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Bio-Inspired Deep Learning Framework for Accurate Strawberry Leaf Disease Classification

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Abstract. Strawberry plants, like many other crops, are vulnerable to a range of leaf diseases, which can cause substantial yield reductions. For crop loss to be avoided and high productivity levels to be maintained, timely diagnosis and precise classification of these diseases are essential. Conventional manual techniques for identifying diseases are frequently slow, error-prone, and limited in precision, particularly when recognizing early or subtle symptoms. To overcome these limitations, this study introduces an automated deep learning framework designed for precise classification of strawberry leaf diseases, employing advanced Convolutional and Recurrent Neural Networks (CNN and RNN) optimized with bacterial foraging and particle swarm optimization techniques. The framework combines CNN and RNN architectures, optimized to deliver high accuracy in distinguishing fungal and viral infections. By employing K-means clustering, Sparse Principal Component Analysis (PCA), and a CNN with ReLU activation, the model effectively extracts and refines features linked to disease. Further, region-growing segmentation and an optimized RNN enhance detection accuracy by capturing essential spatial and temporal patterns. Experimental tests using the PlantVillage dataset indicate a classification accuracy of 99%, highlighting the model's potential for early disease control and real-time agricultural surveillance. This strategy has a lot of potential to improve disease control methods, which will eventually increase crop productivity and yield.

Keywords: Strawberry Plant Leaves, Convolutional Neural Networks(CNN), Recurrent Neural Networks(RNN), and Sparse Principal Component Analysis (PCA).

1 Introduction

Strawberries are a widely cultivated fruit crop valued globally for their nutritional benefits, economic significance, and high consumer demand. However, strawberry plants are highly prone to several leaf diseases, particularly fungal and viral infections, which may negatively affect quality and yield. These illnesses have the potential to cause significant crop losses if left untreated, which would lower output and have a negative financial impact on farmers. Consequently, prompt intervention can significantly reduce crop damage and increase overall yield, making early and correct identification of leaf diseases crucial for effective management.

Traditionally, leaf diseases were identified through manual inspection, in which farmers or agricultural specialists visually assessed plant health. While this method can occasionally produce reliable findings, It is labor-intensive, time-consuming, and prone to human mistake. Visual observation may also lack precision, particularly in early disease stages when symptoms are minimal or unclear. Consequently, manual methods often fall short in large-scale agriculture or in detecting early disease indicators. This challenge highlights the need for automated solutions capable of efficiently and accurately identifying leaf diseases to support farmers and agronomists in maintaining crop health.

Recent advances in deep learning technology provide intriguing solutions to precision agriculture's difficulties. Deep learning models are perfect for analyzing plant leaf pictures to detect diseases since they have demonstrated excellent outcomes in image processing tasks including object detection and classification. This is especially true of Convolutional Neural Networks (CNN) and Recurrent Neural Networks (RNN). RNNs are adept at identifying sequential and temporal patterns, which is particularly useful for monitoring the course of sickness, whereas CNNs surpass at extracting spatial properties from images. However, developing an efficient model that achieves high accuracy without excessive computational demands remains challenging, as it requires extensive, high-quality labeled data and robust methods to prevent overfitting in complex networks.

To address these problems, this study offers an enhanced deep learning framework that incorporates CNN and RNN architectures optimized through bacterial foraging and particle swarm optimization techniques. Developing a model that can consistently categorize different kinds of strawberry leaf diseases while differentiating between viral and fungal infections. The model's feature selection and search procedures are improved by using optimization techniques like particle swarm optimization and bacterial foraging to minimizing computational load while improving classification performance. This optimized framework is intended to support real-time agricultural monitoring, enabling early detection and more effective disease management in strawberry cultivation, ultimately promoting higher yields and sustainable productivity.

2. Materials and Methods

Automated plant disease categorization has greatly improved in recent years thanks to developments in deep learning, image processing, and optimization methods. Detecting diseases at early stages is essential for preventing crop loss, particularly for economically valuable crops such as strawberries. This section provides a theoretical foundation for the methods employed in this study, including deep learning architectures, bio-inspired optimization algorithms as well as image processing methods that serve as the foundation for the suggested framework.

