

IOT ENABLED EFFICIENT PLANT LEAF DISEASE DETECTION AND CLASSIFICATION USING LSTM-FCL NETWORK**¹L. Subash and ²Dr. G. Arulselvi**¹Ph.D. Research Scholar, Department of Computer and Information Science, Faculty of Science, Annamalai University, Annamalainagar, Tamil Nadu, India²Associate Professor, Department of Computer Science and Engineering, Faculty of Engineering and Technology, Annamalai University, Annamalai nagar, Tamil Nadu, India¹l.subashmenon@gmail.com and ²arulselvi_ag2004@yahoo.com**ABSTRACT**

Plant diseases can have a substantial impact on food and agricultural production, resulting in significant losses in terms of quality, quantity, and economic output. Early diagnosis through visual observation is a common method to identify plant disease infection. Certain prominent plant species, such as apple, mango, banana, and groundnut, are cultivated in specific regions worldwide. The prevalence of leaf diseases varies depending on the geographic location of an area. Traditional methods of plant leaf disease detection are often inefficient and time-consuming. This study proposes a novel approach for the automatic detection and classification of plant leaf diseases, utilizing the Long Short-Term Memory Networks with Fully Connected Layer (LSTMs-FCL) deep learning algorithm. The process begins with preprocessing IoT-based leaf photographs to eliminate noise from the images. Subsequently, the segmentation process employs Sorensen Dice similarity with Mask-based Fuzzy C-Means (SDSM-FCM). Following segmentation, the gray-level co-occurrence matrix (GLCM) is applied to the binarized image for feature extraction. Feature selection is performed using the hybrid Osprey optimization with whale optimization algorithm (OOWOA). Finally, categorization is accomplished using the LSTMs-FCL network as a plant leaf diseases classifier capable of distinguishing between healthy and diseased plants. The experimental results demonstrate promising outcomes in terms of classification measures, including accuracy, precision, loss rate, recall, and F-score. A comparative analysis is conducted between the proposed algorithm parameters and existing parameters, revealing the superior performance of the LSTMs-FCL network algorithm, achieving an accuracy of 95.5%.

Keywords: Plant leaf disease, Long Short-Term Memory Networks with Fully Connected Layer (LSTMs-FCL), gray-level co-occurrence matrix (GLCM), Osprey optimization with whale optimization algorithm (OOWOA)

1. INTRODUCTION

Agriculture plays a crucial role as a primary source of sustenance and food for humans. Plant infections can result in significant economic and environmental losses, impacting both the quantity and quality of crops. Therefore, the consistent and accurate diagnosis and detection of plant diseases are paramount important [1, 2]. The conventional method for assessing and detecting plant diseases often relies on professional examination using the naked eye. However, this manual approach is practical only for small-scale assessments in specific regions, and delays in the process can lead to the rapid spread of diseases across crops [3]. Therefore, an automated detection method for plant diseases becomes imperative need. Plant diseases can directly correlate with stunted growth, negatively affecting crop yields. Globally, economic losses due to plant diseases are estimated at approximately \$20 billion annually. The diverse conditions presented by this challenge pose difficulties for researchers, given geographical variations that impact accurate identification [4]. Traditional methods, primarily involving specialists, experts, and manuals, are costly, time-consuming, and reliant on manual operations, making precise representation challenging. Thus, a swift and accurate approach to plant disease detection holds significant economic and environmental benefits for agriculture [5].

Visual identification of soil diseases is a labour-intensive and less precise task, often necessary only in limited areas. Utilizing automated techniques can reduce effort, save time, and enhance precision [6, 7]. Viral infections impede plant growth, leading to yellowing, wilting, and seed drop. Examples of bacterial diseases include leaf

blight, gall blight, and fire blight, while fungal diseases encompass anthracnose, downy mildew, powdery mildew, black spot, and downy mildew [8]. Fungi are responsible for substantial plant damage, with 80% of plant diseases attributed to fungal infections. Protecting plants from diseases is crucial for ensuring both their quality and quantity. Early diagnosis is essential for implementing an effective protective strategy, preventing the spread of diseases [9, 10]. Global losses in agriculture due to tree diseases cost billions annually, underscoring the significance of preventive disease diagnosis [11].

Image processing emerges as an effective method for extracting features from images, segmenting them based on characteristics, highlighting qualities, and classifying individual objects. This approach proves vital in plant disease detection, enabling automatic classification of common diseases and long-term symptoms on plant leaves [12]. Implementing image processing eliminates the need to hire experts for the monotonous task of monitoring large crop fields. Plant disease detection encompasses various steps, including plant leaf image collection, quality enhancement, segmentation, feature extraction, and classification [13]. To detect plant infections early and reduce disease occurrence, traditional observation with the naked eye is ineffective, especially in large crops [14]. Leveraging digital image processing and deep learning technologies enhances the efficiency and accuracy of detecting diseased plants, requiring less effort and time. Classical approaches involve image preprocessing and feature extraction, often integrated into artificial intelligence (AI) techniques such as support vector machines (SVM), k-nearest neighbors (k-NN), fully connected neural networks (FCNN), decision trees, and random forests. In recent years, there has been an increasing reliance on AI-modified methods for image classification tasks. The primary challenge in identifying leaf images lies in accurately outlining the leaf shape. Various shape options have been proposed to describe leaf image shapes [15]. However, there is currently no precise application for classifying leaves into categories after capturing their images and identifying their characteristics. Plant leaf image classification involves categorizing leaves based on their distinct morphological characteristics.

The objective of this work is to focus on classification algorithms and feature optimizations useful for effective classification of leaf diseases in plants. This area is of utmost importance as a good forecasting method will significantly improve crop production. To optimize functions, function optimization algorithms are used, such as the hybrid Osprey optimization algorithm with Whale optimization algorithm (OOWOA). Deep learning algorithms are then applied to a set of optimized features for the classification process. Furthermore, in this work, several measures were tested on given data to determine a priori the expected performance of the compared classifiers on plant leaf disease data sets.

The remainder of the paper is structured as follows: Section 2 provides an overview of the current research landscape on plant diseases, highlighting existing problems and identifying gaps. Section 3 outlines the proposed plant disease system, while Section 4 presents the results and discussions aimed at enhancing performance measurements. Finally, Section 5 concludes the paper by summarizing the system and its key findings.

2. LITERATURE REVIEW

The detection and classification of leaf plant diseases have posed longstanding challenges. Despite numerous research efforts in this field, some studies have fallen short in delivering substantial results.

Darwish et al. [16] proposed an optimized model based on convolutional neural networks (CNN) and the particle swarm optimization algorithm with orthogonal learning for plant disease diagnosis. They addressed dataset imbalance through random oversampling and random undersampling, achieving more accurate results than other pre-existing CNN models. Their work demonstrated competitiveness with models like InceptionV3 and Xception.

Ramesh et al. [17] focused on rice leaf disease detection and classification, utilizing a deep neural network optimized with the Jaya algorithm. They captured images directly from agricultural fields and employed preprocessing techniques such as RGB to HSV conversion, binary image generation, and clustering for disease segmentation. Their deep neural network achieved disease classification using the Jaya optimization algorithm (DNN_JOA).

Abhilasha et al. [18] investigated disease identification in oilseed leaves through deep and diverse learning techniques, particularly focusing on soybean, dwarf palm, and rapeseed. The study emphasized the economic impact of diseases on production and the potential for quick detection to save crop varieties.

