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A Cloud-Based Platform for Leaf Disease Segmentation and Classification using Hybrid Deep Learning Model

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Abstract: This paper presents a cloud-based hybrid deep learning method for classifying leaf diseases. At first, sensors aid in detecting soil factors such as moisture content, pH level, air temperature, and humidity. The hybrid Recurrent Layer based Deep Convolutional Neural Network (RLDCNN) approach consists of five distinct stages: preprocessing, segmentation, handcrafted feature extraction, feature selection, and classification. The preprocessing of image involves removal of noise using Averaged Double Plateau Histogram Equalisation (ADPHE). Afterwards, the specific part of the image that is impacted is divided into segments using an improved Wavelet transform. After the process of segmentation, the GLCM (Gray-Level Co-occurrence Matrix) is used to extract features. The hybrid Fire Hawk with Egret Swarm Optimisation (FHESO) algorithm is a very efficient approach for feature selection, significantly lowering the dimensionality of features. The detection of apple, banana mango and groundnut leaf disease are accomplished via the use of a Recurrent Layer based Deep Convolutional Neural Network (RLDCNN), which is trained using the Deer Hunting Algorithm (DHA) that has been created. The suggested concept is implemented inside a cloud-based collaborative framework to provide immediate assistance to farmers. The experimental findings exhibit favourable outcomes, demonstrating a high level of accuracy, precision, a low rate of loss, recall, and F-score. The RLDCNN network method outperforms previous parameters, obtaining an accuracy of 98.51% according to comparative research.

Keywords: Averaged Double Plateau Histogram Equalization (ADPHE), feature selection, classification, feature extraction, leaf disease, using Recurrent Layer based Deep Convolutional Neural network (RLDCNN) and cloud.

1. INTRODUCTION

The agricultural land mass serves a greater purpose than just being a source of food in the modern world. The Indian economy relies heavily on agricultural production. Hence, the identification of plant diseases has great significance in the agricultural industry [1]. Ensuring timely and accurate detection of plant diseases is essential [2]. However, the complexity of plant diseases, including those with no apparent symptoms, poses challenges for even seasoned pathologists [3]. The wide variety of plant species, fluctuations in disease progression due to climate changes, and rapid disease dissemination further complicate the accurate diagnosis of specific disease [4]. The impact of plant diseases extends beyond agriculture, affecting social, ecological, and economic aspects. Precision agriculture has emerged as a crucial field, with the identification of illnesses from plant leaf photographs being a vital component [5].

Foliar plant diseases, caused by various pathogens and environmental factors, pose a substantial risk to global agricultural output. One notable example is powdery mildew, a fungal infection affecting diverse plants like cucurbits, roses, peas, and others [6]. This disease manifests as a white or grey powdery growth on leaves, stems, and sometimes fruit, hindering photosynthesis and diminishing the plant's capacity to capture sunlight [7]. The economic impact of powdery mildew is significant due to the costly fungicides and cultural methods required for its management [8]. Climate change further complicates disease management, with rising temperatures facilitating disease transmission and expanding its geographical range [9]. An exhaustive approach to managing powdery mildew involves selecting resistant plant varieties, implementing cultural practices, utilizing biological control methods, and developing environmentally friendly strategies, ensuring global food security and promoting sustainable agriculture [10].

Many researchers have explored various technological and scientific approaches to efficiently manage foliar diseases. Genetic engineering, RNA interference technology, and omics technologies have played a crucial role in understanding plant-pathogen interactions [11]. The advancement of CRISPR-Cas9 genome editing techniques allows precise modifications in the genetic makeup of plants, enhancing resistance to diseases with improved accuracy and effectiveness [12]. This technological and scientific exploration sets the stage for the development of a model called Recurrent Layer based Deep Convolutional Neural Network (RLDCNN) with Deer Hunting Algorithm (DHA) for detecting various plant leaf diseases [13]. This model employs a hybrid approach, including noise reduction, wavelet transform, and optimization techniques for leaf disease detection and categorization. Implemented in a cloud-based collaborative framework, this model ensures real-time accessibility for farmers [14-15]. The efficacy of the RLDCNN approach has been verified on benchmark datasets, showcasing its potential for revolutionizing plant disease detection and management.

The subsequent sections of the paper are organised in the following manner: Section 2 presents a comprehensive analysis of the current research environment concerning plant diseases. It emphasises the existing challenges and identifies areas where research is lacking. Section 3 provides an overview of the planned plant disease system, while Section 4 includes the findings and comments focused on improving performance metrics. Section 5 provides a summary of the system and its main discoveries, thereby concluding the article.

2. LITERATURE REVIEW

The identification and categorization of leaf plant diseases have presented enduring difficulties. Despite extensive research endeavours in this domain, several studies have failed to provide significant outcomes. The previous research work pertaining to the study are given below.

Ramesh *et al.* [16] concentrated on identifying and categorising diseases in rice leaves. They achieved this by using a deep neural network that was fine-tuned using the Jaya method. The researchers obtained photos straight from agricultural fields and used preprocessing methods like RGB to HSV conversion, binary image creation, and clustering to segregate diseases. Their deep neural network successfully performed illness classification by using the Jaya optimisation algorithm (DNN_JOA).

In their study, Gautam *et al.* [17] used an ensemble stacked deep learning model to effectively detect and classify diseases affecting mango leaves. The proposed approach entails the process of dividing the images into several sections to isolate the specific region of focus. This secluded region is then fed into a series of deep neural networks. The results obtained from the deep neural networks are combined with a machine learning model to accurately detect leaf illness. This model is used for the diagnosis and classification of several mango leaf diseases, such as Powdery mildew and Anthracnose. The goal involves integrating deep learning models with machine learning techniques to accurately detect and classify illnesses that affect mango leaves.

Hosny *et al.* [18] presented a succinct architecture for a deep convolutional neural network (CNN) that can effectively extract latent feature representations at a sophisticated level. The profound characteristics are then combined with conventional manually designed local binary pattern (LBP) characteristics to capture the subtle texture aspects in plant leaf pictures. The proposed model is trained and evaluated using three publically accessible datasets, namely Apple Leaf, Tomato Leaf, and Grape Leaf. The suggested technique attains validation accuracies of 99%, 96.6%, and 98.5% on the three datasets, respectively. In addition, it achieves test accuracies of 98.8%, 96.5%, and 98.3% on the same datasets, respectively.

Suresh *et al.* [19] introduced a method that combines many machine learning techniques to quickly detect and categorise groundnut leaf disease. The GLD-HML technique relies on the Internet of Things (IoT). Begin by using the improved crow search (ICS) method to demarcate the affected region on the leaf. This stage is crucial for accurately classifying the condition. Furthermore, I suggest using a multi-objective sunflower optimisation (MSO) technique to get the most optimum feature selection from a set of multiple extracted features during the feature extraction stage.

Annrose *et al.* [20] did research on a hybrid deep learning model called HDL-AOA, which utilises the Archimedes optimisation approach, for the purpose of classifying bean illnesses. This research has five distinct categories of beans, with one category representing a state of good health, while the other four categories correlate to particular disorders: Bean halo blight, Pythium infections, Rhizoctonia root rot, and Anthracnose abnormalities. The diseases were acquired from the Soybean Data Set. The hybrid deep learning technique combines wavelet packet decomposition (WPD) with long short-term memory (LSTM). The Wavelet Packet Decomposition (WPD) first partitions the input images into four sub-series. Four Long Short-Term Memory (LSTM) networks were generated, with each network dedicated to a certain sub-series. The accuracy of identifying bean disease may be enhanced by using an Archimedes optimisation algorithm (AOA) in conjunction with numerous single LSTM networks.

Chug *et al.,* [21] have undertaken a study on the detection of plant diseases by using a blend of advanced machine learning methods applied to visual data. The proposed framework consists of 40 unique Hybrid Deep Learning models. These models are composed of a combination of eight different variants of pre-trained deep learning architecture, specifically EfficientNet (B0–B7), which act as feature extractors. Additionally, the framework utilises five machine learning techniques, namely k-Nearest Neighbours (kNN), AdaBoost, Random Forest (RF), Logistic Regression (LR), and Stochastic Gradient Boosting, which serve as classifiers. The current study used the Optuna framework to tune the hyperparameters of these classifiers. The study was carried out by gathering a real-time image dataset of tomato early blight disease from the Indian Agricultural Research Institute.

While the mentioned articles propose innovative solutions for plant disease detection and classification, it's important to acknowledge certain drawbacks in the approaches presented. One common limitation is the potential lack of generalizability across diverse agricultural settings and variations in disease types. The effectiveness of these models may heavily depend on the specific datasets used for training, and their performance might vary when applied to different crops or regions with unique disease manifestations. Additionally, the computational resources required for some deep learning models, especially those involving complex architectures or ensemble methods, could pose challenges for deployment in resource-constrained environments. Moreover, the reliance on extensive preprocessing steps and optimization algorithms might introduce additional complexity and computational overhead. Addressing these drawbacks will be crucial to ensure the practical applicability and scalability of the proposed solutions in real-world agricultural scenarios.

