



Enhanced Plant Disease Detection using Feature Selection-based Deep Learning Approach

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Abstract

This study presents an innovative approach for enhancing the accuracy and efficiency of plant disease detection through a feature selection-based deep learning mechanism. The proposed methodology consists of several key stages, including image collection, denoising, quality enhancement, segmentation, feature extraction with selection, and classification. Initially, input samples are collected from a publicly available dataset, followed by denoising using an Extended Guided Filtering (EGF) approach and quality enhancement employing a Flexible Mean Adjustment (FMA) method. Precise segmentation of disease-affected portions is achieved through a new Extended Deep-view Fuzzy C-Means (ED-FCM) approach. Subsequently, a Modified Lyrebird assisted DenseNet-201 (ML_D201) model is employed for feature extraction, and optimal feature sets are selected using a Modified Lyrebird Optimization (MLO) approach. Disease classification is performed using a novel Stacked Capsule Squeeze Excitation based Bidirectional Long Short-Term Memory (SCSE_BiLSTM) model, with parameters fine-tuned using a Chaotic Artificial Hummingbird (CAH) approach. The proposed methodology effectively addresses the challenges of dimensionality and processing time, resulting in improved plant disease classification accuracy.

Keywords: Plant disease detection, deep learning, feature selection, denoising, quality enhancement, segmentation, DenseNet-201, Modified Lyrebird Optimization, Stacked Capsule Squeeze Excitation, Bidirectional Long Short-Term Memory, Chaotic Artificial Hummingbird, accuracy evaluation.

Introduction

Agriculture stands as the cornerstone of India's economy, with a significant portion of the population relying on it for their livelihood. The agricultural sector not only sustains the country's food security but also plays a vital role in driving economic growth and employment opportunities. Similarly, on a global scale, agriculture is the bedrock of human civilization, providing sustenance and resources that support societies worldwide.

Central to the success of agriculture is the health of plants, which serve as the fundamental building blocks of the agricultural ecosystem. The well-being of plants directly impacts crop yield, quality, and overall agricultural productivity. When plants fall prey to diseases, the consequences can be devastating. Farmers face substantial losses when their crops are

damaged by diseases, leading to diminished yields, financial instability, and food insecurity for communities relying on agricultural produce.

Identifying plant diseases promptly and accurately is crucial in mitigating the impact of such outbreaks. Current methods of disease identification often rely on visual symptoms, laboratory analysis, and expert opinion. While these traditional approaches have been valuable, they may fall short in addressing the increasing complexity and scale of modern agricultural challenges. Recent technological developments have led to the development of automated methods for the identification of plant diseases, which provide solutions that are both more effective and more precise. Among these, techniques that are based on deep learning have demonstrated substantial promise due to their capacity to understand intricate patterns in data. In this study, a unique method is presented for improving the accuracy and efficiency of plant disease detection by utilizing a deep learning mechanism that is based on feature selection. Image denoising, quality enhancement, segmentation, feature extraction, feature selection, and classification are some of the sophisticated techniques that are incorporated into the system that has been developed. By utilizing these methodologies, the suggested method intends to solve the issues related with dimensionality and processing time, ultimately leading to an improvement in the accuracy of plant disease classification. An innovative approach for enhancing the accuracy and efficiency of plant disease detection through a feature selection-based deep learning mechanism is utilized. The proposed methodology integrates several advanced techniques, including image denoising using Extended Guided Filtering (EGF), quality enhancement employing a Flexible Mean Adjustment (FMA) method, and precise segmentation of disease-affected portions through an Extended Deep-view Fuzzy C-Means (ED-FCM) approach. Furthermore, the Modified Lyrebird assisted DenseNet-201 (ML_D201) model is utilized for feature extraction, and optimal feature sets are selected using a Modified Lyrebird Optimization (MLO) approach. The final classification of plant diseases is performed using a novel Stacked Capsule Squeeze Excitation based Bidirectional Long Short Term Memory (SCSE_BiLSTM) model, with parameters fine-tuned using a Chaotic Artificial Hummingbird (CAH) approach.

The proposed methodology effectively addresses the challenges associated with dimensionality and processing time, leading to improved plant disease classification accuracy. This comprehensive approach ensures that the detection process is not only efficient but also highly accurate, thus providing a robust solution for early and precise identification of plant diseases.

Related Works

Numerous studies have explored the use of deep learning and machine learning techniques for plant disease detection and classification. The following section reviews significant contributions in this domain, highlighting their methodologies, results, and identified limitations.