Nirmal et al. [19] explored the classification of pomegranate leaf diseases using image processing and machine learning techniques. Their framework involved image processing steps such as capture, resizing, enhancement, segmentation, region of interest (ROI) extraction, and feature extraction. Machine learning models, including Linear Discriminant Analysis (LDA), K-Nearest Neighbor, Naive Bayes (NB), and ensembles, were employed for disease classification, achieving a notable accuracy of 96.49%.

Parez et al. [20] addressed challenges in plant disease detection by proposing an improved technique, GreenViT, based on Vision Transformers (ViT). The study highlighted the limitations of CNN-based models and demonstrated that GreenViT outperformed state-of-the-art CNN models for plant disease detection through experiments on benchmark datasets.

Suresh et al. [21] presented a novel deep neural network model for tomato soil disease classification using PCA-whale optimization. Their approach involved deriving important features from a publicly available plant dataset and feeding them into a deep neural network for disease classification. The proposed model demonstrated superiority in accuracy and handling missing data compared to classical machine learning techniques.

A significant limitation of the current system is that a majority of research relies on image processing techniques that incorporate intricate steps in image segmentation, leading to a time-intensive process.

- ❖ Numerous diseases exhibit symptoms that lack clear demarcations, often blending with healthy portions of the leaf. Current techniques fall short in detecting such cases, necessitating a robust classification algorithm.
- ❖ Existing methods may be tailored to specific crops or confined to particular agricultural practices, limiting their applicability across diverse agricultural settings.
- ❖ The proposed approach centers around Long Short-T Term Memory Networks with Fully Connected Layer (LSTMs-FCL), offering high accuracy levels in disease classification without the time-intensive nature associated with certain other image processing techniques.
- ❖ In many instances, infections in banana, groundnut, apple, and mango plants manifest across multiple parts of the plant, yet a significant portion of research focuses solely on the leaves.

3. PROPOSED METHODOLOGY

The proposed methodology tests advanced deep learning techniques and IoT-enabled technology to address critical issues related to plant disease detection in agriculture. This study proposes an emphasis on plant leaf disease segmentation and classification consisting of the following steps: preprocessing, image segmentation, feature extraction, feature selection and disease classification. Initially, the raw image is preprocessed to remove noise and other unwanted artifacts and improve image quality. Furthermore, the preprocessed images are segmented using the Sorensen Dice Similarity with Mask based FCM (SDSM-FCM). Next, the most relevant features such as spatial features, transformation, features, edges, boundaries, color, shape, and texture are extracted from the segmented images using the gray-level color matrix (GLCM) technique. Furthermore, for feature selection, a hybrid optimization approach is implemented, which combines Osprey optimization with whale optimization algorithm (OOWOA). Finally, these features are fed when entering the classification phase, which is modeled using Long Short-Term Memory Networks with Fully Connected Layer (LSTMs-FCL) networks for disease identification. Furthermore, to improve the accuracy of LSTM-FCL classification, its weights are adjusted by a new hybrid optimization model. Figure 1 shows that the proposed general methodology has been illustrated.

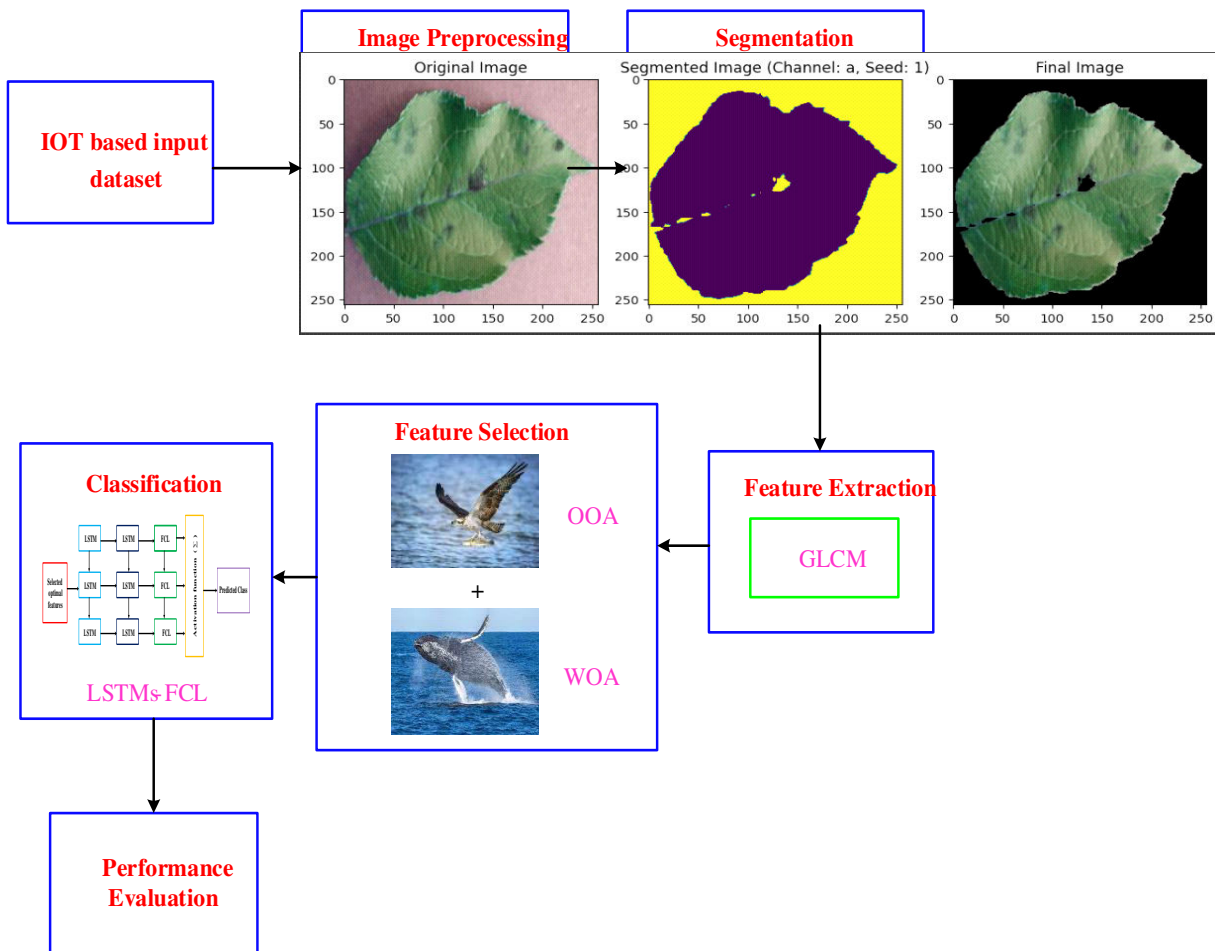


Fig.1: Proposed framework of plant leaf disease recognition

3.1. Dataset Collection

In this article, we utilized the plant village dataset based IoT. This data set contains several leaf diseases found in different fruits and cultivars. The disease classes were chosen from apple, mango, banana and groundnut. Four separate datasets, including Apple leaves [22], Mango leaves [23], Banana leaves [24] and Groundnut leaves [25], were combined into a single dataset, which is available on sites like Kaggle and UCI. The IoT technology-based dataset comprises 21 different classes with a total of 8,731 images including both healthy and diseased leaves, showcasing various diseases affecting these plants. Here, total 8,731 images which are preprocessed and compressed into 7106 images. These images are captured in various IoT based resolutions using different devices including high resolution mobile phones, VGA compatible cameras, mobile phones, digital cameras and DSLR cameras. A healthy variety of each fruit is also available. Infected parts and healthy plants of apple, mango, banana and groundnut were collected from various fields of South India, concentrated in the southern region of Tamil Nadu, including the districts of Madurai, Dindigul, Virudhunagar, Tirunelveli, Tuticorin, Nagercoil, Kanyakumari and some parts across the border between Tamil Nadu and Kerala. Some sample images are illustrated in Fig. 2.