3. PROPOSED METHODOLOGY

A novel technique has been devised to examine and classify leaf spot situations in different plant leaves, with a specific emphasis on evaluating the extent of the problem. The impacted regions often have a circular morphology, while sporadic instances of unusual forms are sometimes reported. The described method is built around a dataset consisting of 8,731 images of leaves obtained from diverse areas. These images were acquired from both local sources and a cloud-based IoT platform. The system consists of six phases: image acquisition, pre-processing, image partitioning, feature extraction, feature selection, and classification. The dataset is sourced from the Kaggle database, which is a cloud storage platform. The first stage entails taking images using IoT-based devices, whereby sensors aid in ascertaining soil properties. Afterwards, the dataset is pre-processed using the Averaged Double Plateau Histogram Equalisation (ADPHE) approach to improve picture quality and remove noise. In the third phase, the Wavelet transform is used for segmentation. This is followed by the fourth phase, which focuses on feature extraction using Grey Level Co-occurrence Matrix (GLCM). Furthermore, leaf traits are used for the purpose of identifying crops. The fifth phase employs the hybrid Fire Hawk with Egret Swarm Optimisation (FHESO) algorithm as a feature selection approach. This algorithm guarantees the extraction of optimised and prominent features while reducing dimensionality. The last stage entails the process of classification, which aids in distinguishing between plants that are in good condition and those that are afflicted with disease. It is essential to highlight that the main goal of using this wide range of methods is to carry out several experiments and determine successful results.

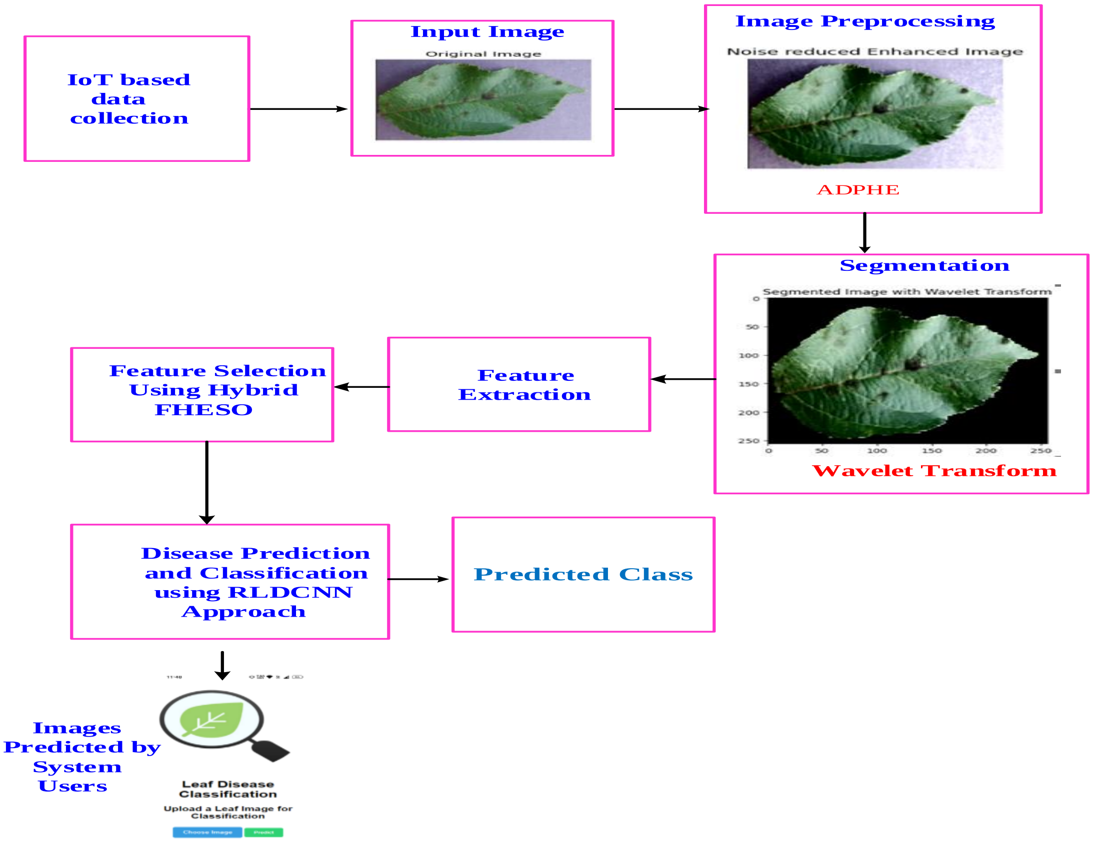


Figure 1. Block diagram for the proposed research methodology

The following descriptions explain the algorithms that are used,

3.1 Internet of Things (IoT) in Smart Agricultural Monitoring System

In the context, the initial stage involves the utilization of sensors to assess the specific environmental conditions surrounding banana, apple, mango, and groundnut plants. The sensors provide crucial data on the moisture content of the soil, its pH level, as well as air temperature and humidity levels, tailored to the unique requirements of each plant species. This data becomes particularly pertinent for banana plants, apple trees, mango trees, and groundnut plants, aiding in the determination of optimal conditions for growth. By understanding the specific environmental factors affecting each type of plant, the system can effectively identify and diagnose potential diseases in banana leaves, apple leaves, mango leaves, and groundnut leaves. This holistic approach allows for informed decision-making to mitigate the impact of diseases and optimize the health and productivity of each plant variety.

3.2 Preprocessing using Double Plateau Histogram Equalization

The supplied image is pre-processed in this stage. First, the input image is cropped, and then the Double Plateau Histogram Equalization (DPHE) technique is used to increase the image contrast level. An image with a higher contrast level contains more details about the texture of the color, shape, etc. However, adding noise to the input images during improvement is possible [22]. This study approach sets the limit based on an average estimate of the intensity of the images pixels to address that issue. ADPHE (Averaged Double Plateau Histogram Equalization) is the name specified to the suggested research approach. To boost the enhancement quality, the suggested ADPHE has been applied independently to the foreground and background regions. To reduce the saturation impact and control the rate of amplification in both regions, two plateau thresholds are used. The lower threshold is designed to avoid merging while maintaining the details with less pixels, while the higher threshold is utilised to prevent over-enhancement. Equations (1) and (2) provide $L_P(x)$ and $U_P(x)$ display the probability density function (PDF) computed by ADPHE in the background and foreground, respectively. LU_T, LL_T are the image's upper and lower thresholds for the background area and UU_T, UL_T as well as foreground portion of the image's upper and lower thresholds.

$$L_P(x) = \begin{Bmatrix} LU_T,\ if\ L_P(x) > LU_T \\ L_P(x),\ if\ \ LL_T < L_P(x) \leq LU_T \\ LL_T,\ if\ 0 \leq L_P(x) \leq LL_T \end{Bmatrix} \tag{1}$$

$$U_P(x) = \begin{Bmatrix} UU_T,\ if\ U_P(x) > UU_T \\ U_P(x),\ if\ \ UL_T < U_P(x) \leq UU_T \\ UL_T,\ if\ 0 \leq U_P(x) \leq UL_T \end{Bmatrix} \tag{2}$$

The values of LL_T, LU_T, UL_T and UU_T are chosen from 0 to 0.0001, 0.0001 to mean L_P, L_P mean to U_P mean, and U_P mean to 1 correspondingly. Here, a shared exponentiation parameter (μ) that affects both the foreground and background is added. Maintaining homogeneity between the two zones is the major goal of utilizing this parameter. Background image's weighted function is,

$$Lw_{pd}(n) = MaxF_0(L_p) * \left(\frac{L_p(n) - MinF_0(L_p)}{MaxF_0(L_p) - MinF_0(L_p)} \right)^{\mu} \tag{3}$$

For the foreground image, the weighted function is,

$$Uw_{pd}(n) = MaxF_0(U_p) * \left(\frac{U_p(n) - MinF_0(U_p)}{MaxF_0(U_p) - MinF_0(U_p)} \right)^{\mu+\eta} \tag{4}$$

The average adjustable parameters are μ and η for exponentiation. These parameters' ideal values are chosen from a range of 0 to 0.5 and 0.5 to 1, respectively.

