

DETERMINATION AND SEGMENTATION OF MAIZE PLANT DISEASE USING IMPROVED GAUSSIAN PARTICLE SWARM OPTIMIZATION ON CONVOLUTION NEURAL NETWORK

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Abstract

Maize Plant diseases are the major concerns in the agricultural domain. But significant loss of yield occurs due to awful techniques. Hence automatic and accurate identification of the quantifying disease is very important. Most of the diseases symptoms are reflected in maize leaves, but diagnosis by experts in laboratories are costly and time-consuming. In this paper, Optimization of Convolution Neural Network is carried out by using Improved Gaussian Conducted Particle Swarm Optimization [IGCPSO] for classifying the maize diseases based on optimization. Initially Contrast Limited Adaptive Histogram Equalization [CLAHE] is framed for partitioning of designated image in to particular non-overlapping segments of similar sizes using deep learning architecture. Preprocessed image is segmented into several segments by employing graph cut segmentation process. Segmented disease regions are useful to extract the discriminative features for remaining process. Color Level Co-occurrence Matrix (CLCM) is a new texture based technique employed to extract informative features related to the diseased region. Improved Gaussian Conducted Particle Swarm optimization is emphasized to generate optimal features by identifying and clustering of important points having similar attributes for classification. In proposed model, experimental analysis using plant village dataset improves performance in terms of dice coefficient, sensitivity, and specificity towards disease identification.

Keyword: Convolution Neural Network, Color Level Co-occurrence Matrix, Graph Cut Segmentation, Particle Swarm Optimization, Contrast Limited Adaptive Histogram Equalization

1. Introduction

Maize is vital food crops around the world which is less equivalent to the production output and plant area of rice and wheat. It is used to development of light industrial products and suitable for cultivation in any climatic condition. However, maize plant disease have enhanced owing to variation in the cultivation systems and pathogen changes to diversifies the infections such as , gray leaf spot, dwarf mosaic, northern leaf blight, brown spot , Curvularia leaf spot, southern leaf blight round spot and rust[1]. Leaf diagnosis by experts in laboratories on basis of severity is costly and time-consuming for early detection of plant disease [2]. Hence automatic and accurate identification of the quantifying disease using image processing techniques is very crucial in monitoring the maize leaf on basis of its appearance and symptoms has become essential to control and manage the crop yield[3].

Machine learning architectures plays a important part in plant disease detection. Especially support vector machines (SVMs) is employed in large extent towards the classification of maize leaf diseases on feature selected using genetic based meta heuristic algorithms[4]. The classification method employing Support Vector Machine is capable in classifying the plant disease only with small samples size as it is not supportive to large number of disease plant samples as it produces the reduced recognition accuracy. Many classification techniques such as Fisher Discriminant principal component analysis (FDPCA) and Support Vector Machine (SVM) and Artificial neural network (ANN) has been employed along image segmentation [5]. Image preprocessing techniques are used to enhance the recognition accuracy for large number of samples, it is unable to meet the high recognition accuracy.

Convolution neural network, a deep learning technique has been proposed in this work by optimizing the PReLU activation function to eliminate the network overfitting issues and it has to provide a timely and accurate detection on determining maize plant diseases [6]. The proposed model has capability in enhancing the scope of the computer vision in precision agriculture along increasing the accuracy of plant protection [7]. Further image preprocessing implementing Contrast Limited Adaptive Histogram Equalization, image Segmentation on implementing the graph cut technique, Feature extraction using color level cooccurrence matrix and feature selection using improved Gaussian conducted particle swarm optimization were implemented to enhance the disease recognition accuracy.

2. Related Work

The determination of maize leaf diseases is carried out employing DMS-Robust Alex net, a deep learning technique. Image enhancement and recognition are combined to avoid severe distortion in transformed images. D. Oppenheim al. [8] proposed that learned features are illustrated as the high level abstract representation of the healthy and diseased maize leaf images. It maintains a spatially local and global correlation employing a local and global connectivity pattern among nodes of deep learning layers. ReLu activation unit has used to generate the class label.

A. Krizhevsky al. [9] who proposed a novel Multiscale CNN model based on Alex Net to identify maize diseases. Features extraction is carried out in the convolution layers to avoid the over fitting issues as disease region contains large number of parameters. S. Chetlur al. [10] proposed that Global pooling layer is processed to change the existing fully-connected layer to manage the transfer learning architecture to handle insufficient sample data with epoch tuning to increase the outcomes of maize diseases recognition. N. Srivastava al. [11] proposed Multi scaling with Convolution Neural Network to generate the class labels for the sparse information in form feature set.

3. Problem statement

The determination and classification of various kinds of maize leaf diseases will lead to various challenges on employing deep learning algorithms. These challenges are due to illumination effects, non linear seed points, extracting the discriminating lesions features, over fitting issues, larger training coverage and accumulation. Reconstruction errors with complex hyper parameter tuning are identified by processing with large maize plant disease dataset.