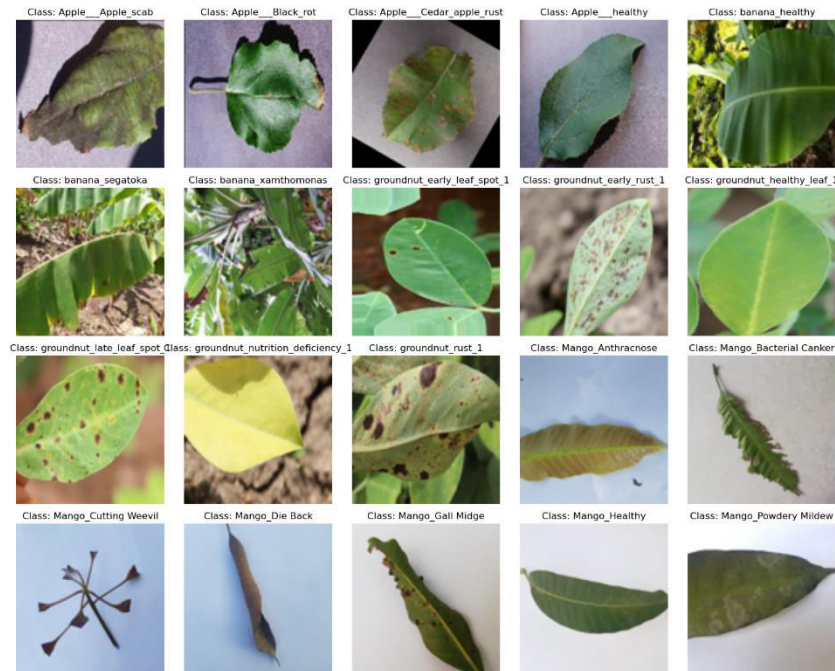


Figure 2: A dataset of sample plant village images for classification purposes

3.2. Image Preprocessing

The pre-processing of images is a crucial step in refining pictures of banana, groundnut, mango, and apple leaves. This involves operations such as cropping, smoothing, and contrast enhancement to eliminate noise and enhance visual quality. The transformed image follows a crucial binary processing phase in which areas of interest are highlighted and details are reduced to a minimum. At the same time, a detailed writing process takes place to perfect all functionalities. This comprehensive pre-processing application ensures that images of banana, groundnut, mango and apple leaves are optimized for sequential analysis, contributing to accurate and meaningful results in agricultural applications.

3.3. Segmentation Process using SDSM-FCM Approach

This study methodology uses the SDSM-FCM algorithm, a robust projected image segmentation technology to accurately identify skin root diseases. By integrating the Sorensen data similarity metric with the black-based fuzzy C-means algorithm, this approach optimally combines the strengths of both methods. Image segmentation can be used mainly by positioning and defining images. Clustering is not monitored by the registered FCM user [26]. The cluster center is generated from the clusters, and the clusters are constructed based on all distances between the specified points. The main advantage of the FCM is its flexibility. However, implementing Euclidean distance that does not contain a large amount of data and randomly selecting centroids can lead to clustering errors. Therefore, the centroid is determined by the standard deviation based on the data, and the input node with the largest deviation again represents the centroid in this study, which represents the Euclidean distance with the Manhattan distance. This approach uses pooling and aims to eliminate the second objective function:

$$OF = \sum \sum D_{ij}^l Dis_{ij} \quad (1)$$

Where D_{ij}^l is the degree of membership of node i to group j , l is the largest real number and Dis_{ij} is the distance between the nodes. First, the centroid is selected and the standard deviation between nodes is calculated, which is expressed as follows:

$$A_x = \sqrt{\frac{\sum \lambda_s - \beta}{\lambda_n}} \quad (2)$$

Where, A_x specifies the center of the group, β indicates the average value, λ_s specifies the sum of numerical features, and λ_n indicates the number of features presented in the plant disease segmentation. After calculating the main image, such as color, texture, image shape, spatial distribution, edge and boundary information, it is calculated based on the Sorensen Mask Dice Similarity (SDSM) calculation. The approach with the largest SDSM in the correct detection class, called, works best, starting from the smallest lesions. There is a volumetric identifier T_1 , where σ_1 is the best performing algorithm and is replaced by σ_2 , σ_3 , which is then replaced by σ_3 in the volumetric identifier T_2 . To apply volumetric identifiers T_n to n^{th} , often after learning σ_n , $(n-1)$ the Data is duplicated during reference. Applying the following fold, the objective is to identify diseases whose volumes occur within the specific thresholds T_n and $T_{(n+1)}$. These thresholds correspond to the optimal performance of the method within this range, which in this context would be $\sigma_{(n+1)}$. The result of the algorithms is the union of these pathological plant segments. This process involves outlining and highlighting areas of the plant, particularly leaves or other plant organs, that have irregularities indicative of disease. The group of plant diseases detected by the algorithm can be accurately expressed as those that include specific thresholds, resulting in a refined understanding of plant disease segmentation.

$$\Omega = \bigcup_n \left\{ F \in \sigma_{n+1} \mid T_n < V(F) \leq T_{(n+1)}, V(F) = \sigma_{(n+1)} \right\} \quad (3)$$

$V(F)$ represents the volume of pixel F detected by the best performing algorithm in the range between the specified thresholds. The distance matrix for the y^{th} -step is then updated as follows:

$$D_{ij}^l = \left(\frac{1}{\sum (Dis_{ij} / Dis_{sv})^{2/l-1}} \right) \quad (4)$$

Where l indicates the iteration step.

The FCM process is ripe for non-convergence. In this way it takes the form of a cluster. The cluster format is displayed,

$$\Psi_S = \{\psi_1, \psi_2, \psi_3, \dots, \psi_n\} \text{ (or) } \Psi_S = \psi_i, \quad i = 1, 2, \dots, n \quad (5)$$

Where, Ψ_S indicates the set of clusters formed and ψ_n defines the number n of clusters.