3.3 Segmentation using Wavelet transform

Segmentation using the Wavelet Transform in plant leaf disease analysis involves a multi-step process to extract meaningful information from leaf images. The Wavelet Transform decomposes the original image into different frequency components, allowing for a detailed analysis of both low and high-frequency details [23]. By setting thresholds on the detail coefficients, high-frequency noise is effectively reduced, and the inverse Wavelet Transform reconstructs a denoised version of the leaf image. Subsequent segmentation techniques are then applied to distinguish healthy and diseased regions, resulting in precise localization of areas potentially affected by diseases. This segmented information serves as a foundation for feature extraction, wherein relevant characteristics are identified within the diseased regions. The user's text is empty. In order to precisely determine the segmentation threshold, the scale is first reduced to create an approximation value for the threshold. The wavelet-based image segmentation approach effectively mitigates the influence of noise. The fundamental principle of this strategy is to partition the histogram of the image by using the binary wavelet transform across many levels of wavelet coefficients. Equation (5) shows the primary components of the wavelet transform.

$$\psi(i) = \frac{1}{\sqrt{x}} \psi^* \left(\frac{i-y}{x} \right) \tag{5}$$

The primary goal of a wavelet is to replace an unlimited trigonometric function base with a limited wavelet foundation. During the wavelet transform procedure, a low-pass and high-pass filter are used to segregate two specific frequency bands from a picture. This approach enables the breakdown of a picture into the components found inside the gaps P_s, W_s^I, W_s^J, W_s^K [24].

$$f_{s-1}(m,n) = P_s + W_s^I + W_s^J + W_s^K$$
$$= 2^{-s} \begin{bmatrix} \sum_{x,y} L_s(x,y)\phi\left(2^{-s}m - x\right)\phi\left(2^{-s}n - y\right) + \\ \sum_{x,y} HL_s(x,y)\phi\left(2^{-s}m - x\right)\phi\left(2^{-s}n - y\right) + \\ \sum_{x,y} LH_s(x,y)\delta\left(2^{-s}m - x\right)\delta\left(2^{-s}n - y\right) + \\ \sum_{x,y} H_s(x,y)\omega\left(2^{-s}m - x\right)\omega\left(2^{-s}n - y\right) \end{bmatrix} \tag{6}$$

The decomposition degree is represented by the variable s. The image sizes are denoted by x and y. The orthonormal basis is represented by $\phi(\square)$, $\omega(\ )$ and $\delta(\ )$. The calculated predictions in the orthogonal domains are shown L_s, LH_s, HL_s, H_s. Here,

$$L_s(a,b) = \sum_{x,y} r(x-2a)\, r(y-2b) L_{s-1}(x,y) \tag{7}$$

$$LH_s(a,b) = \sum_{x,y} r(x-2a)\, q(y-2b) L_{s-1}(x,y) \tag{8}$$

$$HL_s(a,b) = \sum_{x,y} q(x-2a)\, r(y-2b) L_{s-1}(x,y) \tag{9}$$

$$H_s(a,b) = \sum_{x,y} q(x-2a)\, r(y-2b) L_{s-1}(x,y) \tag{10}$$

The location of the low-pass and high-pass filters is unknown $r(\bullet)$ and $q(\bullet)$. Furthermore, the term L_s refers to the portion of the frequency spectrum that is characterised by low frequencies and is specifically intended for the automated calculation of a certain value.

3.4 Handcrafted feature extraction

During this stage, the segmented plant leaf disease is utilized to extract distinctive characteristics or features. These features often encompass various aspects that are pertinent to disease identification and classification. The process involves analyzing color histograms to detect anomalies or discolorations, evaluating texture patterns to identify irregularities associated with diseases, extracting shape descriptors to capture specific disease-related shapes, measuring the size and symmetry of affected areas, detecting edges to identify boundaries altered by diseases, utilizing statistical metrics to quantify pixel value distributions, and assessing the spatial distribution of lesions on the leaf surface. Here using Gray-Level Co-occurrence Matrix (GLCM) approach, which is one of the most considerable characteristics of an image texture descriptors from the noise plant leaf images. This can be attained by looking at the dimensionality of the gray levels in the area. The attributes of each pixel value as well as those of its neighborhood are included in the texture feature. The gray-level co-occurrence matrix seems to be a popular statistical technique for feature extraction. In GLCM, a matrix shows how a pair of pixels' (x,y) values change in accordance to an image's spatial connection. These pixels together make up a feature vector that indicates whether a pixel belongs to color or shape [25]. Angle $(\cdot)$ and displacement (d) between x and y establish the spatial connection. The entire number of gray levels in an image is represented by the width and height of the GLCM matrix. For each plant leaf disease, a few characteristics are recovered after constructing a gray-level cooccurrence matrix.

3.5 Feature selection using hybrid Fire Hawk with Egret Swarm Optimization

In the context of plant leaf disease diagnosis, the hybrid Fire Hawk with Egret Swarm Optimisation (FHESO) feature selection procedure is very beneficial. FHESO combines the Fire Hawk algorithm with the Egret Swarm Optimisation method to find and choose the most relevant characteristics for constructing effective machine learning models for disease categorization. Regarding plant leaf diseases, these features may include a range of attributes such as colour histograms, texture patterns, shape descriptors, and statistical measurements obtained from segmented leaf pictures. The Fire Hawk's exploration component effectively traverses the extensive range of potential solutions, prioritising characteristics that accurately capture subtle disease symptoms. Meanwhile, the Egret Swarm Optimization's collaborative search improves the selection of these characteristics by imitating synchronised foraging patterns, guaranteeing a comprehensive depiction of disease-related attributes. The combined strategy aims to achieve a harmonious blend of exploration and exploitation, resulting in a refined subset of features that include the crucial discriminating information required for precise and dependable detection of plant leaf diseases.

The FHO metaheuristic algorithm simulates the foraging behaviour of fire hawks, considering the acts of sparking and spreading flames, as well as catching prey [26]. At first, a group of alternative solutions is determined by considering the position vectors of the fire hawks and prey. A stochastic initialization approach is used to ascertain the initial placements of these vectors inside the search space.

$$A = \begin{bmatrix} X_1 \\ X_2 \\ . \\ . \\ . \\ X_p \\ . \\ . \\ . \\ X_J \end{bmatrix} = \begin{bmatrix} X_1^1 X_1^2 \ldots X_1^q \ldots X_1^e \\ X_2^1 X_2^2 \ldots X_2^Q \ldots X_2^e \\ \ldots\ldots \\ \ldots\ldots \\ \ldots\ldots \\ X_1^1 X_p^2 \ldots X_p^q \ldots X_p^e \\ \ldots\ldots \\ \ldots\ldots \\ \ldots\ldots \\ X_I^1 X_I^2 \ldots X_I^q \ldots X_N^e \end{bmatrix} \tag{11}$$

$$a_p^q(0) = a_{p.\min}^q + rand.(a_{p.\max}^q - a_{p.\min}^q), \begin{cases} p = 1, 2, \ldots, I \\ q = 1, 2, \ldots., e \end{cases} \tag{12}$$

Let A_p be the pth solution candidate in the search space, e represent the dimension of the problem, J be the total number of solution candidates, a_p^q denote the qth decision variable of the pth solution candidate, $a_p^q(0)$ represent the initial position of the solution candidates, $a_{p.\min}^q$ and $a_{p.\max}^q$ be the minimum and maximum bounds of the qth decision variable for the pth solution candidate. Furthermore, the variable "rand" represents a random integer that is evenly spread between 0 and 1.

The objective function evaluation is used to determine the positions of the Fire Hawks in the search space, considering the provided optimisation problem. Fire Hawks represent solution candidates that possess greater objective function values, while the other solution candidates are regarded as prey. The selected Fire Hawks are used to spread fire around the hunting area to expedite the hunting procedure.

$$RS = \begin{bmatrix} RS_1 \\ RS_2 \\ . \\ . \\ . \\ PR_m \\ . \\ . \\ . \\ RS_i \end{bmatrix}, m = 1, 2, ..., i \tag{13}$$

$$HG = \begin{bmatrix} HG_1 \\ HG_2 \\ . \\ . \\ . \\ HG_1 \\ . \\ . \\ . \\ HG_q \end{bmatrix}, m = 1, 2, ..., i \tag{14}$$

The kth prey is located inside the search space RS_m, relative to the total number of j preys. Similarly, HG_1 the 1st fire hawk is positioned within the search space, taking into account the total number of i fire hawks.

The programme calculates the total distance between the Fire Hawks and their prey in the next step of the procedure. While the other prey is considered to be within the other birds' domain, the Fire Hawk with the highest objective function value selects the nearest prey.

$$C_m^1 = \sqrt{\left(a_2 - a_1\right)^2 + \left(b_2 - b_1\right)^2}, \begin{cases} k = 1, 2, ..., q \\ m = 1, 2, ..., p \end{cases} \tag{15}$$

C_m^1 the total distance between the kth fire hawk and the mth prey is represented by the variable "d". The variable "k" represents the whole number of preys in the exploration location, while "q" represents the total number of fire hawks in the search space. The coordinates of the fire hawks and prey in the search space are represented by $\left(a_1, b_1\right)$ variables "x" and "y".

