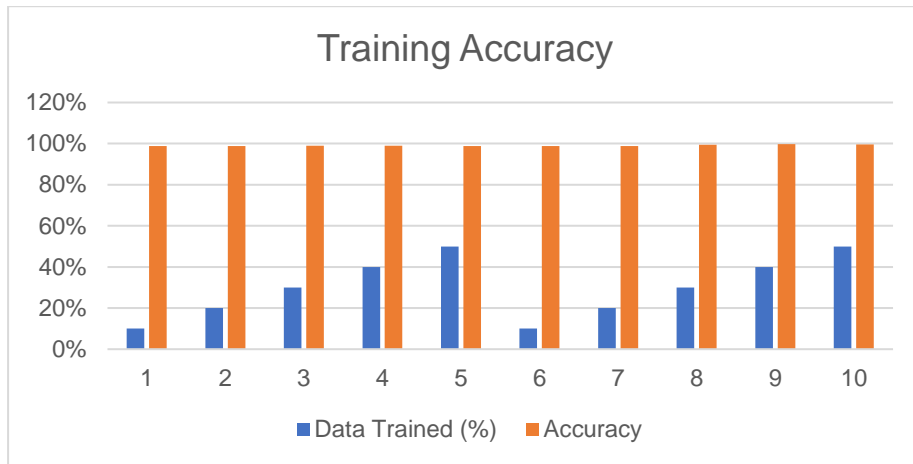















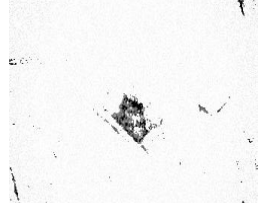


Figure 10. Data Training Accuracy

The accuracy and execution time of the retrieved characteristics are calculated. Figure 11 depicts the reported data training accuracy range, with count 9 displaying the highest accuracy level of 0.9970, indicates that among the different training iterations or configurations, the ninth instance achieved the highest accuracy. This accuracy level suggests that the model trained with this particular configuration performed exceptionally well in classifying the training data. It's important to note that while high training accuracy is desirable, the ultimate goal is to generalize well to unseen data, which is typically assessed through testing accuracy. Nonetheless, achieving a high training accuracy can indicate that the model has effectively learned the patterns present in the training data. Table 2. 20 percent of the 3, 689 total disease-infected tomato crop part segments were evaluated.

Table 3. Result of feature extraction process.

Original Images	Convolution layer	Activation function(Rectifier Linear Unit)	Max Pooling
 Bacterial Wilt			
 Early Blight Disease			
 Late Blight Disease			
 Leaf Mould			