3.4. Feature Extraction Using GLCM approach

Upon segmenting the preprocessed image, the next step involves feature extraction. The objective of this method is to extract meaningful information from the segmented object, showcasing attributes for subsequent processing. In image processing, feature extraction encompasses various aspects, including spatial features, transformations, edges, boundaries, colors, shapes, and textures. The features to be extracted can pertain to color, shape, or texture, with values that may exhibit monotonic behavior within a specific region, making them potent qualifiers for identification in similar images. Image analysis benefits from the extraction of texture features based on the

statistical distribution of pixel intensity. The features derived from the pixel matrix values using the GLCM method [27] form an orientation pattern angle. Six functions are employed in this context, namely:

Contrast: It is the result of measuring the intensity contrast between pixels and their neighbors in the entire image. Contrast value can be obtained using equation (6).

$$C = \sum_{x,y} (x-y)^2 P_{x,y} \quad (6)$$

Correlation: This is a feature that represents the linear relationship of the gray scale of the image. The correlation is between -1 and 1. It can be found using the following formula:

$$Corr = \sum_{x,y} \frac{(x-\alpha_x)*(y-\alpha_y) P_{xy}}{\beta_x \beta_y} \quad (7)$$

Inverse Different Moment (IDM): Measures the smoothness of the image. This parameter reaches its maximum value when the gray levels are similar. This value can be determined using equation (8).

$$IDM = \sum_{xy} \frac{1}{1+(x-y)^2} P(x,y) \quad (8)$$

Energy: The greater the similarity, the greater the energy value. The energy value can be determined by equation (9).

$$EGY = \sum_{x,y=0}^{n-1} (P_{xy})^2 \quad (9)$$

Entropy: If the image does not have a uniform texture, it will have a very small value, which means the entropy is very large. Since entropy is proportional to energy. The value of entropy can be determined using equation (10).

$$ETP = \sum_{xy} P(x,y) \log(P(x,y)) \quad (10)$$

Dissimilarity: When calculating the dissimilarity of a texture, the result is that a high value is similar and a low value is similar. This value must be obtained using equation (11).

$$DSY = \sum_{x,y} P_{xy} |x-y| \quad (11)$$

In feature extraction, the local variation of the image is first measured by GLCM using eqn. (6). Then the uniformity of pixel pairs is represented in the image by using eqn. (7). After that the proposed method calculates the degree to which the GLCM diagonal and the element distribution are closest to one another by using eqn. (8). Next, it determines how the image's gray levels are linearly dependent by using eqn. (9). Then GLCM depicts the texture of the image's intricacy or unpredictability by calculating eqn. (10). In the wake of it calculating the dissimilarity of the texture by using the eqn. (11). In this way, the GLCM extracts all the texture features from the image. For increasing the classification accuracy, the proposed work is selecting the features from the extracted features by using osprey optimization with whale optimization algorithm.

3.5. Feature Selection using Osprey Optimization with whale Optimization Algorithm

Feature selection is an important and ongoing research topic every day. Optimization of a constructed model is necessary to increase classification accuracy. In this study, to increase the accuracy, the proposed work uses the feature selection method, whereby feature selection is a process of selecting similar or relevant features. The

function of feature selection is to reduce some uninformative data, and thus, with some selected features, the measurement process can be accelerated more quickly. Here, a hybrid optimization of Osprey with whale optimization algorithm (OOWOA) is proposed for the best feature selection in this paper. The main objective of this phase is to select the best features that improve accuracy and reduce computation time. OOWOA hybrid search is a metaphysical algorithm for selecting the best features. Ospreys, also known as river hawks or sea hawks and found throughout the world, have clever strategies for catching fish and bringing them to an optimal position for fishing. However, this process can cause convergence problems; Therefore, an update procedure is required to resolve this issue. This requires first establishing the problem variables with their respective positions within the search space [28]. In equation (12) assigns random coordinates to these fishing guilds, defining the exact location within this search space.

$$P_{x,y} = t_y + \alpha_{x,y} \cdot (s_y - t_y), \quad x = 1, 2, \dots, i, \quad y = 1, 2, \dots, j \quad (12)$$

To determine the population matrix of osprey sites $P_{x,y}$, and $\alpha_{x,y}$ it is important to consider the characteristics and dimensions y^{th} of osprey x^{th} . In particular, we need to consider the number of ospreys as well as the number of variables in the problem. In addition, numbers in the interval [0,1] are also important to determine a fitness value for the population. Finally, t_y and s_y are lower bounds and the upper bounds of the problem variables are also taken into account.

$$F = \begin{bmatrix} f(P_1) \\ \cdot \\ f(P_x) \\ \cdot \\ f(P_i) \end{bmatrix}_{i \times 1} \quad (13)$$

The vector F represents the objective function values, and P_i denotes the newly obtained objective function value for the i th osprey. The assessed objective function values serve as the primary criteria for appraising the quality of the candidate. The trajectory of the fishing guild is determined by the vector of objective function values. Through a suitability assessment it is possible to identify a place suitable for the fish population. Then, by chance, the fishermen's guild enters one of these schools of fish and launches a strike. Using (14), if you calculate a new position based on the simulation of movements, will get the grip. Ultimately, this replacement position will enhance the desired outcome below (14).

$$P_{x,y}^{O1} = P_{x,y} + \alpha_{x,y} \cdot (E_{x,y} - D_{x,y} \cdot P_{x,y}) \quad (14)$$

$$P_{x,y}^{O1} = \begin{cases} P_{x,y}^{O1}, & t_y \leq P_{x,y}^{O1} \leq s_y; \\ t_y, & P_{x,y}^{O1} < t_y; \\ s_y, & P_{x,y}^{O1} > s_y. \end{cases} \quad (15)$$

$$P_x^{new} = \begin{cases} P_x^{O1}, & F_x^{O1} < P_x; \\ P_x^{new}, & else. \end{cases} \quad (16)$$

After analyzing the details of the P_x^{O1} first phase of x^{th} osprey, such as its dimension, F_x^{O1} objective function value and food selection, P_x^{new} is the new position of the x^{th} osprey, $\alpha_{x,y}$ and $D_{x,y}$ are random numbers were assigned to both the interval $[0, 1]$ and set $\{1, 2\}$. The Osprey algorithm takes more convergence time, so the convergence time is reduced by using the update function of the Whale Optimization Algorithm [29]. Then a whale updating procedure was applied in order to candidate solution and global optimal solution is first calculated by equation (17). Then the new position is generated by equation (18).

$$\Psi = |G^*(x) - G(x)| \quad (17)$$

$$G(x+1) = \Psi \cdot e^{cr} * \cos(2\pi r) + G^*(x) \quad (18)$$

Where Ψ is constants that define the geometry of the logarithmic spiral, $G^*(x)$ is the global optimal solution, $G(x)$ denotes the position of candidate solution in the current generation, x refers to the number of current iterations and r is randomly generated range in $[-1, 1]$, respectively.

Input: Obtained features sets

Output: Selected optimal features

Begin

Initialize population, fitness, iteration x and maximum iteration Max_x

Compute fitness

Set iteration $x = 1$

While ($x_t \leq Max_x$) **do**

Movements of the osprey by, $P_{x,y}^{O1} = P_{x,y} + \alpha_{x,y} \cdot (E_{x,y} - D_{x,y} \cdot P_{x,y})$

Update the new position

If $F_x^{O1} < P_x$ {

$P_x = P_x^{O1}$

} **else** {

$P_y = P_x$

} **end if**

Obtain the safe position for eat prey using, $\Psi = |G^*(x) - G(x)|$ **Calculate** fitness

Set $x_t = x_t + 1$

End while

Return feature set

End

3.6. Classification using Fully Connected Layer based Long Short-Term Memory Networks

In the classification of plant leaf diseases, the utilization of Long Short-Term Memory with Fully Connected Layer (LSTM-FCL) networks proves advantageous in enhancing the model's ability to capture sequential patterns and dependencies within the data. This architecture typically incorporates LSTM layers [30], well-suited for processing sequential information, followed by Fully Connected Layers responsible for classification. The significance of sequential information is evident in plant leaf disease scenarios, where patterns in disease progression or temporal aspects of leaf images are crucial. The LSTM layers enable the network to learn and retain relevant information over time, while Fully Connected Layers function as classifiers based on the learned features. The process involves pre-processing leaf image data, extracting pertinent features, and feeding them into the LSTM-based architecture. Model training is centered around optimizing weights to accurately categorize plant leaves into disease classifications. It is crucial to implement regularization techniques and validation strategies to ensure the generalization of the model. Through this well-designed architecture, the LSTM based Fully Connected Layer emerges as a robust tool for plant leaf disease classification, effectively leveraging sequential information within the dataset. This component employs the estimated trust value as an input to identify selected features, facilitating the identification of optimal features through automated systems. The order dependency is addressed by employing long-term memory (LSTM) within recurrent neural networks (RNN), where the output of the previous RNN step serves as input for the subsequent step. To mitigate the vanishing gradient issue, the study opts for the fully connected function over the tanh activation function. Figure 3 visually depicts the structure of the proposed LSTM-FCL, showcasing its architecture and design considerations.