In order to light the specified area, the Fire Hawks grab lit branches from the main fire during the algorithm's second step. A few birds, however, are quite excited to use the blazing branches that belong to other Fire Hawks. Accordingly, these two behaviors might be used as location updating strategies in the FHO main search loop, as shown by the following equation:

$$\mathrm{HG}_1^{\mathrm{new}} = HG_1 + \left(s_1 \times \mathrm{GB} - s_2 \times HG_{\mathrm{Near}}\right), k = 1, 2, \ldots, p \tag{16}$$

The location vector of the lth Fire Hawk HG_1 is represented as $\mathrm{HG}_1^{\mathrm{new}}$. The primary ignition GB represents the solution inside the search area. HG_{Near} is another Fire Hawk inside the search area. The movements of Fire Hawks towards the main fire and the other Fire Hawks' territories s_1 and s_2 are determined by random numbers that follow a uniform distribution between 0 and 1.

If the update function's value is improved, the egret swarm optimization algorithm's new location is approved. The egrets have taken the place of the Fire Hawk that was in its prior location. High energy consumption in exchange for perhaps higher rewards is a characteristic of Great Egret with Aggressive Strategy. ESO algorithm defines methods to better simulate egrets' learning habits. $D_{a,x}$ and $D_{b,x}$. $D_{a,x}$ indicate the direction change based on the same group of egrets' ideal position. $D_{b,x}$ signifies a direction shift accomplished in accordance with all egrets' ideal positions [29].

$$D_{b,x} = \frac{P_x^{best} - P_x}{\left|P_x^{best} - P_x\right|} * \frac{f_x^{best} - f_x}{\left|f_x^{best} - f_x\right|} + D_x^{best} \tag{17}$$

$$D_{g,x} = \frac{P_g^{best} - P_x}{\left|P_g^{best} - P_x\right|} * \frac{f_g^{best} - f_x}{\left|f_g^{best} - f_x\right|} + D_g^{best} \tag{18}$$

Where P_g^{best} and P_x^{best} stand for the respective global historical ideal position and individual historical optimal position. The goal function is f. D_x^{best} indicates the historical change in the ideal direction depending on the position of the same group of egrets. D_g^{best} indicates the historical change in the ideal direction based on the ideal location of all egrets. The position update method may include these operations by using the following equation:

$$\mathrm{RS}_j^{\mathrm{new}} = \mathrm{RS}_j + \left(s_3 \times \mathrm{HG}_1 - s_4 \times R\mathrm{S}_1\right), \begin{cases} k = 1, 2, \ldots, q. \\ j = 1, 2, \ldots, s. \end{cases} \tag{19}$$

$$\mathrm{RS}_j^{\mathrm{new}} = \mathrm{RS}_j + \left(s_5 \times \mathrm{HG}_{\mathrm{Alter}} - s_6 \times R\mathrm{S}\right), \begin{cases} m = 1, 2, \ldots, j. \\ j = 1, 2, \ldots, s. \end{cases} \tag{20}$$

The location $\mathrm{RS}_j^{\mathrm{new}}$ vector of the jth prey RS_j, enclosed by the lth fire hawk, is represented as HG_1. $\mathrm{HG}_{\mathrm{Alter}}$ Denotes an additional fire hawk inside the search area. $R\mathrm{S}$ Indicates a secure location outside the jurisdiction of the lth Fire Hawk. The movements of preys towards the other Fire Hawks and the safe spot beyond the domain s_5 and s_6 are determined by uniformly distributed random values between 0 and 1.

3.6 Classification using Recurrent Layer based Deep Convolutional Neural network

The suggested study technique presents a Recurrent Layer based Deep Convolutional Neural Network (RLDCNN) for identifying and categorizing different plant leaf diseases. Deep learning neural networks, characterized by their ability to deeply learn intricate patterns from inputs, are chosen for their superior outcomes in complex tasks such as disease identification. However, a common challenge in deep learning is the generalization error problem, leading to overfitting. To address these issues, the research methodology incorporates a recurrent layer. This layer dynamically adjusts the weight and bias values during the recurrent layer based on the network's performance, thereby mitigating overfitting concerns. The classifier, empowered by RLDCNN, is designed to predict whether an input image depicts a normal plant leaf or a leaf affected by disease. Deep learning algorithms, particularly Convolutional Neural Networks (CNNs), excel in autonomously extracting patterns and relevant features from raw data. In the context of plant leaf disease classification, the application of CNNs proves effective, leveraging their proficiency in image processing to identify and categorize various plant leaf diseases [27]. The utilization of RLDCNN in this research methodology represents a promising advancement in leveraging deep learning techniques for precise and efficient plant leaf disease diagnosis.

Input layer

A collection of input images is stored in the input layer as an array of integers that only contains the pixels of the image. Images are transformed into a matrix array using calculations depending on the image's size and pixel count.

Convolution layer

The convolution layer is responsible for deriving identifiable characteristics from the input picture. The input matrix is converted into smaller sets 3×3 of reduced matrices, often referred to as filters. In the convolution layer, the filters are applied to each part of the input matrix, resulting in a tensor of feature maps. The primary purpose of convoluting the input matrix is to decrease the number of weights that need to be learnt. This includes both the collection of high-level features and the collection of low-level information, such as colors, orientation, edges, and padding. The number of convolution layers may be varied depending on the desired features to be returned [28]. The bottom layer is used for extracting basic qualities; however, the uppermost layer is employed for extracting a diverse range of characteristics. As the number of layers increases, more functionality may be removed. The input picture undergoes convolution when 2D digital filters are applied. The value of each pixel is modified as a result of this process, which depends on neighboring pixels. Consequently, the picture undergoes a transition from a representation based on individual pixels to a map that highlights certain features. Every point on the generated feature map may be evaluated as:

$$N_{Px} = \sum_{k\in S} \alpha_k * \beta_k \tag{21}$$

N_{Px} represents the novel value of a preset pixel and α_k while the old adjacent pixels are multiplied by the filter components β_k .

Pooling layer

The grouping layer reduces the size of the images. To create a value, the adjacent image pixels are concatenated into a deterministic component. Retaining the highest or typical pixel value. The suggested framework calls for the most possible pooling.

Recurrent neural network (RNN) layer

In the proposed methodology, the Recurrent Neural Network (RNN) layer is tightly integrated with the input data dimensions, forming a close connection between the class dimensions and the input data. During the training phase of the RNN layer, adjustments are made to the bias settings, which play a crucial role in influencing the learning process. The modification of bias settings is specific to the current learning process, contributing to the adaptability of the network to the given data. Simultaneously, outputs from the clustering layer are gathered with various weights, reflecting the importance assigned to different features or patterns. These weighted outputs are then fed into the RNN layer, allowing the network to capture sequential dependencies and temporal information effectively. The complex interaction among bias adjustments, weighted outputs, and the RNN layer improves the network's capacity to acquire and identify significant patterns from the input data, which is crucial in tasks like plant leaf disease detection and classification.

A. **Forget layer:** The forget gate eliminates data that is no longer relevant to the state of the cell. Within this layer, two inputs undergo iteration, weight matrices are multiplied, and ultimately a bias is included. The forgetting process may be described using Equation (23) below:

$$F_l = \varpi\left(\varepsilon_f\left[o_{h-1}, \omega_i\right] + b_f\right) \tag{22}$$

In the given context, F_l the symbol represents the output of the forget gate, while ε_f and b_f reflect the weight and bias values for the input. The ϖ symbolises the sigmoid function, and o_{h-1} represents the output of the previous LSTM unit at time $h-1$.

B. **Input layer:** This layer utilises the sigmoid function to first guide the input and filter values, acting as a gateway to oblivion. Equation (24) represents the expression of the input layer.

$$I_l = \varpi\left(\varepsilon_i\left[o_{h-1}, \omega_i\right] + b_i\right) \tag{23}$$

Where, I_l defines the outcome of the input layer, ε_i and b_i indicates the weight and bias values of the input layer. The calculation for the tanh expression is given in equation (25),

$$T_l = \tan sig\left(\varepsilon_t\left[o_{h-1}, \omega_i\right] + b_t\right) \tag{24}$$

Here, Tl denotes the output layer using the hyperbolic tangent function (tanh), whereas ε_t and b_t the weight and bias values of the input layer are represented by the tan sig function.

C. **Output layer:** The block's input and memory are used to determine the output. The expression for the output layer is derived in equation (26),

$$A_l = \varpi\left(\varepsilon_a\left[o_{h-1}, \omega_i\right] + b_a\right) \tag{25}$$

Where, A_l denotes the output gate, ε_a and b_a indicates the weight and bias values of the output layer in equation (26). Thus, the RLDCNN predicts the plant leaf as healthy and disease leaf.