4. Proposed Model

In this section, Convolution Network is modeled along Improved Gaussian Conduced particle Swarm optimization for disease classification is carried out in the plant

village dataset on segmenting the leaf diseases using Region growing segmentation and feature extracted on the segmented regions using Color Level Co-occurrence Matrix is represented in the Figure 1 is as follows

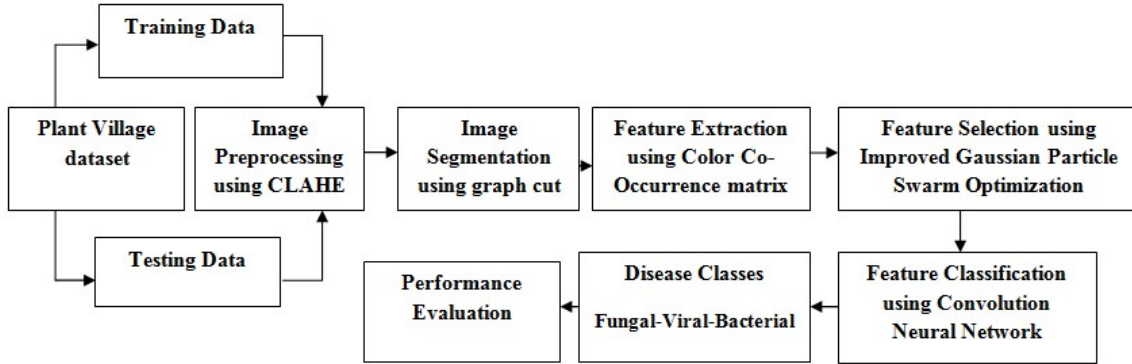


Figure 1: Architecture of Improved Gaussian Particle Swarm Optimization

4.1 Image Pre-processing – Contrast Limited Adaptive Histogram Equalization

Contrast Limited Adaptive Histogram Equalization (CLAHE) has considered as image quality enhancing mechanism to enlarge the contrast of the lesion (disease) features in the images. It is framed on basis of the partition of the expected image to definite non-overlapping regions of similar sizes using architecture of deep learning [12]. CLAHE is framed with partition of the targeted image of equal sizes. For 1028×1028 images, the entire elements is irregularly selected which is identical to 64 attained by similarly image partitioning by 8 in all direction.

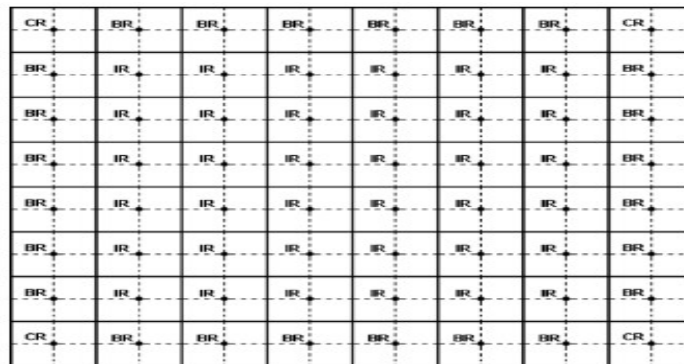


Figure 2: Partition of the Input Image using CLAHE technique

For an instance, the maize leaf disease image segments are represented in Figure 2. These partition outcomes are shown in three various clusters of regions.

Structure of Leaf Regions in a 512×512 Square Images

- The initial outcome is considered as Corner Regions (CR) containing maize image of four sides.
- The next outcome of region is considered as Border Regions (BR) composed of 24 regions including all regions on the image border, excluding the corner regions.
- The final outcome is considered as inner regions consisting of all the remaining 36 regions.

4.1.1 Limit based Histogram Computation

During enhancing the image enhancement, image histogram for every part of the sample has to be determined with respect to range of contrast improvement, a Clipping histogram with a clip limit. Then computed histogram is transformed on a condition that its height should not vary beyond the clip limit. In this process, number of pixels has to be counted for each grayscale in that region. Group of all grayscale counts is considered as region histogram. CLAHE expression of histogram equalization is straightforward for IR group.

4.1.2 Cumulative Distribution Functions

Determination of Cumulative Distribution Function is employed to compute the histogram equalization and for grayscale mapping. These histogram processes of the Cumulative Distribution method are applied to convert into a linear density method from the grayscale density method. On utilizing the CLAHE method, each image pixel is mapped by merging the mapping parts of segment results of the four nearest parts. Further it requires some primary consideration to the regions in CR and BR groups. When the leaves images noises are removed, then image improving techniques are applied to extend the image quality.

The numbers of pixels and grayscales of each region are represented as M and N

If $h_{ij}(n)$ for $n = (0, 1, 2, 3, 4, \dots, N-2, N-1)$ where n is the image histogram of $H(i, j)$ partitioned part

Compute CDF

It is enhanced by $(N - 1)$ for mapping of grayscale images

$$F_{i,j}(n) = \frac{(k-1)}{l} \sum_{k=0}^n x_{h_{i,j}(k)} \quad n = 1, 2, 3, 4, \dots, N-2, -1 \quad [1]$$

Further the highly improved maize leaf disease images are obtained. The following process is to extract leaf disease region in the image employing image segmentation method.