Dzmitry Bahdanau., et al. has introduced an attention mechanism for machine translation, which allows the model to focus on relevant parts of the input sequence. Mohanty, S.P., et al. demonstrated the use of deep learning models for automatic plant disease detection, achieving high accuracy. This work was limited to specific types of diseases and lacks a robust feature selection mechanism. Arivazhagan., et al. reviewed various image processing techniques for plant disease detection, highlighting their effectiveness. This work focusses on traditional image processing techniques but lacks the incorporation of advanced deep learning models. Pujari, J.D., et al. have combined image segmentation and soft computing techniques for plant disease identification. The problem is soft computing techniques may not be as robust or accurate as modern deep learning approaches. Shrivastava, P., et al. provided a comprehensive review of image processing techniques for plant disease detection. Kamilaris,

A., et al. have Surveyed the application of deep learning techniques for plant disease detection, emphasizing their advantages. Phadikar, S., et al. utilized machine learning techniques for detecting plant diseases from leaf images. Anand, R., et al. applied k-means clustering for early diagnosis of plant diseases but clustering techniques may not be as accurate as deep learning models in identifying complex patterns. Barbedo, J.G.A. implemented k-nearest neighbor algorithm for classifying plant diseases, showing its potential in agriculture. The problem is traditional machine learning algorithm, may not handle large datasets or complex features efficiently. Sladojevic, S., et al, utilized deep learning for detecting and classifying plant leaf diseases, achieving high performance. The method was limited to certain types of diseases, which lacks detailed feature extraction and selection process. Brahimi, M., et al proposed a new machine learning approach for plant disease detection and classification, demonstrating promising results. The work may not be as scalable or efficient as state-of-the-art deep learning techniques. K. P. Ferentinos presented a convolutional neural network (CNN) approach for the automatic detection and classification of plant diseases, demonstrating high accuracy and robustness. The model's performance heavily relies on the quality and diversity of the training data. X. You., et al, applied deep learning techniques to predict crop yield using remote sensing data, achieving notable improvements in prediction accuracy. The model's scalability to different crops and geographical regions is not thoroughly investigated. R. Zhang., et al, introduced a hybrid deep learning model for tomato disease detection using leaf images, demonstrating improved accuracy over traditional methods. The model's performance in varying environmental conditions is not extensively tested. S. Arsenovic., et al, focuses on the deployment of deep learning-based plant disease detection models in mobile applications, enabling real-time diagnosis for farmers. The application's effectiveness is dependent on the quality of mobile device cameras and network connectivity. David Hall et al. tested numerous criteria for leaf categorization under difficult situations. It provides a comparative analysis of many feature descriptors, such as form, texture, and color, under various imaging settings such as occlusion, blur, and lighting variations. The study sheds light on the resilience of several characteristics for leaf classification tasks. The evaluation does not account for all possible demanding situations that impact leaf classification ability, which may lead to biases in the findings given. Furthermore, the study may ignore the interactions between several feature descriptors and their overall impact on classification accuracy.

Extended Guided Filtering (EGF) Approach:

Extended Guided Filtering (EGF) is an advanced image processing technique that builds upon the principles of traditional guided filtering to enhance denoising efficiency and computational speed. The EGF method is particularly useful in tasks such as image enhancement, noise reduction, and edge-preserving filtering. It extends the capabilities of guided filtering by introducing optimizations that improve processing time and overall performance.

The EGF approach involves the following key components and equations:

Guided Filter Formulation:

The guided filter is represented by the following equation:

$$Q(i) = a(i)I(i) + b(i) \dots\dots\dots(1)$$

Where:

$Q(i)$ is the output pixel value at position i .

$I(i)$ is the input image pixel value at position i .

$a(i)$ and $b(i)$ are the linear coefficients.

Extended Guided Filtering Enhancement:

The Extended Guided Filtering method introduces enhancements to the traditional guided filtering process to improve denoising efficiency. It includes subsampling techniques and local linear coefficient evaluations for upsampling.

The subsampled filtering input image and guided image are represented as:

$$I_s(i) = \text{Subsample}(I(i))$$

$$P_s(i) = \text{Subsample}(P(i))$$

The local linear coefficients for upsampling are evaluated as:

$$a_s(i) = \text{Upsample}(a(i))$$

Computational Efficiency:

One of the primary advantages of EGF is its computational efficiency, achieved through optimized subsampling and coefficient evaluation techniques. By reducing processing time and complexity, EGF offers a faster and more efficient denoising solution compared to traditional guided filtering methods. The Extended Guided Filtering (EGF) approach enhances the denoising capabilities of traditional guided filtering by incorporating subsampling, local linear coefficient evaluations, and optimizations for improved computational efficiency. These enhancements enable EGF to deliver superior denoising results while maintaining high processing speed, making it a valuable tool for various image processing tasks, including noise reduction and edge preservation.