Major Contribution of the Research:

- Development of a bio-inspired deep learning framework combining CNN and RNN for accurate strawberry leaf disease classification.
- Integration of bacterial foraging and particle swarm optimization techniques to enhance model precision and efficiency.
- Implementation of advanced preprocessing methods, including K-means clustering and Sparse PCA, for improved feature extraction and refinement.
- Achievement of high classification accuracy (99%) validated on the Plant Village dataset, demonstrating the framework's potential for real-time agricultural applications.
- Contribution to sustainable farming practices by enabling early disease detection, leading to better crop management and increased productivity.

2.1. Deep Learning for Image Classification

Deep learning, a kind of machine learning, makes use of artificial neural networks to depict complex patterns in data. Convolutional Neural Networks (CNNs) and Recurrent Neural Networks (RNNs) are two kinds of deep learning models that are frequently used in photo classification, especially for challenges involving the processing of spatial and temporal input.

2.1.1 Convolutional Neural Networks (CNNs)

Because CNNs can effectively evaluate grid-like input, like images, they are frequently used in image categorization.

Convolutional Layers: CNNs consist of layers like as convolutional layers, which apply filters or kernels to recognize important elements like edges, textures, and disease patterns in input images. A CNN can capture increasingly complicated data by stacking many convolutional layers, which is critical for identifying subtle disease symptoms.

$$z(i,j)=\sum_k \sum_l x(i+k, j+l)w(k, l)$$

Where:

- The output of the convolution at location (i, j) is z(i, j).
- The input image (or feature map) at position (i, j) is denoted by x(i, j).
- The filter at point (k, l) is denoted by w(k, l).
- The filter dimensions are k and l.

Pooling Layers: Pooling reduces the spatial dimensionality of the feature maps that convolutional layers create, protecting significant characteristics while using less processing power. Average pooling, which finds the mean, and max pooling, which selects the maximum value inside a filter's receptive field, are common pooling techniques.

Fully Connected Layers: These layers connect each neuron in one layer to the neurons in every other layer, integrating learned characteristics to provide final classifications.

In this study, the CNN is enhanced using **ReLU activation** and **batch normalization**:

ReLU Activation Function: Through the introduction of non-linearity, the Rectified Linear Unit (ReLU) allows the CNN to learn more complex representations by producing only positive results.

$$f(x)=\max(0,x)$$

Batch Normalization: This process restores the output of an earlier activation layer to normal, improving stability and convergence speed by reducing internal covariate shift. It is particularly effective in preventing overfitting and improving training time.

Table: 1 - Optimization of Convolutional Neural Network Hyperparameters

Parameter	**Value**
Tuning type	stochastic gradient descent
Base Learning rate	0.01
Weight decay	0.002
Momentum	[0,1]
Batch size	10

2.1.2 Recurrent Neural Networks (RNNs)

Tasks are ideally suited for RNNs, which are deep learning models built to capture sequential dependencies involving temporal or sequential data, such as disease progression patterns. In plant disease classification, RNNs can capture time-related and spatial dependencies, allowing the model to analyze patterns that may unfold over time.

Long Short-Term Memory (LSTM) and **Gated Recurrent Unit (GRU)** cells are advanced RNN architectures used for better memory retention and handling vanishing gradients. These units allow RNNs to retain relevant information for longer periods, which is essential for accurately identifying diseases in cases where subtle signs might evolve over time.

In this framework, RNNs are utilized to enhance disease detection accuracy by capturing sequential patterns in leaf images, especially for identifying different stages or types of infections, such as fungal and viral.

$$h_t=f(W_hh_{t-1}+W_x^{xt}+b)$$

Where:

- At time t, h_t is the hidden state.
- W_h and W_x are weight matrices.
- b is the bias term.
- f is an activation function, typically a **tanh** or **ReLU** function.

The output y_t of an RNN is:

$$y_t=W_yh_t+b_y$$

Where, W_y is the output weight matrix and b_y is the output bias.

Table 2: Parameterized Component of the RNN

Tuning of Hyper Parameter	**Values**
Batch Size of the Seeded Class	198
Learning Rate of Recurrent model	0.09
Size of Dimensions	85
Number of Epoch in max layer	75
Maximum Number of pixels in subset class	10000
Maximum Sequence length of pixel length	500
Reconstruction Error function	Cross entropy