Classification layer

The most recent CNN scale is used to categorize the output of the RNN at various levels. The Soft-max activation function is used in this layer of the suggested architecture to ascertain the technique of categorization.

Soft-max function

A crucial element is thought to be the activation functions that CNNs use. The activation function serves the objective of introducing nonlinearity into the neuron's output. The suggested framework employs the soft-max function for decision-making. It is a straightforward and uncomplicated kind of activation. The numbers 0 and 1 define the boundaries of the output range. This tool is used for both multi-class and binary classification process.

$$\rho(G_i) = \frac{e^{G_i}}{\sum_{i=1}^{j} e^{G_i}} \tag{26}$$

The input to the classification layer is represented by the i , while the result is indexed by the $i = 1,.....,....j$. The following section examines the effectiveness of the suggested research approach. The proposed RLDCNN structural design, seen in Figure 2, elucidates the role of the recurrent neural network layer.

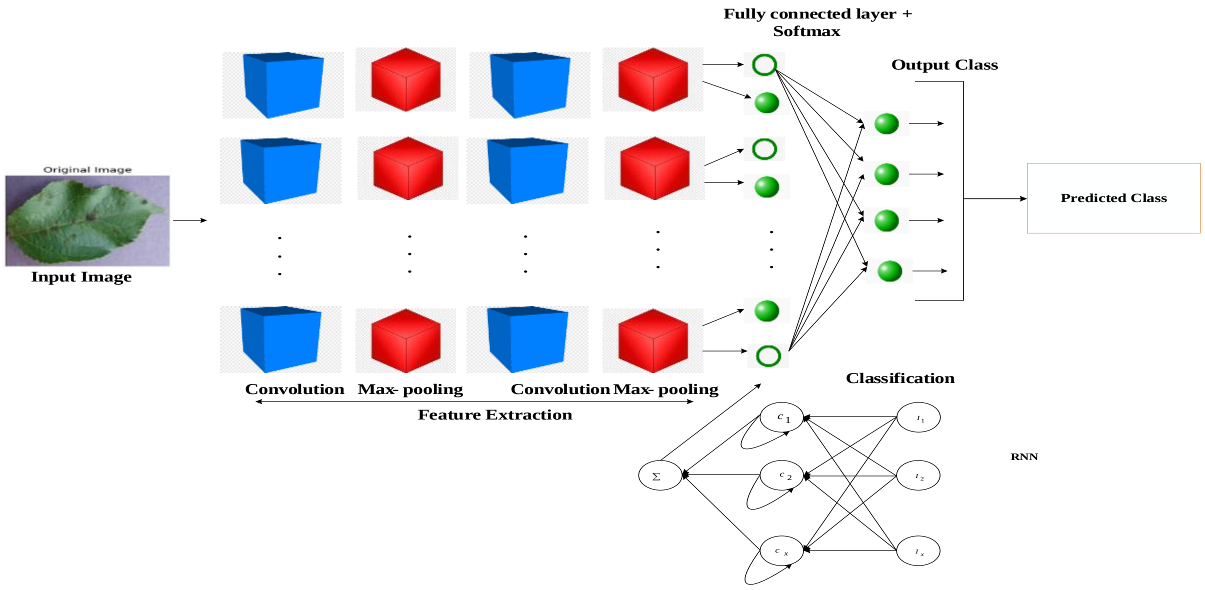


Fig.2. Architecture of RLDCNN classifier

The update weighting process of RLDCNN using the Deer hunting Algorithm

The process of update weighting an RLDCNN for plant leaf disease classification using the DHA algorithm [29] involves several key steps. First, a dataset comprising labeled images of healthy and diseased plant leaves is collected and preprocessed through resizing and augmentation. The RLDCNN architecture, tailored for leaf disease classification, is designed, incorporating convolutional layers for feature selection. The new position of the deer hunting is accepted if it improves the value of the objective function. The previous position of the coatis is replaced with the new position of the deer hunting. The deer hunting optimization algorithm saves the best solutions obtained so far over the course of iteration, and this information can be used to improve solutions in deer hunting. The safe position is then obtained using the deer hunting updating procedure, which is derived in equation (27).

$$S_{It+1} = S_L - d * w_{scope} * \left| E \times S_E - S_{It} \right| \tag{27}$$

Where,

$$d = 0.25 * \log\left(I + \frac{1}{I_{\max}} \right) * R \tag{28}$$

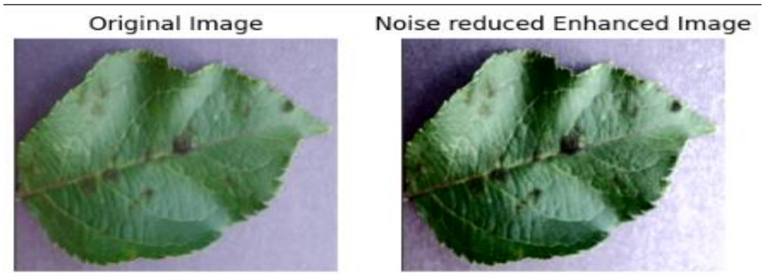
The ensuing position of hunters at any given moment is symbolized as S_L. The encircling conduct is represented by E. The random integer, derived from wind velocity within the range of [0, 2], is designated as w_{scope}. The coefficient vectors are labeled as d. Within this algorithm, the hunters' positions are iteratively refreshed with the best solution at each repetition. The optimal solution is achieved when $|S_L| \geq 1$ is minimized. If $|S_L| < 1$ does not reach the minimized state, a random selection is made among the hunters.

4. RESULTS AND DISCUSSION

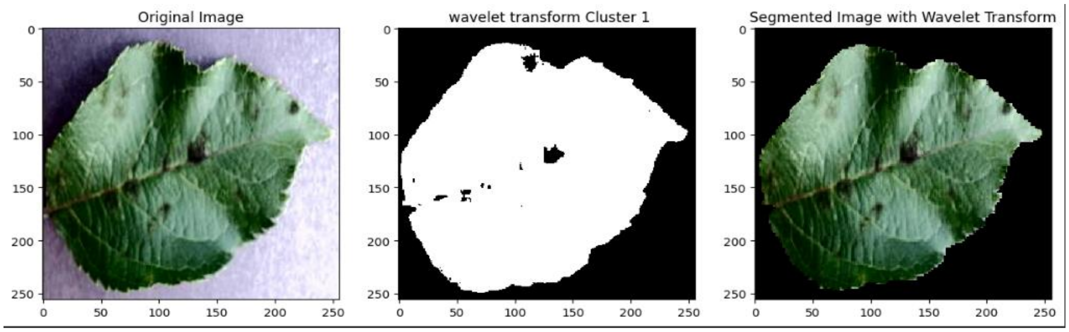
The performance of the RLDCNN approach in detecting plant leaf diseases is examined in this part. The evaluation is conducted using a Kaggle and UCI dataset consisting of the total images 8,731 is preprocessed and compressed into 6525 images, as shown in Table 1. The dataset has 21 distinct class labels. The study of various leaf disease categories in our dataset is shown in Table 1. The Apple dataset [30] comprises four diseases: apple scab, black rot, and cedar apple rust. Moreover, a sturdy class is provided for the purpose of classification. The mango dataset [31] has eight disease classes: anthracnose, bacterial canker, cutting weevil, die back, gall midge, powdery mildew, and scooty mould. Furthermore, a lesson that focuses on providing nourishment is also included. The banana dataset [32] consists of three clearly defined classes: Healthy, Segatoka, and Xamthomonas. The groundnut dataset [33] consists of six unique classes: Early leaf spot, Early rust, Healthy leaf, Late leaf spot, Nutrition shortage, and Groundnut rust. The recommended study approach is implemented using the PYTHON programming language on a Jupyter laptop including an Intel Core i5 CPU, 32 GB of RAM, and an NVIDIA AMD GPU with 6 GB of memory workspace.

Table 1. Details on Dataset

Classes	**Leaf Disease**	**No of Images**
Apple	Apple Scab	320
	Black Rot	320
	Cedar Apple Rust	320
	Apple Healthy	320
Banana	Healthy	155
	Segatoka	320
	Xamthomonas	320
Groundnut	Early leaf spot	320
	Early rust	320
	Healthy leaf	320
	Late leaf spot	320
	Nutrition deficiency	320
	Groundnut rust	320
Mango	Anthracnose	320
	Bacterial Canker	320
	Cutting Weevil	320
	Die Back	290
	Gall Midge	320
	Healthy	320
	Powdery Mildew	320
	Scooty Mould	320
Total class	21	



(a)



(b)

Fig.3. (a) Preprocessed image and (b) Segmented Image

The study of the hybrid RLDCNN model is shown in Figure 3:(a) depicts the original photographs of the sample and their pre-processed variants. Next, the segmented images are shown in Figure 3(b).