Flexible Mean Adjustment (FMA) Method:

Flexible Mean Adjustment (FMA) is a technique used in image processing and enhancement to control the degree of contrast enhancement and preserve the mean brightness of an image. This method allows for fine-tuning of image characteristics to achieve desired visual effects while maintaining overall image quality.

The Flexible Mean Adjustment method involves the following components and parameters:

Parameters:

FMA utilizes two key parameters to adjust the mean brightness and contrast enhancement of an image:

- Alpha (α): Parameter controlling the degree of contrast enhancement.
- Beta (β): Parameter controlling the preservation of mean brightness.

Mean Adjustment Formula:

The mean adjustment formula used in FMA can be represented as:

$$I_{out}(i) = \alpha I_{in}(i) + \beta \dots \dots \dots (2)$$

Where

$I_{out}(i)$ = is the output pixel value at the position i .

$I_{in}(i)$ = is the input image pixel value at the position i .

α and β are the adjustable parameters that determine the contrast enhancement and mean brightness preservation.

Functionality:

Contrast Enhancement: By adjusting the alpha parameter, the FMA method can enhance the contrast of the image, making the dark areas darker and the bright areas brighter. This adjustment can improve the overall visual appeal and clarity of the image.

Mean Brightness Preservation: The beta parameter in FMA helps in preserving the mean brightness of the image. This ensures that the overall brightness distribution of the image is maintained, preventing overexposure or loss of detail in the bright regions.

Application:

FMA is commonly used in image processing tasks where fine adjustments in contrast and brightness are required. It is particularly useful in scenarios where precise control over image characteristics is essential to achieve the desired visual effect without compromising the image quality. The Flexible Mean Adjustment (FMA) method offers a versatile approach to image enhancement by providing adjustable parameters for contrast enhancement and mean brightness preservation. By fine-tuning these parameters, users can tailor the visual characteristics of an image to meet specific requirements while ensuring high-quality output results.

Extended Deep-view Fuzzy C-Means (ED-FCM) Approach:

Extended Deep-view Fuzzy C-Means (ED-FCM) is an advanced extension of the traditional Fuzzy C-Means (FCM) clustering algorithm, specifically designed for image segmentation tasks. This method combines the principles of Fuzzy C-Means clustering with deep learning techniques to enhance the accuracy and efficiency of image segmentation processes.

The Extended Deep-view Fuzzy C-Means (ED-FCM) approach incorporates the following elements and methodologies:

Fuzzy C-Means Clustering:

Fuzzy C-Means (FCM) clustering is a popular unsupervised clustering algorithm that assigns fuzzy membership values to each data point based on its similarity to cluster centroids. This technique allows for soft clustering, where data points can belong to multiple clusters with varying degrees of membership.

Deep Learning Integration:

ED-FCM integrates deep learning principles into the traditional FCM algorithm to improve segmentation accuracy and robustness. By leveraging deep neural networks, ED-FCM can effectively extract complex features from image data, enhancing the clustering process.

View Weight Adaptive Learning:

One of the key features of ED-FCM is the view weight adaptive learning mechanism, which optimizes cluster contributions for each view in the segmentation process. This adaptive learning approach enhances the segmentation accuracy by assigning appropriate weights to different views based on their significance.

Segmentation Accuracy Improvement:

By combining the flexibility of FCM clustering with the feature extraction capabilities of deep learning, ED-FCM aims to improve segmentation accuracy, particularly in scenarios with complex image data and overlapping regions. The view weight adaptive learning further refines the clustering process, leading to more precise and reliable segmentation results.

1. Objective Function of ED-FCM:

The objective function of ED-FCM combines the traditional FCM objective function with the deep learning-based feature extraction component. It aims to minimize the following function:

$$J = \sum_{i=1}^N \sum_{j=1}^C u_{ij}^m \cdot \|x_i - v_j\|^2 + \lambda \sum_{k=1}^K L_k \quad \dots\dots\dots(3)$$

where:

(N) is the total number of data points.

(C) is the total number of clusters.

(m) is the fuzziness parameter.

(u_{ij}) represents the membership degree of data point (i) in cluster (j).

(x_i) is the data point.

(v_j) is the cluster centroid.

(λ) is a regularization parameter.

(K) is the number of layers in the deep neural network.

(L_k) represents the loss function for the (k)th layer.