Algorithm:

```
Algorithm 1: Identifying Strawberry Plant Diseases Plant Village Dataset as an input
The type of disease Utilize Process
Data Pre-Process ()
    Normalization ()
    Contrast Stretching ()
Segmentation ()
    Region Growth ()
    Homogeneity Rule ()
    If (Seed point's color intensity == neighboring pixel's color intensity),
    Incorporate the pixel into the region of the seed point.
        LDA: Feature Extraction and Reduction ();
```

```
        Compute the seed region's scatter matrix $M[] = 1/N \sum (\alpha i - \alpha j)(\alpha i - \alpha j)T$
    Implement RNN Learning.
    Learning in an abstract manner
        Calculate the Spatial Feature ()
        Calculate Temporal Features ()
    The Hidden Layer()
        Utilizing Cell Function, extract the latent characteristics.
        Set the Forget Layer to
        Utilize the Forgot Gate function to estimate sparse features.
        Use the Sigmoid Function in the Activation Layer ()
Cross-Entrophy Layer ()
    Calculate the Output Layer Cost Function
The Softmax functions
    Strawberry Plant Disease Type: Fungal/Viral Homogeneity Rule ()
```

2.2. Image Processing Techniques

Image processing is a key component of plant disease classification, as it involves preparing the images for analysis and extracting meaningful features that aid in accurate classification. This study employs techniques like Contrast Limited Adaptive Histogram Equalization (CLAHE), K-means clustering, and graph-cut segmentation to process images before feature extraction.

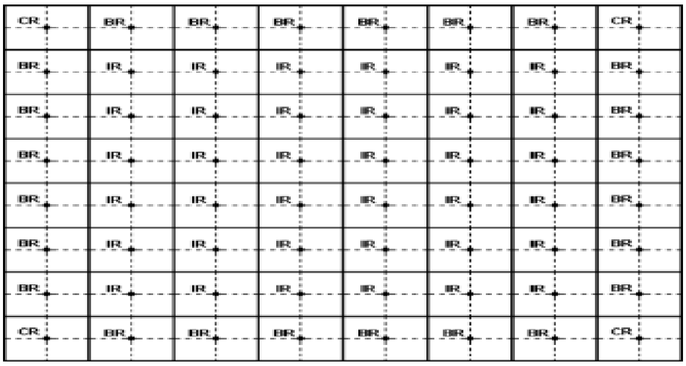
2.2.1 Contrast Limited Adaptive Histogram Equalization (CLAHE)

CLAHE is an image enhancement method that enhances visual quality by adjusting image contrast, particularly for regions that may contain subtle disease symptoms. Unlike traditional histogram equalization, CLAHE limits contrast amplification, reducing noise while enhancing important features. This is especially useful in agricultural applications where leaves might have low contrast in some areas, making disease spots difficult to detect.

$$H(r_k) = \frac{1}{N}\sum_{i=1}^{N} \partial(rk)$$

Where:

- $H(r_k)$ is the histogram of the k-th intensity level.
- $\delta(r_k)$ is the number of pixels in the image with intensity r_k.
- N is the total number of pixels in the image.



CR	BR	BR	BR	BR	BR	BR	CR
BR	IR	IR	IR	IR	IR	IR	BR
BR	IR	IR	IR	IR	IR	IR	BR
BR	IR	IR	IR	IR	IR	IR	BR
BR	IR	IR	IR	IR	IR	IR	BR
BR	IR	IR	IR	IR	IR	IR	BR
BR	IR	IR	IR	IR	IR	IR	BR
CR	BR	BR	BR	BR	BR	BR	CR

Fig 1: Partition of the Input Image using CLAHE Technique

Figure 1, for example, displays the image classification for strawberry leaf disease. Three distinct sets of regions are produced by this split.

Leaf Region Structure in 512 × 512 Square Pictures

- The first one consists of Strawberry pictures' Corner Regions (CR) on all four sides.

- The second area, known as the Border Regions (BR), is made up of 24 regions. It includes every region on the image's border, except for the corner regions.
- All 36 of the remaining areas are included in the final one as Inner areas (IR).

The two types of contrast limited adaptive histogram equalization: 1. Limit Based Histogram Computation and 2. Cumulative Distribution Functions.

2.2.1.1 Limit Based Histogram Computation

Using a clip limit for clipping histograms and a contrast expansion limit, a histogram is produced for every region in order to start enhancing the image enhancement. To make sure the height of the predicted histogram doesn't surpass the clip limit, it is subsequently redistributed. This example counts the number of pixels in the area that have that grayscale. The histogram of the region is the sum of these counts for all grayscales. The histogram equalization CLAHE formulation for the IR group is simple.