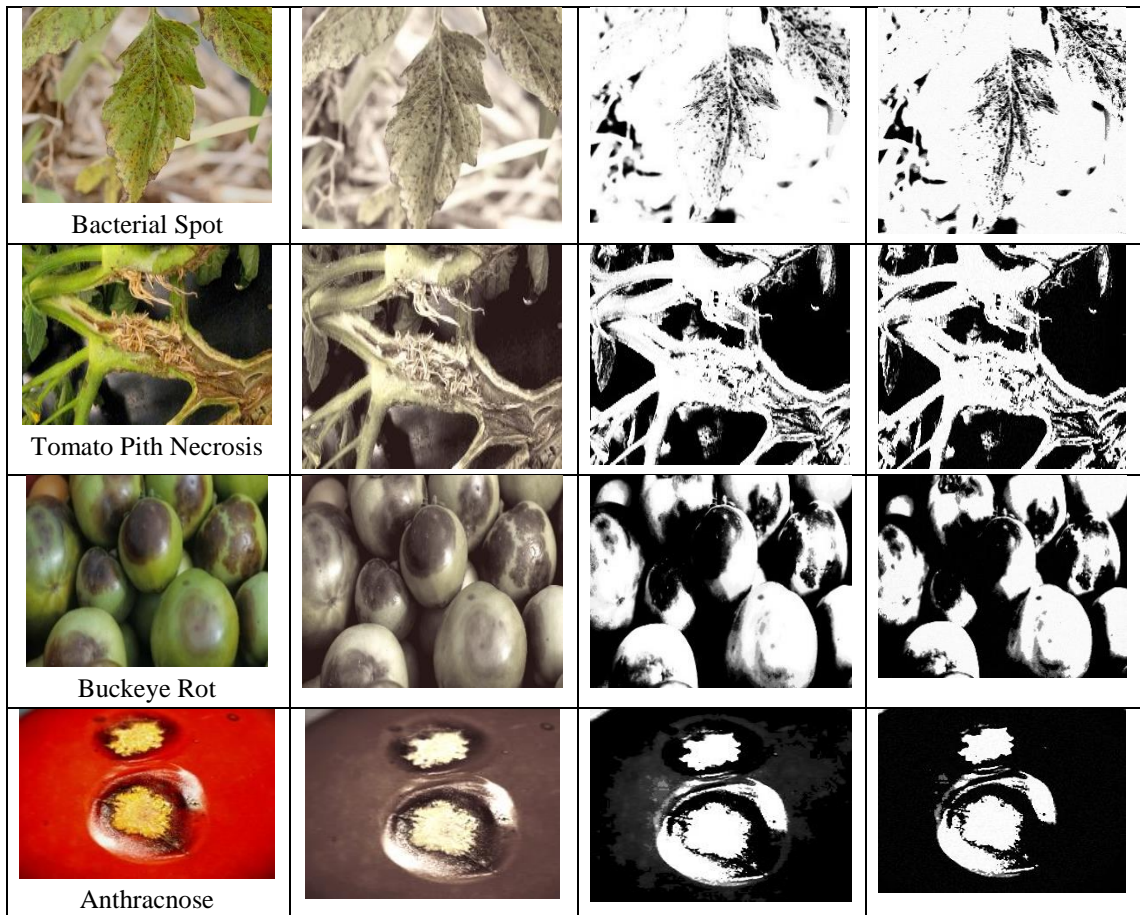


Table 2 categorises the features that were gathered using convolutional neural networks. A variety of diseased tomato crop sections are identified using various procedures. Utilising a classification technique, the final flattening and output production steps are completed. With various classifiers like The terms "back propagation neural network (BPNN), feed forward neural network (FFNN), recurrent neural network (RNN), convolutional neural network (CNN), and deep neural network (DNN), the proposed VMRN's accuracy is evaluated. Utilising a MATLAB tool, the proposed VMRN model tested with tomato crop parts is evaluated. Table 2 provides a thorough analysis F-Measures, sensitivity, and specificity are examples of accuracy metrics.

Table 4. Comparative comparison using the suggested VMRN for various classifiers

Classifiers	Sensitivity	Specificity	F-measures
DNN	72.111	93.005	69.251
CNN	82.211	93.706	72.101
RNN	74.737	93.750	68.512
BPNN	69.372	92.970	67.927
FFNN	66.775	91.930	64.940
VMRN	84.826	95.267	80.867

To verify the ideal prediction procedure, a comparison is made to determine the sensitivity, specificity, and F-measures. As indicated in table 4, different classifiers are tried on the diseased tomato crop halves. With every classifier, the identification procedure is put to the test using various bacterial attacks discovered on tomato crop. The Feed Forward Neural Network had the lowest sensitivity, and the proposed VMRN model had the highest sensitivity values. The same testing and implementation for specificity also indicated that VMRN had the best specificity (95.267%), and that Feed Forward Neural Network (FFNN) had the lowest specificity (91.930%). The lowest specificity point, which has a 93.750% range, is very near to the performance of the RNN. The F-Measure calculation was also performed with several classifiers; the proposed VMRN produced results with a high range of 80.867%, and the Feed Forward Neural Network (FFNN) produced results with a low range of F-Measure.

Table 5. Accuracy of the proposed VMRN model

Organizers of Classes	Accuracy
DNN	91.356
CNN	92.819
RNN	93.608
BPNN	93.496
FFNN	93.256
VMRN	98.940

The suggested VMRN's accuracy was tested using the same assortment of classifiers as before. Each affected area of the tomato crop parts is predicted and identified separately. Results are calculated after applying the set of testing variables gathered using convolution methods to several classifiers with various iterations. In comparison to previous classifiers, Table 5 demonstrates that the suggested VMRN model performs best, obtaining a score of 98.940%. The least accurate method for locating the diseased area of tomato crop parts was found to be deep neural network (DNN), which had an accuracy rating of 91.356%.

XIII. CONCLUSION

The image processing technique employed for identifying disease-affected areas of tomato crops stands as a promising research avenue. Traditional approaches to identification have encountered practical challenges, such as time constraints and accuracy issues with classification algorithms when identifying diseased components. Moreover, previous methods of image processing often underutilized the activation function, hindering the full potential of disease identification. However, the proposed VMRN (Vector Machine Recurrent Neural with Manual Activation Function) framework suggests that the identification process remains viable even without automatic activation functions. This framework justifies the combination of automatic and systematic activation functions, emphasizing their significance in enhancing accuracy and efficiency. Furthermore, the integration of RNNs with CNNs presents a promising approach to improving the accuracy of the identification process. This combination allows for the seamless integration of temporal and spatial information, resulting in more robust and precise disease detection in tomato crops. Overall, exploring novel methods that leverage advanced neural network architectures and activation functions holds immense potential for revolutionizing disease identification in agriculture, particularly in the context of tomato crop management.