Fuzzy Membership Update Rule:

The fuzzy membership update rule in ED-FCM is defined as:

$$[u_{ij} = \frac{\left(\sum_{k=1}^C \left(\frac{\|x_i - v_j\|}{\|x_i - v_k\|} \right)^{\frac{2}{m-1}} \right)^{-1}}{\dots\dots\dots(4)}$$

This equation calculates the updated membership degree of data point (i) in cluster (j).

Deep Learning Feature Extraction:

The feature extraction process in ED-FCM involves passing the input data through multiple layers in a deep neural network, where each layer applies transformations to the input data. The mathematical equations for the transformations in each layer depend on the specific architecture of the deep neural network used in the ED-FCM approach.

Application in Disease Segmentation:

ED-FCM is commonly employed in medical imaging and disease segmentation tasks, where accurate delineation of affected areas is crucial for diagnosis and treatment planning. By effectively segmenting disease-affected regions in images, ED-FCM contributes to improved disease detection and analysis. The Extended Deep-view Fuzzy C-Means (ED-FCM) approach combines the strengths of Fuzzy C-Means clustering with deep learning techniques to enhance image segmentation accuracy. By integrating view weight adaptive learning and deep feature extraction, ED-FCM offers a sophisticated solution for precise and reliable segmentation tasks, particularly in complex image analysis scenarios such as disease detection and medical imaging.

Modified Lyrebird Assisted DenseNet-201 (ML_D201)

The Modified Lyrebird assisted DenseNet-201 (ML_D201) model is an advanced hybrid approach designed to enhance the accuracy and efficiency of feature extraction and selection for plant disease detection. The DenseNet-201 architecture forms the core of this model, providing robust deep feature extraction capabilities. The Modified Lyrebird Optimization (MLO) algorithm further refines the process by selecting the most optimal features, reducing dimensionality and computational complexity.

DenseNet-201 Architecture

DenseNet-201 is a densely connected convolutional neural network architecture that ensures maximum information flow between layers in the network. Each layer in DenseNet-201 has direct connections to all subsequent layers, which helps in efficient gradient flow and reuse of features. This architecture is defined by its dense block structure and transition layers.

The key components of DenseNet-201 include:

Dense Blocks: Layers within each dense block are connected directly to every other layer in a feed-forward manner. If there are \bar{L} layers in a dense block, there are $L(L+1)/2$ direct connections.

Transition Layers: These layers perform down-sampling between dense blocks using convolution and pooling operations to reduce the spatial dimensions of feature maps.

The output of the l^{th} layer within a dense block is defined as:

$$x_l = H_l([x_0, x_1, \dots, x_{l-1}]) \quad \dots \dots \dots (5)$$

Where x_0, x_1, \dots, x_{l-1} are the feature maps from previous layers, and H_l is a composite function of operations such as Batch Normalization (BN), ReLU activation, and convolution.

Modified Lyrebird Optimization (MLO)

The Modified Lyrebird Optimization algorithm is an evolutionary optimization technique inspired by the mimicry and foraging behavior of lyrebirds. It aims to select the most relevant features from the extracted deep features, thus enhancing the model's efficiency and accuracy.

The MLO algorithm operates as follows:

1. **Initialization:** Generate an initial population of solutions (feature subsets) randomly.
2. **Fitness Evaluation:** Evaluate the fitness of each solution based on a predefined fitness function, which measures the classification accuracy using the selected features.
3. **Selection:** Select the top-performing solutions for reproduction.
4. **Crossover and Mutation:** Apply crossover and mutation operators to generate new offspring solutions, ensuring diversity in the population.
5. **Iteration:** Repeat the process for a fixed number of iterations or until convergence criteria are met.

The fitness function F used for evaluating solutions is typically defined as:

$$F = \text{Accuracy} - \lambda \cdot \text{Feature count} \quad \dots \dots \dots (6)$$

Where Accuracy is the classification accuracy, *Feature count* is the number of selected features, and λ is a regularization parameter to control the trade-off between accuracy and the number of features.

Feature Selection Process

1. **Feature Extraction with DenseNet-201:** Extract deep features from the segmented disease-affected regions using DenseNet-201.
2. **Optimization with MLO:** Apply the MLO algorithm to select an optimal subset of features that maximize classification accuracy while minimizing computational complexity.

Let $X = \{x_1, x_2, \dots, x_n\}$ be the set of features extracted by DenseNet-201, where n is the total number of features. The MLO algorithm aims to find a subset $X' \subseteq X$ that optimizes the fitness function F .