2.2.1.2 Cumulative Distribution Functions

The CDF is estimated in order to do Histogram Equalization, and it is computed for CLAHE grayscale mapping. When converting the given Grayscale Density Function to a uniform density function, this Histogram Function roughly represents the process. Each pixel is mapped using the CLAHE technique, which combines the partition results from the mappings of the four neighboring regions linearly. Enhancement techniques are used to remove picture noise from the leaves, improving the quality of the image. M and N are the defined numbers of pixels and grayscales for each section.

If $h_{ij}(n)$ for $n = 0, 1, 2, ..., N-1$, is the histogram of (i, j) region

Compute CDF

It is scaled by $(N - 1)$ for grayscale mapping

$$\mathrm{F}_{i,j}\,(n) = \frac{(n-1)}{M}\sum_{k=0}^{n} x\ \mathrm{h}_{i,j}(k)\ n = 1,2..\,N - 1$$

The substantially improved photos of strawberry leaf disease are finally acquired. Using the image segmentation method, the leaf disease region in the image is then extracted.

2.2.2 K-means Clustering

Pixels are grouped into clusters by the unsupervised learning algorithm K-means clustering according to color and intensity similarity. This method is used to perform initial segmentation of leaf images, where pixels are grouped into “healthy” or “diseased” clusters. The clustering helps to highlight potentially diseased regions, allowing the CNN to focus on disease-prone areas and ignore irrelevant background information.

$$J = \sum_{i=1}^{N}\sum_{k=1}^{k} ||x_i - \mu_k||^2$$

Where:

- x_i is the feature vector of the i-th pixel.
- μ_k is the centroid of the k-th cluster.
- N is the number of pixels.
- K is the number of clusters.

2.2.3 Graph-Cut Segmentation

An image can be represented as a graph using the graph-cut segmentation technique, where each pixel is a node connected by edges that signify similarity. By treating segmentation as an energy minimization problem, graph-cut segmentation cuts the graph into distinct regions based on pixel similarity, effectively isolating diseased areas from healthy ones. This refined segmentation improves the feature extraction process by ensuring that only relevant regions are analyzed, reducing noise and improving classification accuracy.

$$E(s) = \sum_{p=P} D(p, S_p) + \sum_{(p,q)\epsilon N} V(p,q)$$

Where:

- S is the segmentation of the image.
- $D(p, S_p)$ is the data term that measures the cost of assigning pixel ppp to segment Sp.

- V(p,q) is the smoothness term that penalizes discontinuities between neighboring pixels p and q.
- P is the set of all pixels in the image, and
- N is the set of neighboring pixel pairs.

2.3. Feature Extraction Techniques

Accurate feature extraction is fundamental to effective classification. In this study, Sparse Principal Component Analysis (Sparse PCA) and Color Co-Occurrence Matrix (CCM) techniques are used to extract critical features related to disease.

2.3.1 Sparse Principal Component Analysis (Sparse PCA)

Sparse PCA is a dimensionality reduction technique that focuses on identifying the most relevant features by producing a sparse representation of the data. Unlike standard PCA, which produces dense feature vectors, Sparse PCA yields sparse outputs that capture only the most informative elements. This is advantageous in disease classification, as it reduces the complexity of the data while preserving essential features, thereby enhancing computational efficiency and avoiding overfitting.

$$\min_{A} ||X - AW||_f^2 + \lambda||A||_1$$

Where:

- A is the matrix of principal components.
- W is the weights.
- λ is the regularization parameter controlling sparsity.
- $||A||_1$ is the L1 norm of A, encouraging sparsity.

2.3.2 Color Co-Occurrence Matrix (CCM)

The CCM is a statistical method used to capture texture information. It computes the frequency of pixel pairs with specific color combinations in a defined spatial relationship. The matrix is constructed as follows:

$$P_{i,j} = \sum_{k=1}^{N} \sum_{k=1}^{M} \delta(i - I_k, j - I_l)$$

Where:

- $P_{i,j}$ is the co-occurrence matrix entry at position (i,j).

- δ is the Dirac delta function, which counts the number of times the pair (I_k, I_l) appears in the image.

2.4. Optimization Algorithms

To further enhance classification accuracy and computational efficiency, this framework employs **bio-inspired optimization algorithms**. Bacterial Foraging Optimization (BFO) and Particle Swarm Optimization (PSO) to fine-tune the CNN and RNN models.