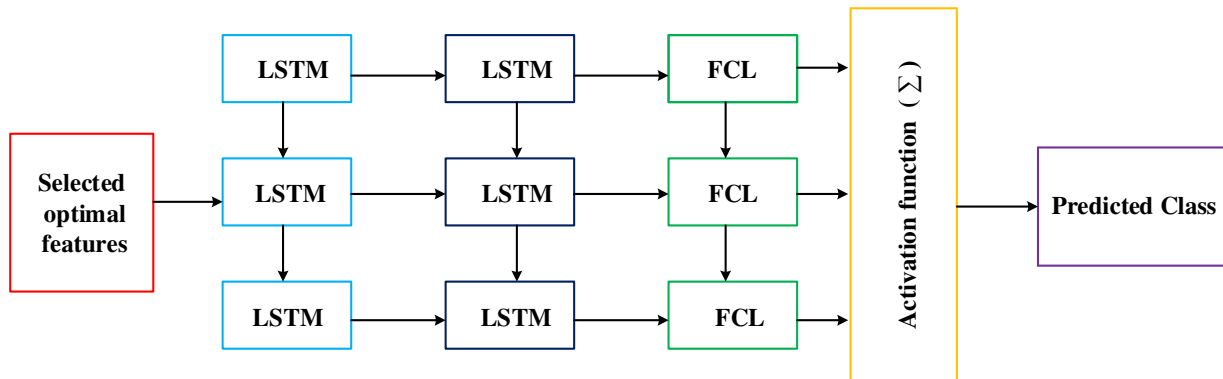


Figure 3: Structure for LSTM-FCL

Forget layer: Data that is no longer relevant to the condition of the cell is deleted by the forget gate. In this layer, two inputs are iterated, weight matrices are multiplied, and finally a bias is introduced. Equation (19) below shows how to describe the forgetting process:

$$L_{fg} = \sigma(\lambda_f [Y_{h-1}, \mu_i] + B_f) \quad (19)$$

Where, L_{fg} denotes the forget gate output, λ_f and B_f indicates the weight value and bias values for input value, σ specifies the sigmoid function, and Y_{h-1} represents the output of the last LSTM unit at time $h-1$.

Input layer: The selected features by using Osprey optimization with whale optimization algorithm is given to the input of LSTM layer. The input and filter values are initially directed by this layer's employment of the sigmoid function to serve as a portal to oblivion. The input layer's expression is represented as follows:

$$L_i = \sigma(\lambda_i [Y_{h-1} - \mu_i] + B_i) \quad (20)$$

Where, L_i defines the outcome of the input layer, λ_f and B_f indicates the weight and bias values of the input layer. The calculation for the tanh expression is given in equation (21),

$$L_{fc} = \tan \text{sig}(\lambda_i [Y_{h-1}, \mu_i] + B_i) \quad (21)$$

Here, L_{fc} specifies the fully connected output layer, λ_f and B_f indicates the weight and bias values of the tansig function of input layer.

Output layer: The block's input and memory are used to determine the output. The expression for the output layer is derived as follows,

$$L_o = \sigma(\lambda_a [Y_{h-1}, \mu_i] + B_a) \quad (22)$$

Where, L_o denotes the output gate, λ_f and B_f indicates the weight and bias values of the output layer. Thus, the LSTMs-FCL classify the features as healthy leaf and identification of leaf disease.

4. RESULTS AND DISCUSSION

Tests for detecting and classifying banana, apple, mango, and groundnut plant leaf diseases were conducted using the PYTHON programming language on a laptop with an Intel Core i5 processor and 32 GB of RAM, equipped with an NVIDIA AMD GPU with 6 GB of memory. The experiment aimed to demonstrate the proposed image classification method across four distinct image categories. The proposed system utilizes the SDSM-FCM to visualize image data and additional image features. Moreover, with the added functionality of LSTM-FCL operations, the fully connected head classifies the image as either an infected leaf plant or a healthy leaf plant. The following is an example of the proposed classifier, presenting accuracy percentages in seconds. Simultaneously, a confusion matrix is constructed to calculate accuracy, precision, recall, and F1 score for the classification. Table 1 presents an analysis of the different classes of leaf diseases within our dataset. There are four diseases in the Apple dataset: apple scab, black rot and cedar apple rust. In addition, a healthy class is included for classification purposes. For the mango dataset, eight disease classes have been picked: anthracnose, bacterial canker, cutting weevil, die back, gall midge, powdery mildew and scooty mould. Moreover, a healthy class is also included. The banana dataset contains three classes such as Healthy, Segatoka and Xanthomonas. The groundnut dataset also includes six classes-Early leaf spot, Early rust, Healthy leaf, Late leaf spot, Nutrition deficiency and Groundnut rust. Figure 4(a) depicts the simulation results of the classification images with the disease in which the LSTM-FCL is efficiently classified the disease leaf. For example, if the apple leaf is input image, then the proposed work is classified the leaf is healthy or unhealthy. if the leaf is unhealthy then proposed system is check what kind of disease is occur in the apple leaf. Figure 4(b) illustrates the outcome, showcasing the original plant leaf disease image, the segmented image, and the final image. These visual representations contribute to a comprehensive understanding of the proposed method's performance in disease detection and image classification.

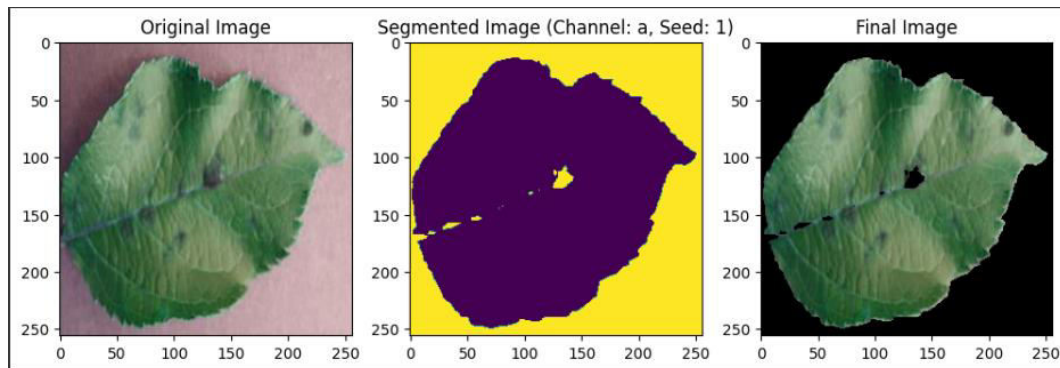
Table.1: Various leaf disease classes in our dataset

Classes	Leaf Disease	No of Images
Apple	Apple Scab	399
	Black Rot	402
	Cedar Apple Rust	355
	Apple Healthy	395
Banana	Healthy	122