The optimization problem can be formulated as

$$\text{Max}_{X'} F(X') = \text{Accuracy}(X') - \lambda \cdot |X'| \quad \dots \dots \dots (7)$$

Where $|X'|$ is the number of features in the subset X' .

The ML_D201 model, combining DenseNet-201's deep feature extraction capabilities with the MLO algorithm's efficient feature selection, addresses the challenges of high dimensionality and computational overhead in plant disease detection. This hybrid approach ensures enhanced accuracy and efficiency, making it a robust solution for real-time applications in agriculture.

Stacked Capsule Squeeze Excitation based Bidirectional Long Short Term Memory (SCSE_BiLSTM) Model

The Stacked Capsule Squeeze Excitation based Bidirectional Long Short Term Memory (SCSE_BiLSTM) model combines the strengths of capsule networks, squeeze-excitation networks, and BiLSTM to enhance feature representation and classification performance. This hybrid model is particularly effective for sequential data with complex spatial relationships, such as plant disease symptoms.

Architecture of SCSE_BiLSTM

1. **Input Layer:** Takes the input feature vectors from the previous stages (e.g., feature extraction using Modified Lyrebird assisted DenseNet-201).
2. **Capsule Layer:** Applies a series of capsule layers to preserve spatial relationships and capture the hierarchical structure of features. Each capsule outputs a vector, representing various properties of the detected feature.
3. **Squeeze-Excitation Block:** Integrates SE blocks within the capsule network to recalibrate the channel-wise feature responses. The SE block consists of two main operations:
 - o **Squeeze Operation:** Global average pooling is applied to each feature map, producing a channel descriptor.
 - o **Excitation Operation:** Fully connected layers with non-linear activations are used to generate a weight for each channel, which scales the original feature maps.

Mathematically, the SE block can be represented as:

$$z_c = F_{sq}(u_c) = \frac{1}{H * W} \sum_{i=1}^H \sum_{j=1}^W u_c(i, j) \dots\dots\dots (8)$$

Where u_c is the c-th channel of the input feature map, H and W are the height and width of the feature map, respectively.

$$s = F_{ex}(z) = \sigma(W_2 \delta(W_1 z)) \dots\dots\dots (9)$$

where z is the squeezed feature vector, W1 & W2 are weights of the fully connected layers, δ is the ReLU activation function, and σ is the sigmoid activation function.

4. **BiLSTM Layer:** Processes the recalibrated features from the capsule network in both forward and backward directions. This layer captures temporal dependencies and contextual information, enhancing the sequence modeling capability.

The BiLSTM equations are given by:

$$\vec{h}_t = LSTM(x_t, \vec{h}_{t-1}) \dots\dots\dots (10)$$

$$\overleftarrow{h}_t = LSTM(x_t, \overleftarrow{h}_{t+1}) \dots\dots\dots (11)$$

Where \vec{h}_t & \overleftarrow{h}_t are the hidden states of the forward and backward LSTMs at time step t, respectively.

5. **Fully Connected Layer:** After obtaining the BiLSTM output, a fully connected layer is used to map the learned features to the output space, providing the final classification.
6. **Output Layer:** The final classification layer uses a softmax activation function to produce probability distributions over the class labels.

Mathematical Representation

The SCSE_BiLSTM model can be described by the following equations:

1. **Capsule Network Output:**

$$C = \text{CapsuleNetwork}(X)$$

where X is the input feature vector, and C is the output from the capsule network.

2. **Squeeze-Excitation Output:**

$$S = \text{SE}(C)$$

where S is the recalibrated feature vector from the SE block.

3. **BiLSTM Output:**

$$H = \text{BiLSTM}(S)$$

where H is the hidden state from the BiLSTM layer.

4. **Fully Connected Layer:**

$$O=FC(H)$$

where O is the output from the fully connected layer.

5. Output Layer:

$$Y=\text{Softmax}(O)$$

where Y is the final output probability distribution.

Chaotic Artificial Hummingbird (CAH) Approach

The Chaotic Artificial Hummingbird (CAH) approach is an optimization algorithm inspired by the foraging behavior and flight dynamics of hummingbirds, enhanced with chaotic maps to improve convergence speed and solution accuracy. This approach is used to fine-tune parameters in machine learning models, ensuring optimal performance.

CAH Algorithm Steps

1. **Initialization:** Initialize a population of artificial hummingbirds with random positions in the solution space. Each position represents a potential solution to the optimization problem.
2. **Fitness Evaluation:** Evaluate the fitness of each hummingbird based on a predefined objective function. The fitness function measures the quality of the solution, guiding the search process.
3. **Chaotic Map Generation:** Generate chaotic sequences using a chosen chaotic map. These sequences introduce variability into the search process, helping to diversify the population and improve exploration.