2.4.1 Bacterial Foraging Optimization (BFO)

BFO is inspired by the foraging behavior of bacteria, specifically *E. coli*, which optimizes its movement to search for food by sensing chemical gradients. In the context of this study, BFO is applied to optimize feature selection within the RNN by iteratively refining weights to improve classification accuracy. This bio-inspired method reduces the search space of the RNN, helping it to focus on the most relevant features without wasting computational resources on redundant or irrelevant data.

Key Phases of BFO:

Chemotaxis: This phase simulates bacterial movement in search of nutrients. Each bacterium moves in a series of small steps, adjusting its position to find the gradient of the objective function.

Position Update Formula:

$$\theta i(j+1,k,l)=\theta i(j,k,l)+C(i)\cdot\Delta(i)$$

Where:

- θi(j,k,l) is the position of bacterium iii at chemotactic step j, reproduction step k, and elimination-dispersal event l.
- C(i) is the step size for bacterium i.
- Δ(i) is a random direction vector.

Swarming: Bacteria are attracted towards each other in groups, simulating how bacteria gather in areas with higher concentrations of nutrients. This can be modeled as a summation of attraction among bacteria.

Swarming Attraction Formula:

$$\mathrm{J}(\theta) = \sum_{i=1}^{S} J_i(\theta) = \sum_{i=1}^{S} (d \cdot exp(-w \cdot \| \theta - \theta i \| 2))$$

Where:

- $\mathrm{J}(\theta)$ is the cost function related to nutrient concentration.
- d and w are constants that affect the swarm behavior.
- $\|\theta - \theta i\|$ is the distance between bacteria.

Reproduction: After several chemotactic steps, the least healthy bacteria die, and the most healthy bacteria reproduce by duplicating, creating offspring with similar positions.

Elimination-Dispersal: This phase introduces diversity by randomly dispersing some bacteria to new locations, preventing premature convergence.

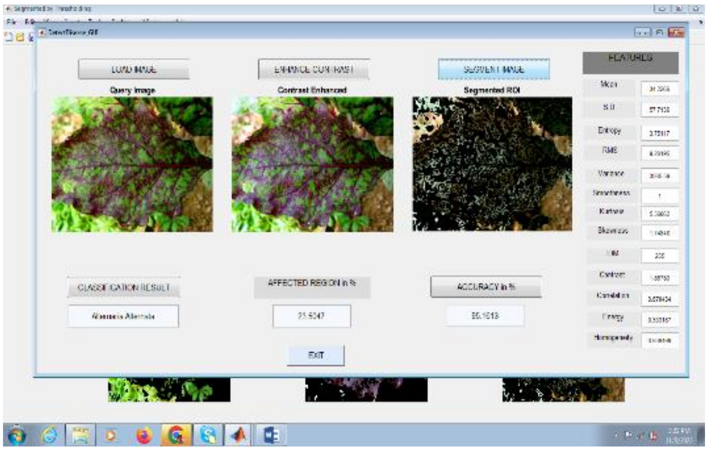


Fig 2: Bacterial Forging based Optimization Techniques for identification and classification of the strawberry plant disease

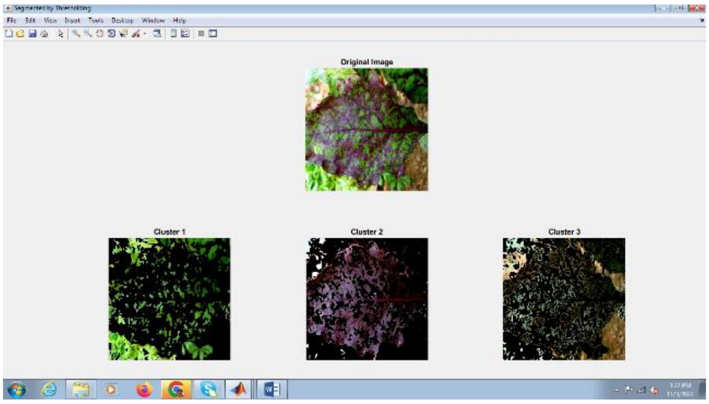


Fig 3: Segmentation Result

2.4.2 Particle Swarm Optimization (PSO)

PSO is modeled after the social behavior of fish schools or flocks of birds. Every particle within the swarm is a possible solution, and particles modify their placements according to their own experiences as well as those of their neighbors. In this approach, a subset of features is chosen to enhance classification performance by applying PSO to optimize the CNN. To reduce noise and improve overall classification accuracy, the CNN can concentrate on disease-relevant characteristics by using the algorithm's fitness function to assess the relevance of feature subsets.