4.1 Performance Evaluation

According to the precision, recall, accuracy, and F-Measure metrics, the proposed hybrid RLDCNN for plant leaf disease classification is compared to the existing fully connected layer-based classifier with long-short-term memory networks (FCL-LSTM) and Allied Layered Deep Convolutional Neural Network (ALDCNN).

Accuracy

The Accuracy of the forecast is determined by calculating the average of all true instances. The calculation is performed using the designated equation:

$$Accuracy = \frac{True\,Positive + True\,Negative}{True\,Positive + True\,Negative + Fasle\,Positive + Fasle\,Negative} \tag{29}$$

Precision

Precision is the ratio of genuine positives to the total number of positive forecasts. The equation below represents the computation of Precision.

$$\Pr ecision = \frac{True\,Positive}{True\,Positive + Fasle\,Positive} \tag{30}$$

Recall

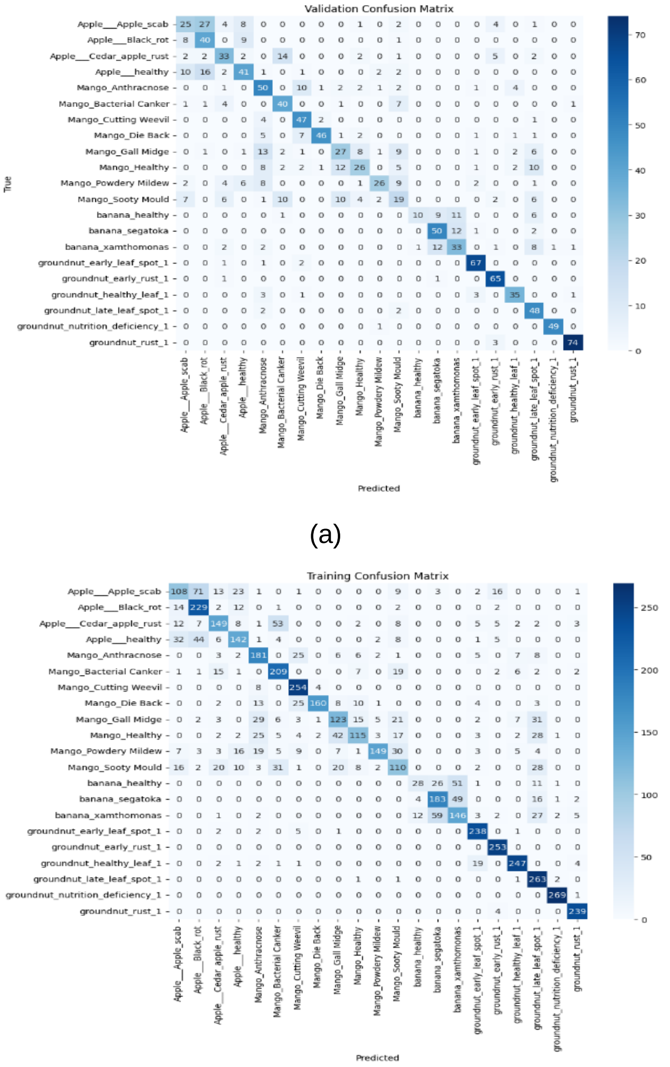
The Recall is a metric that quantifies the effectiveness of our approach in identifying True Positives. Consequently, Recall provides us with the number of apple, banana, mango and groundnut plants that we correctly detected as having leaf disease out of the total number of plants that really have the illness.

$$\Pr ecision = \frac{True\,Positive}{True\,Positive + Fasle\,Negative} \tag{31}$$

F1 Score

The F1 score succinctly summarises a model's prediction effectiveness and is determined by two often conflicting variables, accuracy and recall.

$$\text{F-Measure=}2 * \frac{\Pr ecision * \operatorname{Re} call}{\Pr ecision + \operatorname{Re} call} \tag{32}$$



Validation Confusion Matrix

	Apple___Apple_scab	Apple___Black_rot	Apple___Cedar_apple_rust	Apple___healthy	Mango_Anthracnose	Mango_Bacterial Canker	Mango_Cutting Weevil	Mango_Die Back	Mango_Gall Midge	Mango_Healthy	Mango_Powdery Mildew	Mango_Sooty Mould	banana_healthy	banana_segatoka	banana_xamthomonas	groundnut_early_leaf_spot_1	groundnut_early_rust_1	groundnut_healthy_leaf_1	groundnut_late_leaf_spot_1	groundnut_nutrition_deficiency_1	groundnut_rust_1
Apple___Apple_scab	25	27	4	8	0	0	0	0	0	1	0	2	0	0	0	0	4	0	1	0	0
Apple___Black_rot	8	40	0	9	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Apple___Cedar_apple_rust	2	2	33	2	0	14	0	0	0	2	0	1	0	0	0	0	5	0	2	0	0
Apple___healthy	10	16	2	41	1	0	1	0	0	0	2	2	0	0	0	0	0	0	0	0	0
Mango_Anthracnose	0	0	1	0	50	0	10	1	2	2	1	2	0	0	0	1	0	4	0	0	0
Mango_Bacterial Canker	1	1	4	0	0	40	0	0	1	0	0	7	0	0	0	0	0	0	0	0	1
Mango_Cutting Weevil	0	0	0	0	4	0	47	2	0	0	0	0	0	0	0	0	0	0	1	0	0
Mango_Die Back	0	0	0	0	5	0	7	46	1	2	0	0	0	0	0	1	0	1	1	0	0
Mango_Gall Midge	0	1	0	1	13	2	1	0	27	8	1	9	0	0	0	1	0	2	6	0	0
Mango_Healthy	0	0	0	0	8	2	2	1	12	26	0	5	0	0	0	1	0	2	10	0	0
Mango_Powdery Mildew	2	0	4	6	8	0	0	0	0	1	26	9	0	0	0	2	0	0	1	0	0
Mango_Sooty Mould	7	0	6	0	1	10	0	0	10	4	2	19	0	0	0	0	2	0	6	0	0
banana_healthy	0	0	0	0	0	1	0	0	0	0	0	0	10	9	11	0	0	0	6	0	0
banana_segatoka	0	0	0	0	0	0	0	0	0	0	0	0	0	50	12	1	0	0	2	0	0
banana_xamthomonas	0	0	2	0	2	0	0	0	0	0	0	0	1	12	33	0	1	0	8	1	1
groundnut_early_leaf_spot_1	0	0	1	0	1	0	2	0	0	0	0	0	0	0	0	67	0	0	0	0	0
groundnut_early_rust_1	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	65	0	0	0	0
groundnut_healthy_leaf_1	0	0	0	0	3	0	1	0	0	0	0	0	0	0	0	3	0	35	0	0	1
groundnut_late_leaf_spot_1	0	0	0	0	2	0	0	0	0	0	0	2	0	0	0	0	0	0	48	0	0
groundnut_nutrition_deficiency_1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	49	0
groundnut_rust_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	74

(a)