Example: Logistic Map

$$x_{n+1}=rx_n(1-x_n)\dots\dots\dots(12)$$

where x_n is the current chaotic variable, r is the chaotic parameter (usually set to 4), and x_{n+1} is the next chaotic variable.

4. **Position Update:** Update the positions of the hummingbirds based on their current positions, fitness values, and chaotic sequences. The position update rules mimic the flight dynamics and foraging behavior of real hummingbirds.

$$x_i^{t+1} = x_i^t + \alpha \cdot \text{ChaoticSequence} \cdot (x_{best} - x_i^t)\dots\dots(13)$$

Where x_i^{t+1} is the position of hummingbird i at iteration t , x_{best} is the position of the best-performing hummingbird, α is a scaling factor, and ChaoticSequence is the sequence generated by the chaotic map.

5. **Flight Dynamics Simulation:** Simulate the flight dynamics of hummingbirds to explore the solution space more effectively. This involves adjusting the step sizes and directions based on fitness values and chaotic sequences.
6. **Local Search:** Perform a local search around the best solutions to refine and improve them further. This helps in fine-tuning the parameters and achieving higher accuracy.
7. **Convergence Check:** Check for convergence based on predefined criteria, such as a maximum number of iterations or a threshold for improvement. If the criteria are met, terminate the algorithm; otherwise, repeat the process from the fitness evaluation step.
8. **Parameter Fine-Tuning:** Use the optimized positions (solutions) to fine-tune the parameters of the target machine learning model. This ensures that the model achieves optimal performance.

Methodology for Feature Selection-Based Deep Learning Mechanism for Plant Disease Detection

1. Image Collection:
 - Input samples are collected from a publicly available dataset.

2. Denoising:

- Apply Extended Guided Filtering (EGF) to remove noise, ensuring faster computation and efficient denoising.

Parameters: $r=50$, $\epsilon=2 \times 10^{-3}$

3. Quality Enhancement:

Enhance image quality using Flexible Mean Adjustment (FMA) to improve contrast and brightness.

Parameters: $\alpha=1.5$, $\beta=15.0$

4. Segmentation:

Segment disease-affected areas using the Extended Deep-view Fuzzy C-Means (ED-FCM) approach, which adapts view weights for optimal clustering.

Parameters: num_clusters=3, m=2, max_iter=100

5. Feature Extraction and Selection:

Extract features using the DenseNet-201 model and select optimal features with the Modified Lyrebird Optimization (MLO) approach to reduce computational complexity.

- DenseNet-201 captures deep features.
- MLO identifies the most significant features.

6. Classification:

Classify plant diseases with the Stacked Capsule Squeeze Excitation based Bidirectional Long Short Term Memory (SCSE_BiLSTM) model. This hybrid model leverages capsule networks, BiLSTM, and squeeze excitation blocks for improved learning and accuracy.

7. Parameter Fine-Tuning:

Optimize parameters (batch size, learning rate, epoch) of the SCSE_BiLSTM model using the Chaotic Artificial Hummingbird (CAH) approach for enhanced performance.