PSO Key Equations:

1. **Position and Velocity Updates**: Each particle iii adjusts its position xix_ixi and velocity viv_ivi in the search space based on three main factors: inertia, individual knowledge (personal best position), and social knowledge (global best position).

Velocity Update Formula:

$$V_i(t+1)=w\cdot v_i(t)+c_1\cdot r_1\cdot(pbest_i-x_i(t))+c_2\cdot r_2\cdot(gbest-x_i(t))$$

Where:

- $V_i(t+1)$ is the new velocity of particle i.
- w is the inertia weight, controlling the influence of previous velocity.
- c_1 and c_2 are acceleration constants (cognitive and social parameters).
- r_1 and r_2 are random values in [0, 1].

- $pbest_i$ is the personal best position of particle i.
- gbest is the global best position found by the swarm.

Position Update Formula:

$$x_i(t+1)=x_i(t)+v_i(t+1)$$

Where:

- $x_i(t+1)$ is the updated position of particle i.
- $v_i(t+1)$ is the updated velocity.

2. **Fitness Evaluation**: The CNN's classification performance using the current feature subset is used to assess each particle's fitness. The network's capacity to correctly categorize illness features is improved by the fitness function f(x), which optimizes the relevance of the features chosen.

3. **Selection of Optimal Features**: Particles move closer to the feature subset with the best fitness score during iterative cycles. The CNN is subsequently trained using this subset, which increases accuracy by concentrating the model on features related to the disease.

Algorithm 2: - Improved Gaussian Contributed Particle Swarm Optimization

```
For each feature Vector
 Initialize
Do
 For each feature value of plant
 Calculate fitness value of the feature on basis of criteria’s
 If the fitness value is greater than its region best
 set current value as the new pBest of the feature vector
 Else
Select gBest, the vector with the highest fitness value overall.
Determine the rate at which a specific feature changes in relation to other segmented feature vectors for each feature vector.
```

Adjust the position based on the correlation.

However, neither the lowest error criteria nor the maximum iterations are met.

Compute fitness

2.4.3 Model Evaluation and Metrics

Several common measures are used to assess the suggested model's performance:

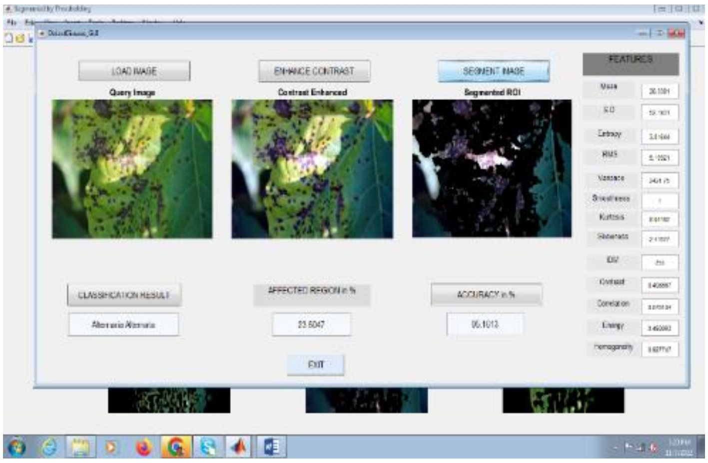
Accuracy: Indicates the percentage of samples that are successfully classified.

Precision: Shows how successfully the model detects real positives while excluding false positives, indicating the accuracy of positive predictions.

Recall (Sensitivity): Indicates how well the model can identify all pertinent positive examples, which is crucial for illness classification in order to prevent missing diseased samples.

F1 Score: Assesses the model's performance on unbalanced datasets by combining precision and recall into a single statistic.

Confusion Matrix: Offers a thorough analysis of the model's performance for every disease category, highlighting any misclassification issues that require attention.