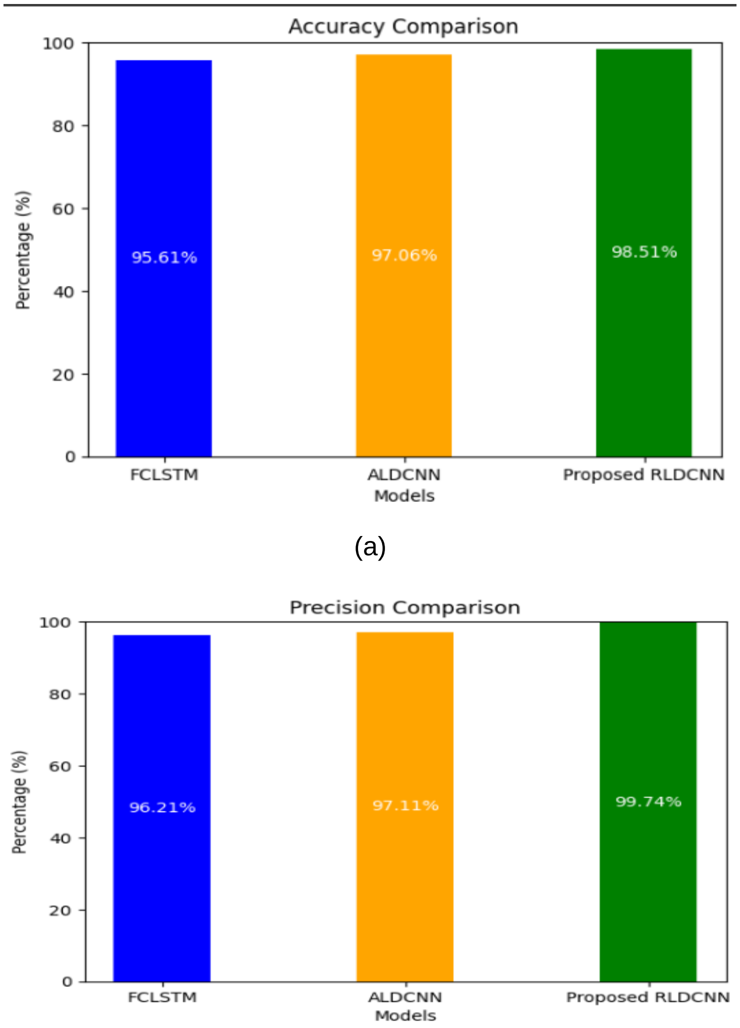
Training Confusion Matrix

	Apple___Apple_scab	Apple___Black_rot	Apple___Cedar_apple_rust	Apple___healthy	Mango_Anthracnose	Mango_Bacterial Canker	Mango_Cutting Weevil	Mango_Die Back	Mango_Gall Midge	Mango_Healthy	Mango_Powdery Mildew	Mango_Sooty Mould	banana_healthy	banana_segatoka	banana_xamthomonas	groundnut_early_leaf_spot_1	groundnut_early_rust_1	groundnut_healthy_leaf_1	groundnut_late_leaf_spot_1	groundnut_nutrition_deficiency_1	groundnut_rust_1
Apple___Apple_scab	108	71	13	23	1	0	1	0	0	0	0	9	0	3	0	2	16	0	0	0	1
Apple___Black_rot	14	229	2	12	0	1	0	0	0	0	0	2	0	0	0	0	2	0	0	0	0
Apple___Cedar_apple_rust	12	7	149	8	1	53	0	0	0	2	0	8	0	0	0	5	5	2	2	0	3
Apple___healthy	32	44	6	142	1	4	0	0	0	0	2	8	0	0	0	1	5	0	0	0	0
Mango_Anthracnose	0	0	3	2	181	0	25	0	6	6	2	1	0	0	0	5	0	7	8	0	0
Mango_Bacterial Canker	1	1	15	1	0	209	0	0	0	7	0	19	0	0	0	0	2	6	2	0	2
Mango_Cutting Weevil	0	0	0	0	8	0	254	4	0	0	0	0	0	0	0	0	0	0	0	0	0
Mango_Die Back	0	0	2	0	13	0	25	160	8	10	1	0	0	0	0	4	0	0	3	0	0
Mango_Gall Midge	0	2	3	0	29	6	3	1	123	15	5	21	0	0	0	2	0	7	31	0	0
Mango_Healthy	0	0	2	2	25	5	4	2	42	115	3	17	0	0	0	3	0	2	28	1	0
Mango_Powdery Mildew	7	3	3	16	19	5	9	0	7	1	149	30	0	0	0	3	0	5	4	0	0
Mango_Sooty Mould	16	2	20	10	3	31	1	0	20	8	2	110	0	0	0	2	0	0	28	0	0
banana_healthy	0	0	0	0	0	0	0	0	0	0	0	0	28	26	51	1	0	0	11	1	0
banana_segatoka	0	0	0	0	0	0	0	0	0	0	0	0	4	183	49	0	0	0	16	1	2
banana_xamthomonas	0	0	1	0	2	0	0	0	0	0	0	0	12	59	146	3	2	0	27	2	5
groundnut_early_leaf_spot_1	0	0	2	0	2	0	5	0	1	0	0	0	0	0	0	238	0	1	0	0	0
groundnut_early_rust_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	253	0	0	0	0
groundnut_healthy_leaf_1	0	0	2	1	2	1	1	0	0	0	0	0	0	0	0	19	0	247	0	0	4
groundnut_late_leaf_spot_1	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	1	263	2	0
groundnut_nutrition_deficiency_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	269	1
groundnut_rust_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	239

(b)

Fig.4. Simulation Output of Confusion Matrix (a) Test and (b) Training dataset

Figure 4 displays the simulation outcome using two confusion matrices: (a) for the test dataset and (b) for the training dataset in the context of classifying plant leaf diseases. The confusion matrix of the test dataset gives a comprehensive analysis of the model's accuracy on data that it has not been trained on, providing valuable information on the number of true positives, true negatives, false positives, and false negatives. Conversely, the confusion matrix of the training dataset demonstrates the level of proficiency the model has acquired from the data it was trained on. Differences between these matrices might indicate possible problems such as overfitting or underfitting, providing guidance to academics and practitioners in improving the model's accuracy and ability to apply to real-world situations. The data presented in these confusion matrices is crucial for evaluating the resilience and dependability of the plant leaf disease classification model.

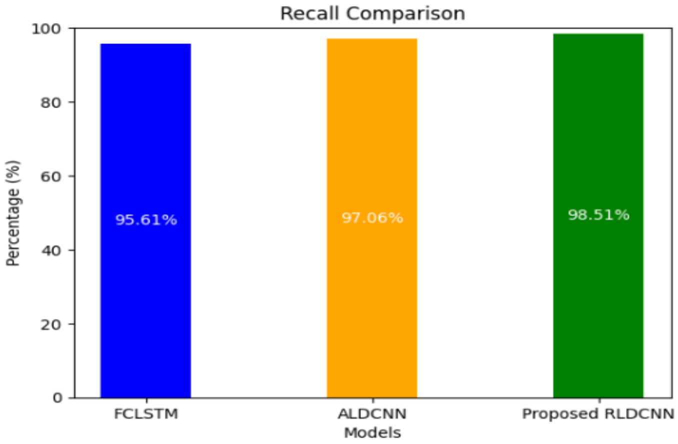


(a)

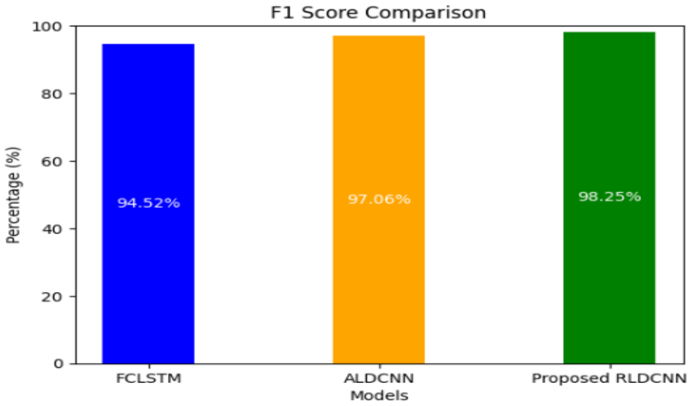
(b)

Fig.5. Simulation Output of (a) Accuracy and (b) Precision

Figure 5 displays the results of the simulation for classifying plant leaf diseases, highlighting important metrics like accuracy and precision. Accuracy measures the extent to which the model's predictions are right, including its capacity to accurately detect both healthy and damaged plant leaves. Figure 5(b) illustrates precision, which highlights the exactness of positive predictions, particularly the model's capacity to accurately identify plant leaves that are impacted by illnesses. The recommended approach has accuracy and precision levels above 98%. The proposed methodology's accuracy and precision provide improved outcomes in comparison to the current ALDCNN and FCLSTM. Given that the proposed approach has a more pronounced activation function.



(a)



(b)

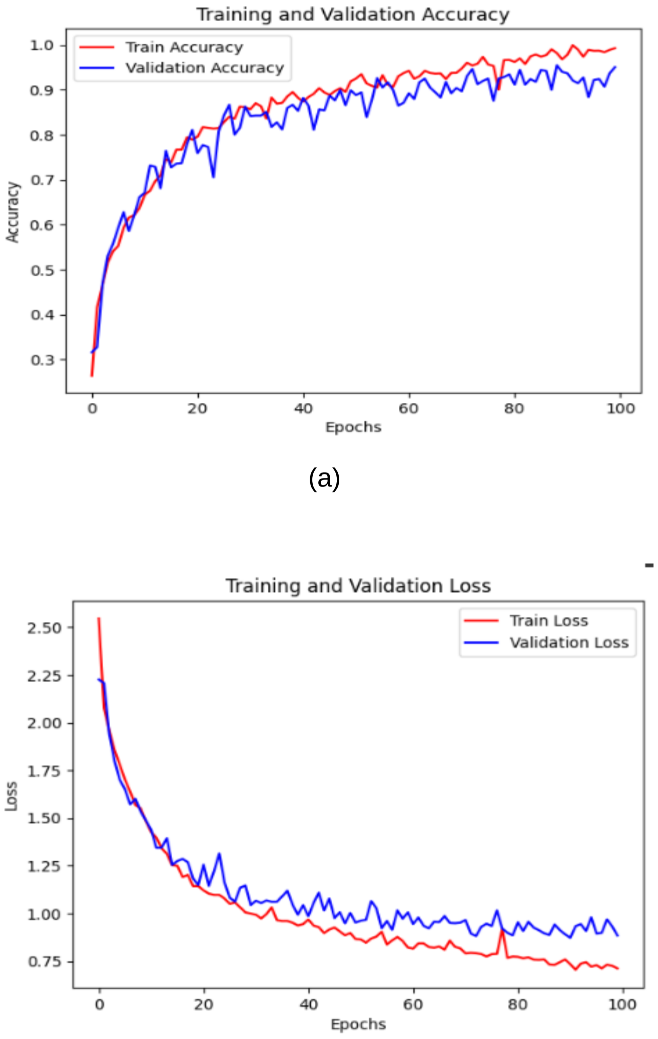
Fig.6. Simulation Output of (a) Recall and (b) F1 score