	Segatoka	258
	Xanthomonas	663
Groundnut	Early leaf spot	335
	Early rust	304
	Healthy leaf	322
	Late leaf spot	340
	Nutrition deficiency	319
	Groundnut rust	331
	Mango	Anthraxnose
Bacterial Canker		337
Cutting Weevil		315
Die Back		316
Gall Midge		310
Healthy		307
Powdery Mildew		328
Scooty Mould		326
Total class		21



(a)



(b)

Figure 4: Output of plant leaf disease (a) prediction and (b) Segmented image

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4.1. Performance Evaluation

To assess the effectiveness of the proposed model, a confusion matrix is constructed, providing a tabular representation of the model's performance. Figure 5 displays the confusion matrix for the proposed model, which comprises four essential elements:

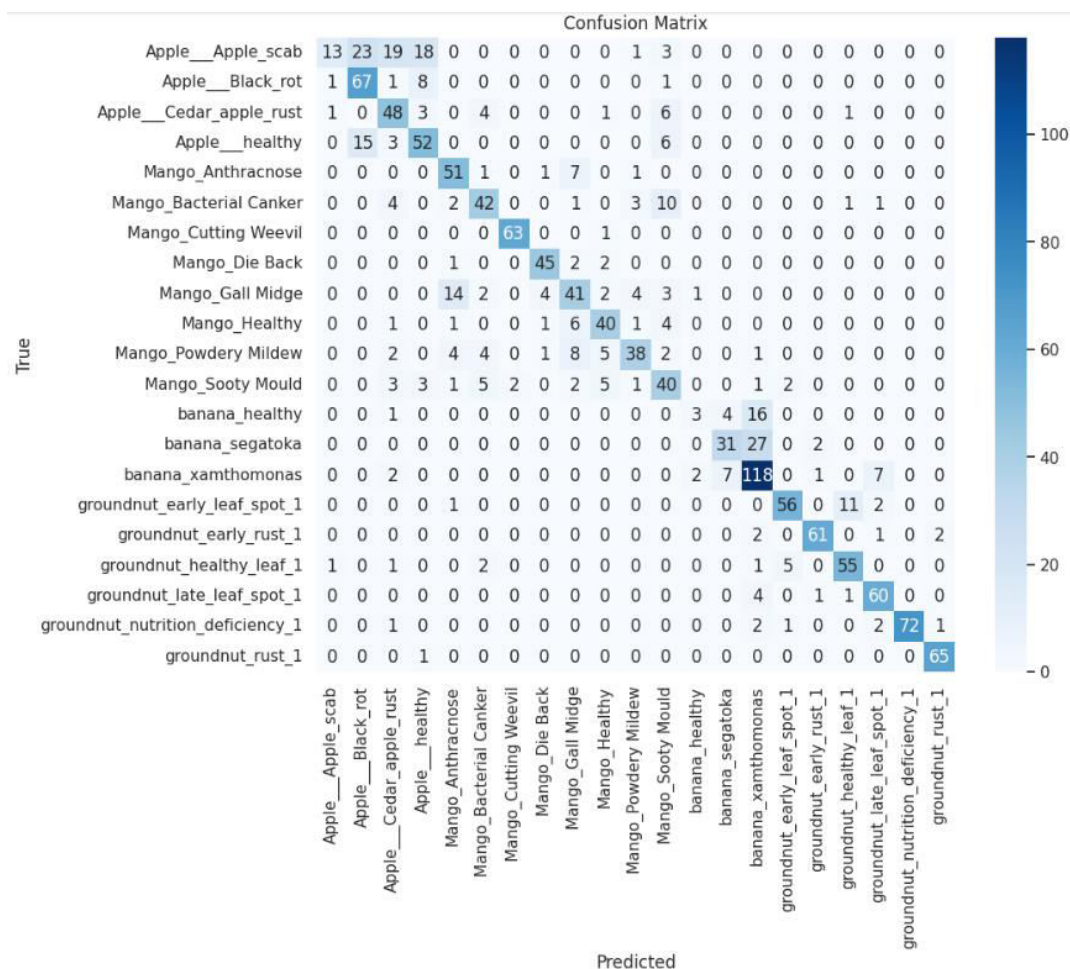
True Positive (TP): The proposed model predicts true, and the actual outcome is indeed true.

True Negative (TN): The proposed model predicts false, and the actual outcome is indeed false.

False Positive (FP): The proposed model predicts true, but the actual outcome is false.

False Negative (FN): The proposed model predicts false, but the actual outcome is true.

This matrix serves as a comprehensive tool to evaluate the efficiency and performance of the proposed model in distinguishing between true and false predictions.



(a)

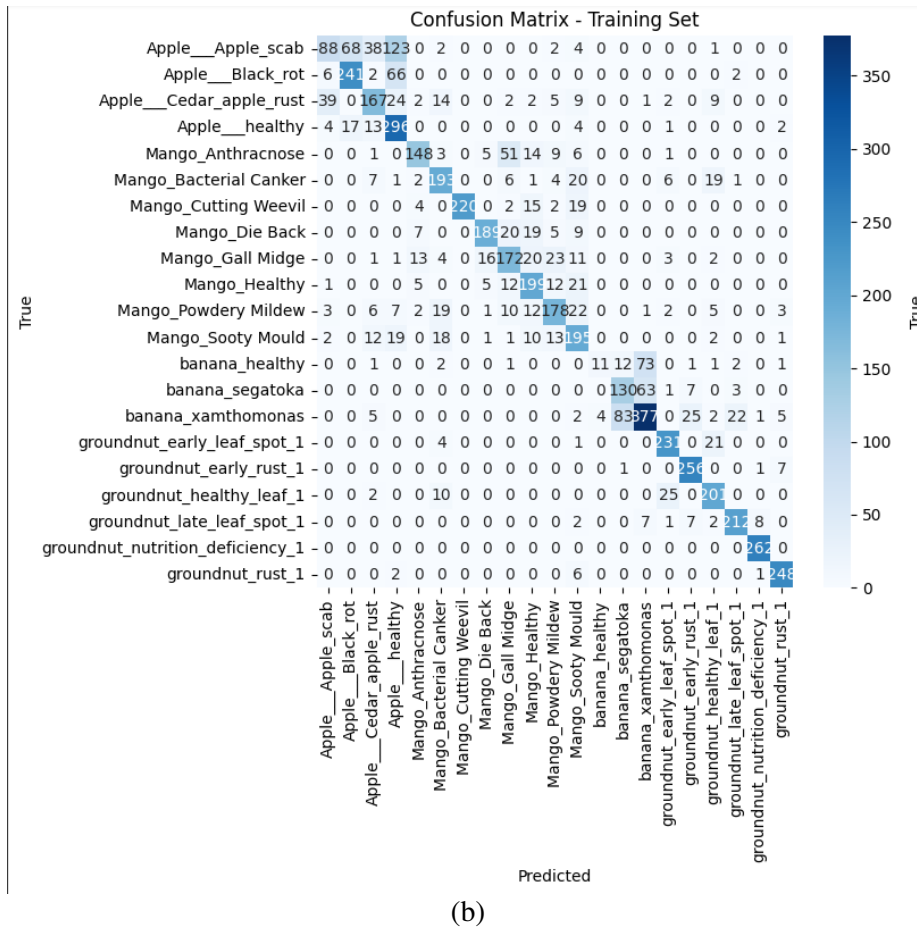


Figure 5: Output of confusion matrix (a) Test and (b) Training dataset

In examining the misclassification between groups, the study employs the confusion matrix as an assessment metric. Each row in the matrix represents an example of the expected class, while each column represents an example of the original class. The confusion matrix visually depicts the number of correct and incorrect predictions made by the classification model in comparison to the actual output. The diagonal elements indicate correctly classified classes, while the off-diagonal elements represent misclassified classes, as illustrated in Figure 5. After calculating the confusion matrix, the model achieved an accuracy of 96.5% on the training set and 95.5% on the testing set. This accuracy is determined by summing the diagonal elements and dividing the result by the total number of entries in the matrix. To prove the efficiency of the proposed FCL-LSTM model, an experiment is conducted using CNN and ordinary LSTM models on the collected dataset and the achieved results are presented in Figures 6 and 7.