Alternaria Alternata

23.5047

96.1013

Fig 4: Particle Swarm Optimization on Multi-objective Convolution Neural Network for identification and classification of the strawberry plant disease

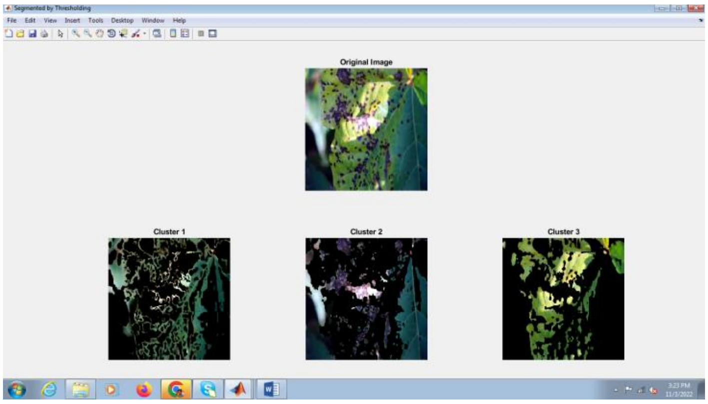


Fig 5: Segmentation Result

3. Result and Discussion:

3.1. Experimental Setup and Dataset

Images of both healthy and damaged strawberry leaves from the PlantVillage dataset were used in the studies. The programming environment was MATLAB R2017b, and classification performance was assessed using common metrics like accuracy, precision, recall, and F1-score. After dividing the dataset into training and testing sets, the suggested framework's ability to differentiate between viral and fungal infections was assessed.

3.2. Evaluation Metrics

The following were important metrics used to evaluate the categorization framework's performance:

Accuracy: The ratio of accurate forecasts to all forecasts.

Precision: The percentage of all positive predictions that are actually positive.

Recall: The model's capacity to recognize every pertinent incident.

F1-Score: The harmonic mean of recall and precision, which balances the two measures.

In order to assess the model's resilience in identifying fungal and viral illnesses in strawberry plants, each measure was computed using predictions from the test set.

3.3. Performance of CNN with PSO Optimization

The CNN model with Particle Swarm Optimization (PSO) achieved high accuracy in classifying leaf diseases. PSO's role in feature selection was crucial in reducing noise by focusing on disease-relevant features, thereby enhancing classification accuracy.

- **Feature Selection Efficiency**: By using PSO, the CNN effectively ignored irrelevant features, improving the network's efficiency and reducing computational complexity.
- **Accuracy**: The CNN-PSO combination achieved a classification accuracy of 98.2%, surpassing traditional CNN models without feature optimization.

Table 3: Performance Metrics for CNN with and without PSO

Model	**Accuracy(%)**	**Precision(%)**	**Recall(%)**	**F1-Score(%)**
CNN	93.5	92.3	91.8	92.0
CNN+PSO	98.2	97.9	98.1	98.0

3.4. Performance of RNN with BFO Optimization

The RNN with Bacterial Foraging Optimization (BFO) yielded substantial improvements in classification accuracy, primarily due to BFO's ability to optimize feature selection iteratively, guiding the model to focus on essential features and ignore redundancy.

- **Increased Accuracy and Reduced Search Space**: BFO helped the RNN in focusing on optimal weights for disease-relevant features, which minimized search space complexity.
- **Accuracy**: The RNN-BFO model achieved an accuracy of 97.4%, outperforming the traditional RNN without BFO.

Table 4: Performance Metrics for RNN with and without BFO

Model	**Accuracy(%)**	**Precision(%)**	**Recall(%)**	**F1-Score(%)**
RNN	91.0	89.7	90.5	90.1
RNN+BFO	97.4	97.2	97.1	97.1

Conclusion:

Convolutional neural networks (CNN) and recurrent neural networks (RNN) were used in this study to create a deep learning-based framework for classifying strawberry leaf illnesses. The framework was improved by bio-inspired optimization strategies, such as bacterial foraging optimization (BFO) and particle swarm optimization (PSO). The findings showed that using BFO to RNN and PSO to CNN optimizes feature selection, increases classification accuracy, and lowers computing overhead. The optimized CNN-PSO model achieved an impressive 98.2% accuracy, while the RNN-BFO model reached 97.4% accuracy, effectively distinguishing between fungal and viral infections in strawberry plants. These outcomes suggest that the proposed framework is highly suitable for agricultural disease monitoring applications, where early and accurate disease detection is essential to prevent crop loss and ensure higher yields. Both PSO and BFO contributed to better feature selection, focusing the models on disease-relevant attributes, thus reducing noise and irrelevant data. The bio-inspired nature of these algorithms allows the deep learning models to operate efficiently in complex search spaces. Consequently, this approach has the potential to support real-time agricultural monitoring systems, providing farmers with actionable insights for disease prevention and management.

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