Figure 6 shows a comparative study of the recall and F1-score measures. The recall value of the suggested RLDCNN technique is 98.51%, while the ALDCNN value is 98.06% and the FCLSTM value is 95.61%. However, the ALDCNN and FCLSTM methods achieve lower recall values compared to the proposed research strategy. The recommended research technique utilises an allied layered function-based output layer and a better activation function for classifying plant leaf diseases. The F1-score of the proposed RLDCNN approach is much greater than that of current techniques such as the ALDCNN method (98.06%) and the FCLSTM technique (94.52%). Specifically, the F1-score of the RLDCNN method is 98.25%. The graphical depiction clearly illustrates the higher performance of the proposed strategy compared to current techniques in the field of plant leaf disease classification.

Table.2. Comparison analysis of statistical measurement

Methods	**Accuracy** (%)	**Precision** (%)	**Recall** (%)	**F1-score** (%)
Proposed RLDCNN	98.51	99.74	98.51	98.25
ALDCNN	97.06	97.11	97.06	97.06
FCLSTM	95.61	96.21	95.61	94.52

Table 2 presents an elaborate comparison of statistical metrics for several approaches used to classify plant leaf diseases, namely the Proposed hybrid RLDCNN, ALDCNN, and FCLSTM. The performance metrics of three classification approaches, namely Proposed RLDCNN, ALDCNN, and FCLSTM, were assessed. Out of all the options, the Proposed RLDCNN showed exceptional performance, achieving an accuracy of 98.51%, precision and recall rates of 99.74% each, and an F1-score of 98.25%. The ALDCNN model demonstrated impressive performance, with an accuracy of 97.06% and precision and recall rates likewise at 97.06%. The FCLSTM model, albeit maintaining a commendable accuracy of 95.61%, exhibited slightly diminished precision, recall, and F1-score metrics at 96.21% and 94.52% respectively [34-35]. The metrics together demonstrate that the Proposed RLDCNN approach surpasses other methods in terms of overall classification performance, surpassing them in different important categories.

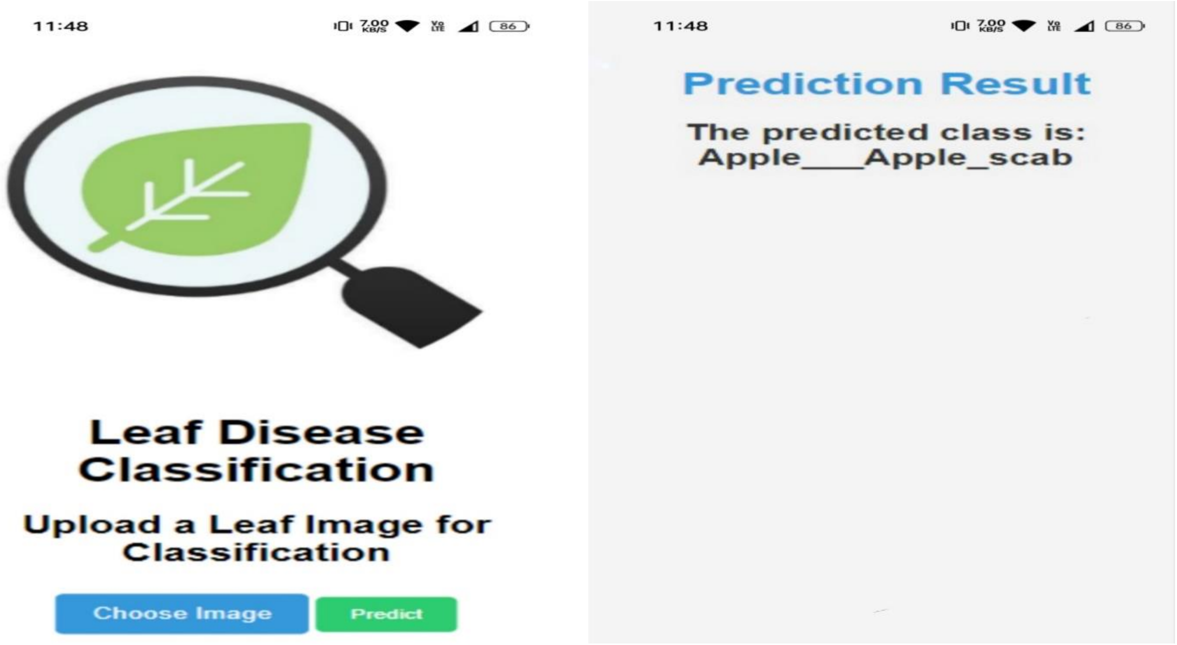


(a)

(b)

Fig.7. Comparison analysis of (a) Classifier accuracy and (b) Loss rate

Figure 7 presents a graphical representation of the training process, illustrating the progression of accuracy and loss measures over time. During the training process, the model regularly achieved an accuracy of roughly 0.995, demonstrating a high degree of precision in its predictions. Concurrently, the loss rate reached a stable value of about 1, indicating a minimal amount of inaccuracy in the model's categorization. The findings confirm the successful training of the hybrid RLDCNN model, indicating that it has proficiently acquired the patterns and characteristics required for classifying and identifying diseases in apple, mango, banana, and groundnut plants. The model's high accuracy and low loss indicate its suitability for practical use, inspiring confidence in its capacity to accurately and reliably identify diseases in many plant species. When the learning rate is 0.01 and the epoch is 10, its accuracy values are at the same level, so it stops with epoch 10.



Leaf Disease Classification

Upload a Leaf Image for Classification

Prediction Result

The predicted class is: Apple___Apple_scab

Fig. 8. Plant leaf disease prediction in application

When the user clicks the login button, the programme initiates a connection with the web server. Afterwards, users are given the choice to submit a picture of a leaf. After the user chooses and uploads a photograph, the programme utilises its capabilities to identify and categorise the leaf as either healthy or sick. Figure 8 depicts the UI, showcasing a button that, once being pushed, unveils comprehensive information pertaining to the identified plant leaf ailment.

5. CONCLUSION

This study presents a novel hybrid RLDCNN model designed for the cloud-based segmentation and classification of several plant leaf diseases. The suggested approach is a classification technique that involves collecting images using cloud-based technology, preprocessing the images, segmenting them, extracting relevant features, selecting the most important features, and finally classifying the images. Initially, a cloud-based system captures photographs and then enhances the visual quality of the input images. The ADPHE clustering technique is used to partition the distinct components and regular components. Furthermore, the investigation conducted utilising the FHESO shown that the chosen characteristic does not result in any loss of data during disease diagnosis. The performance of the proposed Recurrent Layer based Deep Convolutional Neural network (RLDCNN) classification approach is evaluated by comparing it with an FCL-LSTM and ALDCNN, based on measurements of metrics such as classification accuracy, precision, recall, and F-measure. The Python script is used to construct the RLDCNN network model, which is designed for classifying leaf diseases of plants. The first experiment demonstrates that the first RLDCNN algorithm has a high level of classification accuracy, thereby confirming its effectiveness. The RLDCNN algorithm achieved an accuracy of 98.51% based on the findings. This method is a very reliable and accurate system with a minimal margin of error. The testing results demonstrated the superior performance of the hybrid RLDCNN approach compared to other models. Construct the model using a hybrid Reinforcement Learning Deep Convolutional Neural Network (RLDCNN) to develop a web application that can operate autonomously on a smartphone.

The future scope of this project includes the incorporation of the identification of supplementary agricultural illnesses, which will subsequently undergo testing in a real-world agricultural setting. Enhance the programmer's utility by including other functionalities, such as disease treatment capabilities. The system might potentially be constructed using an alternative dataset or picture of a distinct plant species. Get ready for If the platform supports many languages, so that it may be used worldwide.

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