REFERENCES

- [1] S. P. Mohanty, D. P. Hughes and M. Salathé, "Using Deep Learning for Image-Based Plant Disease Detection", *Frontiers in Plant Science*, vol. 7, 2016.
- [2] G. Wang, Y. Sun and J. Wang, "Automatic Image-Based Plant Disease Severity Estimation Using Deep Learning", *Computational Intelligence and Neuroscience*, vol. 2017, pp. 1-8, 2017.
- [3] E. Fujita, Y. Kawasaki, H. Uga, S. Kagiwada and H. Iyatomi, "Basic Investigation on a Robust and Practical Plant Diagnostic System", *IEEE Proc. on Machine Learning and Applications*, pp. 989-992, 2016.
- [4] S. Sladojevic, M. Arsenovic, A. Anderla, D. Culibrk and D. Stefanovic, "Deep Neural Networks Based Recognition of Plant Diseases by Leaf Image Classification", *Computational Intelligence and Neuroscience*, vol. 2016, pp. 1-11, 2016.
- [5] Fuentes, S. Yoon, S. Kim and D. Park, "A Robust Deep-Learning-Based Detector for Real-Time Tomato Plant Diseases and Pests Recognition", *Sensors*, vol. 17, no. 9, 2017.
- [6] J. Lu, J. Hu, G. Zhao, F. Mei and C. Zhang, "An in-field automatic wheat disease diagnosis system", *Computers and Electronics in Agriculture*, vol. 142, pp. 369-379, 2017.
- [7] D. P. Hughes and M. Salathé, "An open access repository of images on plant health to enable the development of mobile disease diagnostics", *CoRR*, vol. abs/1511.08060, 2015.

- [8] S. Ren, K. He, R. Girshick and J. Sun, "Faster R-CNN: Towards Real-Time Object Detection with Region Proposal Networks", *IEEE Trans. on Pattern Analysis and Machine Intelligence*, vol. 39, no. 6, pp. 1137-1149, 2017.
- [9] W. Liu, D. Anguelov, D. Erhan, C. Szegedy, S. Reed, C.-Y. Fu, et al., "SSD: Single Shot MultiBox Detector", *ECCV 2016 Lecture Notes in Computer Science*, pp. 21-37, 2016.
- [10] J. Dai, Y. Li, K. He and J. Sun, "R-FCN: Object Detection via Region-based Fully Convolutional Networks", *Advances in Neural Information Processing Systems*, vol. 29, pp. 379-387, 2016.
- [11] J. Dai, H. Qi, Y. Xiong, Y. Li, G. Zhang, H. Hu, et al., "Deformable convolutional networks", *CoRR*, vol. abs/1703.06211, 2017.
- [12] K. He, X. Zhang, S. Ren and J. Sun, "Deep Residual Learning for Image Recognition", *IEEE Proc. on Computer Vision and Pattern Recognition*, pp. 770-778, 2016.
- [13] Fatma Zohra Rekad, David Edward Llewelyn Cooke., et al, "Characterization of *Phytophthora infestans* populations in north-western Algeria during 2008–2014", *Fungal Biology*, Volume 121, Issue 5, 2017, Pages 467- 477, ISSN 1878-6146, <https://doi.org/10.1016/j.funbio.2017.01.004>.
- [14] ANDREA P. ZULUAGA., et al," Transcriptional dynamics of *Phytophthora infestans* during sequential stages of hemibiotrophic infection of tomato", *MOLECULAR PLANT PATHOLOGY* (2016) 17(1), 29–41
- [15] E. Mine Soylu, SonerSoylu&Sener Kurt," Antimicrobial activities of the essential oils of various plants against tomato late blight disease agent *Phytophthora infestans*", *Mycopathologia* (2006) 161: 119–128.
- [16] Yushi Luan, Jun Cui, Weichen Wang & Jun MengPublished: 25 October 2016 MiR1918 enhances tomato sensitivity to *Phytophthora infestans* infection.
- [17] Luan, Y., Cui, J., Wang, W. et al. MiR1918 enhances tomato sensitivity to *Phytophthora infestans* infection. *Sci Rep* 6, 35858 (2016). <https://doi.org/10.1038/srep35858>.