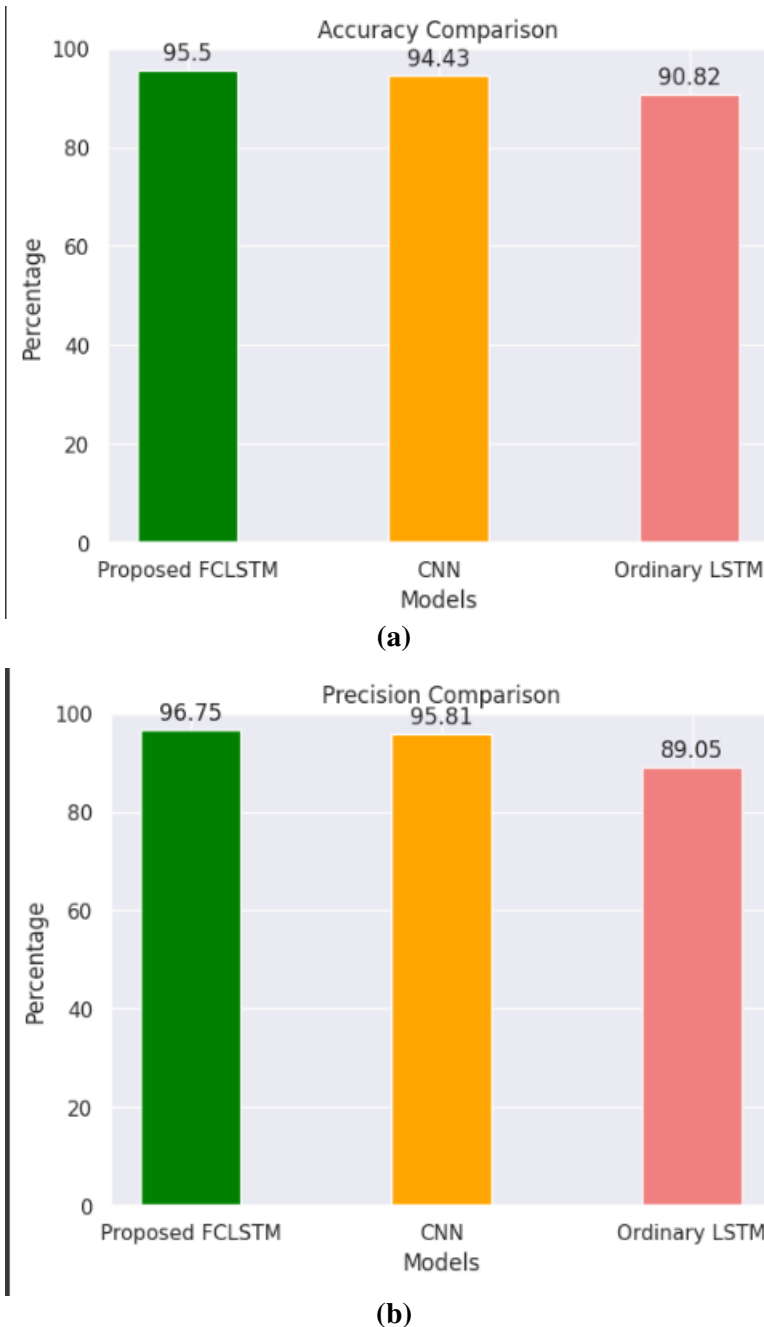


Figure 6: Performance Evaluation of (a) Accuracy and (b) Precision

Figure 6 provides a summary of the performance of the proposed models in detecting plant leaf diseases on the test images used. The evaluation includes an analysis of accuracy and precision for the plant leaf disease classification based on the LSTM-FCL model, comparing it to conventional CNN and ordinary LSTM approaches. The proposed methodology achieves an accuracy exceeding 95.5%, outperforming the CNN models (94.43%) and the ordinary LSTM approach (90.82%). The precision of the proposed LSTM-FCL network model in classifying plant leaf diseases is notably high at 96.75%. This suggests that the proposed method for plant leaf disease classification yields superior results compared to existing research approaches.