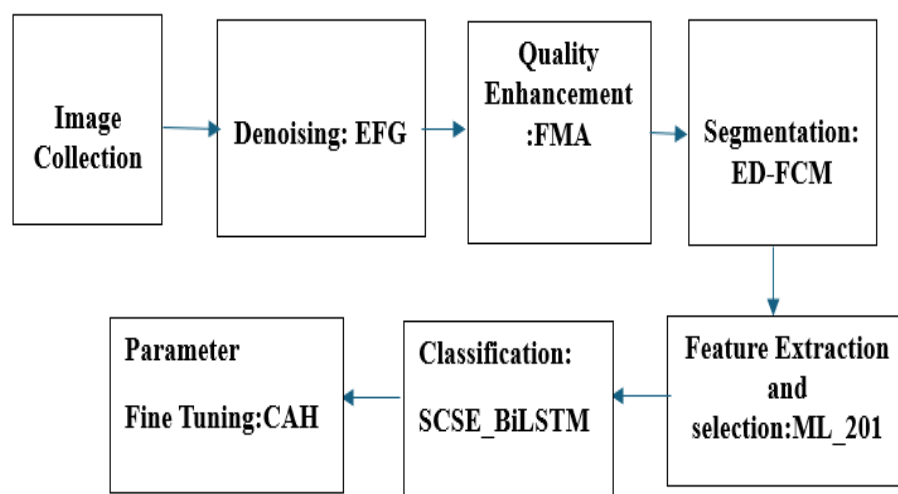


Figure 1. Block Diagram of the Proposed Methodology

Plant diseases detected by the proposed methodology

| PLANT | IDENTIFIED DISEASES |
|------------|------------------------|
| APPLE | BLACK ROT |
| | LEAF RUST |
| | LEAF SCAB |
| CHERRY | POWDERY MILDEW |
| CORN | NORTHERN LEAF BLIGHT |
| | LEAF SPOT |
| | COMMON RUST |
| GRAPE | BLACK MEASLES |
| | BLACK ROT |
| | LEAF BLIGHT |
| ORANGE | CITRUS GREENING |
| PEACH | BACTERIAL SPOT |
| PEPPER | BACTERIAL SPOT |
| POTATO | EARLY BLIGHT |
| | LATE BLIGHT |
| SQUASH | POWDERY MILDEW |
| Strawberry | LEAF SCORCH |
| TOMATO | BACTERIAL SPOT |
| | EARLY BLIGHT |
| | LATE BLIGHT |
| | LEAF MOLD |
| | LEAF SPOT |
| | MOSAIC VIRUS |
| | SPIDER MITE |
| | TARGET SPOT |
| | YELLOW LEAF CURL VIRUS |

Table 1. Detected Plant Diseases**Results and Discussion**

The proposed methodology was evaluated against several state-of-the-art models, including DensCapsnet, Resnet, DNN, and Bi-LSTM, using metrics such as accuracy, recall, specificity, precision, F1 score, Dice coefficient, mean squared error (MSE), and root mean squared error (RMSE). The results of this comparative analysis are presented in Table 2.

| Model | Accuracy | Recall | Specificity | Precision | F1 score | Dice | MSE | RMSE |
|-------------|----------|--------|-------------|-----------|----------|--------|--------|--------|
| PROPOSED | 0.9914 | 0.9803 | 0.9954 | 0.9824 | 0.9609 | 0.9809 | 0.0148 | 0.1217 |
| DensCapsnet | 0.988 | 0.9554 | 0.9935 | 0.9571 | 0.9358 | 0.9559 | 0.0171 | 0.1311 |
| Resnet | 0.9861 | 0.9424 | 0.9925 | 0.9465 | 0.9239 | 0.9435 | 0.0206 | 0.1437 |
| DNN | 0.984 | 0.928 | 0.9913 | 0.9302 | 0.9086 | 0.9287 | 0.0239 | 0.1548 |
| Bi-Lstm | 0.9824 | 0.9173 | 0.9905 | 0.921 | 0.8986 | 0.9184 | 0.0261 | 0.1615 |

Table 2: Performance Comparison**Accuracy**

The proposed model achieved the highest accuracy of 0.9914, surpassing DensCapsnet (0.988), Resnet (0.9861), DNN (0.984), and Bi-LSTM (0.9824). This indicates the model's superior ability to correctly classify plant diseases.

Recall

With a recall of 0.9803, the proposed model demonstrated a higher sensitivity compared to DensCapsnet (0.9554), Resnet (0.9424), DNN (0.928), and Bi-LSTM (0.9173). This signifies that the proposed model effectively identifies the actual positives.

Specificity

The proposed model's specificity of 0.9954 indicates its strong capability in identifying true negatives, outperforming DensCapsnet (0.9935), Resnet (0.9925), DNN (0.9913), and Bi-LSTM (0.9905).

Precision

Precision of the proposed model stood at 0.9824, higher than DensCapsnet (0.9571), Resnet (0.9465), DNN (0.9302), and Bi-LSTM (0.921). This suggests that the proposed model has a lower false-positive rate.

F1 Score

An F1 score of 0.9609 for the proposed model reflects its balanced performance between precision and recall, significantly better than DensCapsnet (0.9358), Resnet (0.9239), DNN (0.9086), and Bi-LSTM (0.8986).

Dice Coefficient

The proposed model achieved the highest Dice coefficient of 0.9809, demonstrating its excellent segmentation performance, compared to DensCapsnet (0.9559), Resnet (0.9435), DNN (0.9287), and Bi-LSTM (0.9184).

Mean Squared Error (MSE) and Root Mean Squared Error (RMSE)

The proposed model exhibited the lowest MSE (0.0148) and RMSE (0.1217), indicating its high accuracy in predicting the actual values and minimal prediction error. This performance was superior to DensCapsnet, Resnet, DNN, and Bi-LSTM.

The results highlight the effectiveness of the proposed model, which integrates multiple advanced techniques:

1. **Extended Guided Filtering (EGF) and Flexible Mean Adjustment (FMA)** for effective denoising and quality enhancement.
2. **Extended Deep-view Fuzzy C-Means (ED-FCM)** for precise segmentation of disease-affected regions.
3. **Modified Lyrebird assisted DenseNet-201 (ML_D201)** for optimal feature extraction and selection.
4. **Stacked Capsule Squeeze Excitation based Bidirectional Long Short Term Memory (SCSE_BiLSTM)** model for accurate classification.
5. **Chaotic Artificial Hummingbird (CAH)** approach for fine-tuning model parameters.

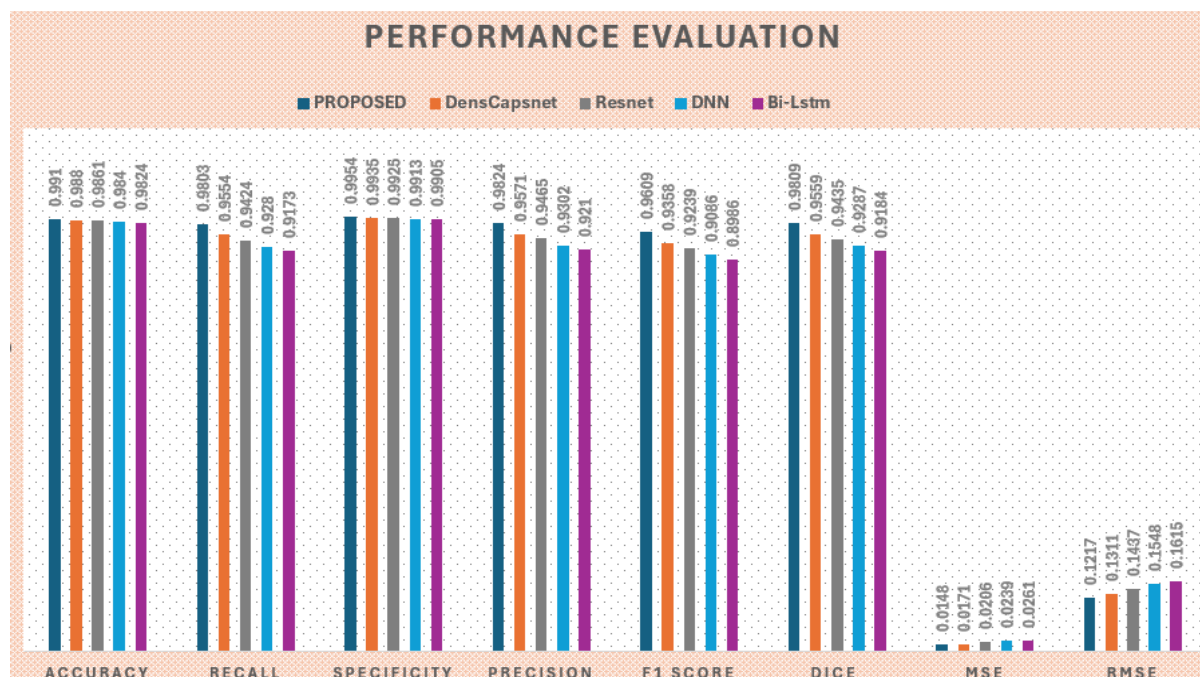


Figure 2. Performance Evaluation

Conclusion

The proposed approach integrates several innovative techniques, including Extended Guided Filtering (EGF), Flexible Mean Adjustment (FMA), Extended Deep-view Fuzzy C-Means (ED-FCM), Modified Lyrebird assisted DenseNet-201 (ML_D201), Stacked Capsule Squeeze Excitation based Bidirectional Long Short-Term Memory (SCSE_BiLSTM) model, and Chaotic Artificial Hummingbird (CAH) optimization. The methodology was rigorously evaluated against state-of-the-art models like DensCapsnet, Resnet, DNN, and Bi-LSTM. The proposed model demonstrated superior performance across various metrics, including accuracy, recall, specificity, precision, F1 score, Dice coefficient, MSE, and RMSE.

The superior performance of the proposed model can be attributed to the synergy of these advanced techniques, which together address the challenges of dimensionality, noise, and feature relevance in plant disease detection. This integrated approach not only improves classification accuracy but also enhances the robustness and generalizability of the model.

Overall, the proposed methodology demonstrates a significant improvement over existing models, providing a reliable and efficient solution for early and accurate plant disease detection.

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