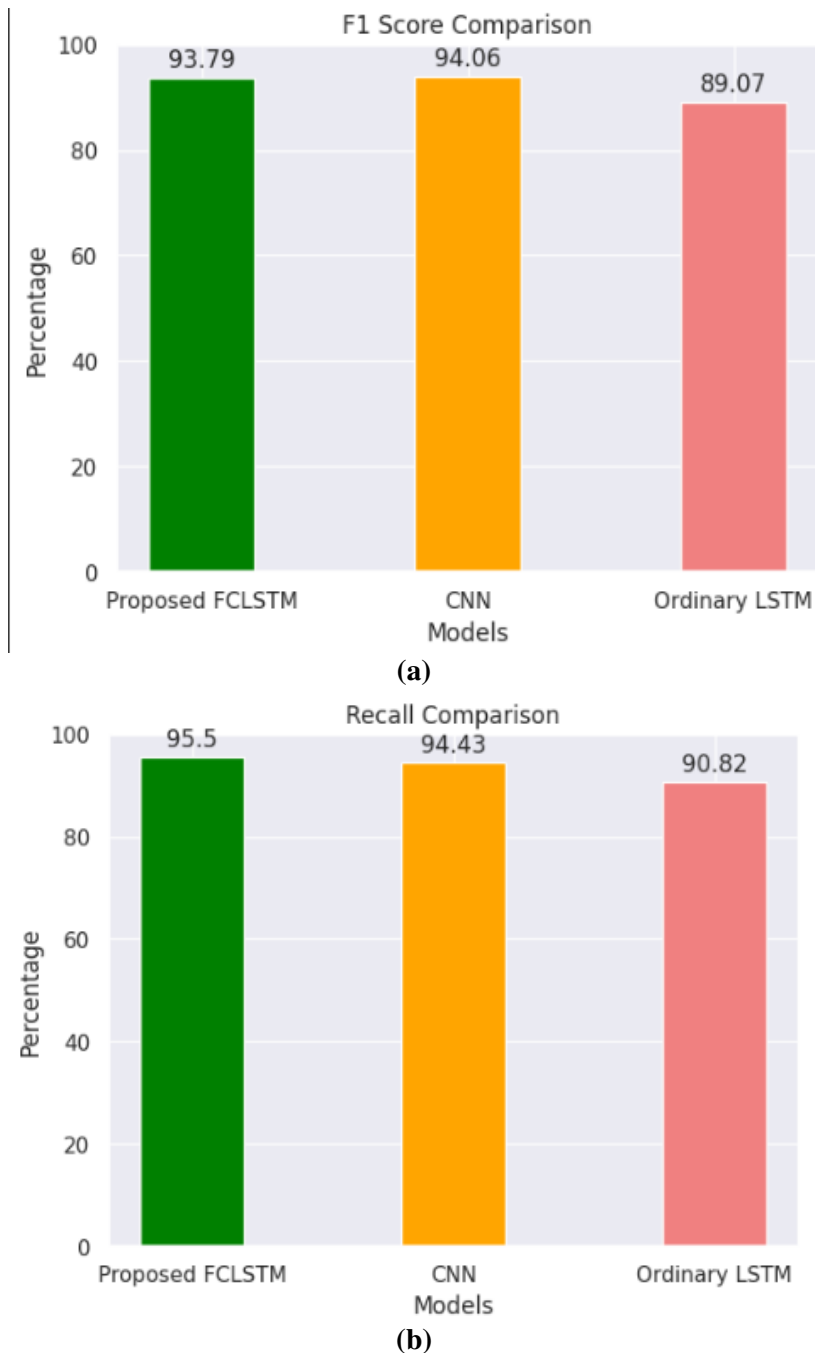
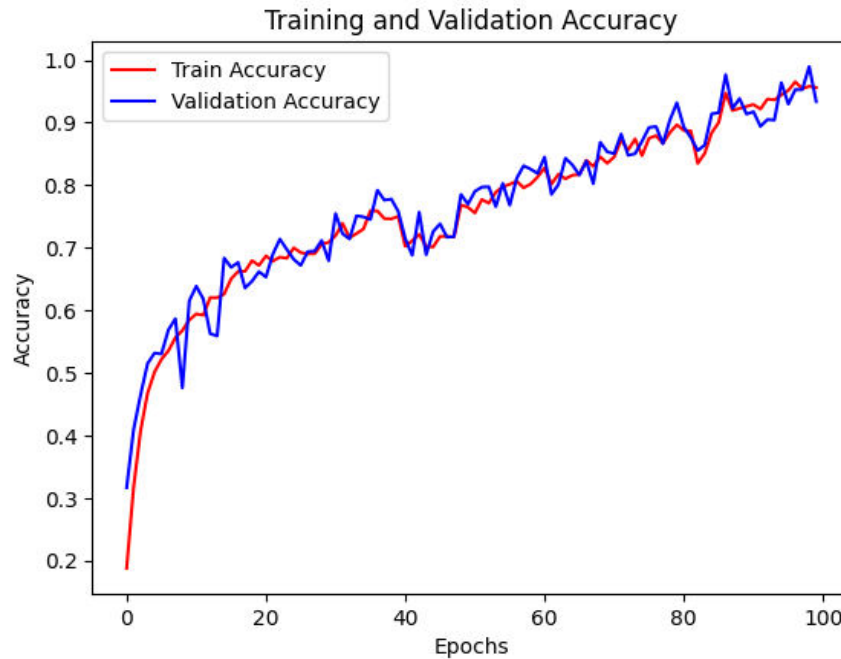


Figure 7: Performance Evaluation of (a) F1-score and (b) Recall

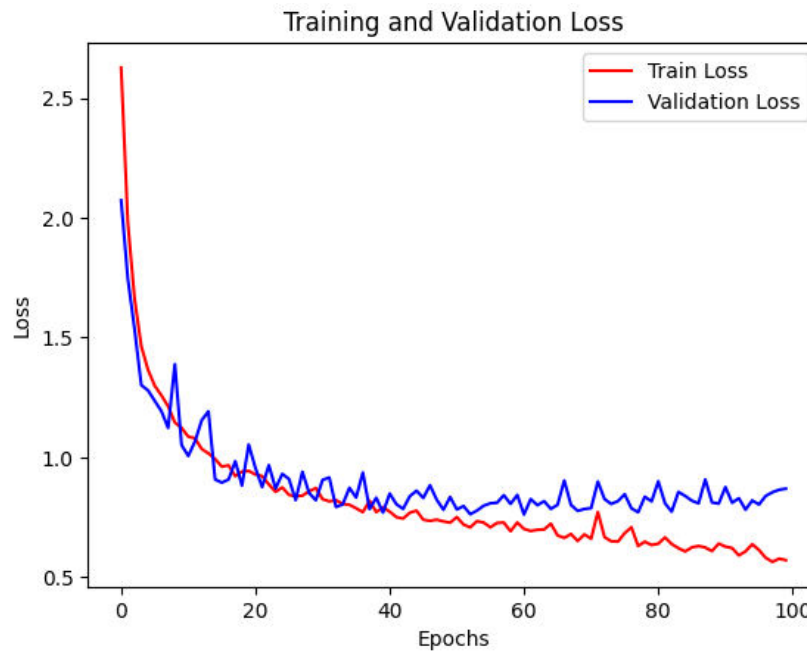
Figure 7 illustrates the F1-score and recall analysis comparing the proposed method with existing CNN and Ordinary LSTM approaches. The F1-score and recall values of the proposed method are above 92%, while both CNN and Ordinary LSTM exhibit lower F1-score and recall values in comparison. This discrepancy can be attributed to the superior utilization of the fully connected function and distribution function in the proposed research methodology for plant leaf disease classification. Table 2 provides a comprehensive analysis of the results, showcasing the performance of the proposed method against existing approaches across various measures [31-32].

Table 2: Result Analysis of Proposed Methods and Existing approach in terms of Different Measures

Methods	Accuracy	Precision	Recall	F1-Score
Ordinary LSTM	90.82	89.05	89.07	90.82
CNN	94.43	95.81	94.06	94.43
Proposed LSTM-FCL	95.5	96.75	93.79	95.5



(a)



(b)

Figure 8: Performance Evaluation of (a) Loss rate and (b) Classifier accuracy

The performance analysis in terms of accuracy and loss is shown in Fig. 8. Based on the 75/25 ratio, both training and test sets are split. The image size is 224 x 224 pixels larger. The training and testing performances in terms of accuracy and loss are shown in Fig. 8(a) and (b). here, 14 epochs were selected for this experiment. Fig. 8(a) shows 14 epochs with 100% accuracy, with accuracy levels varying between 0.7% and 0.9% of training accuracy and testing accuracy between 0.53% and 0.9%. According to Figure 8(b), the training loss varies between 2.5% and 0.5. Likewise, the validation loss varies between 2.3% and 1.2%. The proposed LSTM-FCL networks require higher training precision and testing accuracy as well as training and testing losses in terms of plant leaf disease classification.

5. CONCLUSION

In this paper, fully connected layer-based classifier with long-short-term memory networks (LSTM-FCL) was used to classify leaf diseases in plants. The proposed method is a classification method that includes feature extraction, feature selection and classification after the preprocessing stage. First, a preprocessing step to improve the visual quality of the input images. The SDSM-FCM clustering method is used to segment the different parts and normal parts. Thanks to the features selected in the study using the hybrid Osprey optimization algorithm with the Whale optimization algorithm, there is no data loss in disease diagnosis. The performance of the proposed LSTM-FCL classification method is compared with a convolutional neural network (CNN) and an ordinary LSTM based on measurements of parameters such as classification accuracy, precision, recall and F-measure. The LSTM-FCL model for classifying leaf diseases of plants is implemented in Python software. From the first experiment, the first LSTM-FCL algorithm shows the classification accuracy, proving that the first one is effective. From the results of the LSTM-FCL algorithm, the accuracy is 95.5%. This system is a robust system whose results have a high accuracy rate and a low error rate. In future research, we will focus on these shortcomings and work to improve accuracy and classification algorithms.

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