4.2 Image Segmentation – Graph Cut Segmentation

Diseased maize leaves images are segmented into numerous segments by applying graph cut segmentation process. Image Segmentation is applied to segment the disease infected regions of the maize leaves. Graph Cut is implemented for the image segmentation on the features and characteristics of image in form of graph and its dependency [13]. It has two important parts, initially inside segmentation areas which are considered as image region to estimate the image pixel conformity including the image's features, and the regularization of the image pixel to flatten the image pixel boundaries of the image segmented regions (ROI) by placing the image spatial information. Some of commonly affected disease images of maize leaves are shown in Figure 3

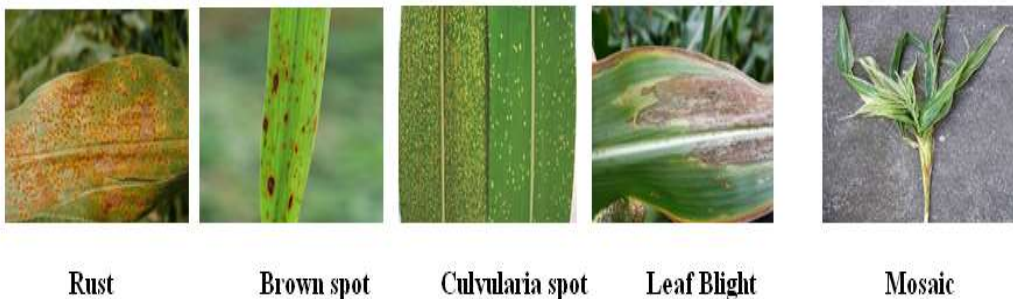


Figure 3: Disease infected Maize Crop leaves

An appropriate dataset of images from plant village dataset with five different categories namely Rust, Brown spot, Culvularia Blight and Mosaic are considered for classification.

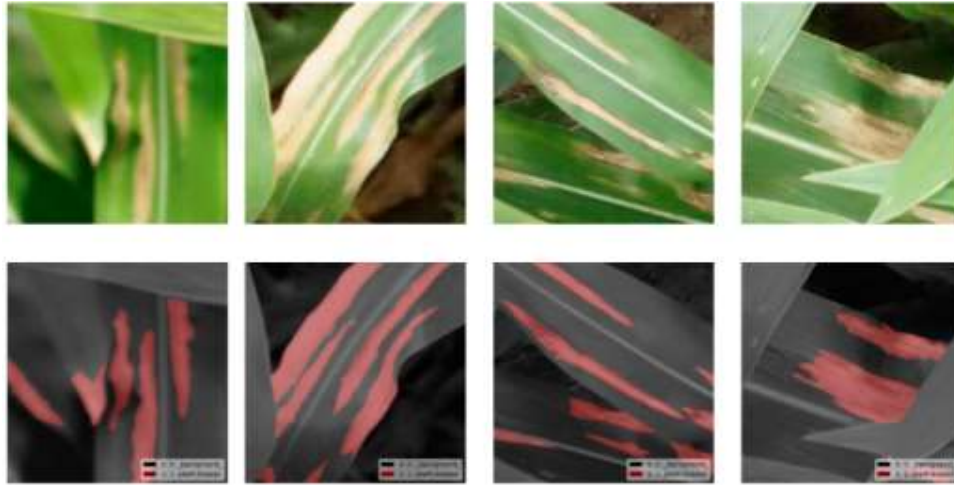


Figure 4: Disease infected segments of the Maize Crop using Graph Cut Technique

Figure 4 represents the disease infected segmentation of the maize disease infected image. Graph cut is represented as constructed graph G_{GC} through a combination of seed set containing the energy minimization process for region of interest segmenting in an image. Transmission of the graph into maximum flow is represented as MF. Graph containing a set of P image vertices represents the pixel and a set of edges H representing the image neighboring vertices where, G_{GC} is indicated as represented

$$G_{gc}=(P,H) +(1-\Delta).O_{reg}(u) \quad [2]$$

Define Map to cluster the pixel of the image. The Map composed of the two vertices is considered as energy function G_{func} and data O_{data} . Typically, a weight factor is offered with two parts; hence, the energy function can be indicated by

$$G_{func}(u)=\Delta.O_{data}(u) +(1-\Delta).O_{reg}(u) \quad [3]$$

Where the weight of the image pixel has the range $0 \leq \Delta \leq 1$ to offer a relative image segments

Energy function of each part can be implemented to map the image data into different segment containing the disease segment of the maize crop for better processing of the disease types in deep learning architecture with recognition accuracy.

4.3 Feature Extraction- Color Level Co-occurrence Matrix

Feature extraction is employed using Color Level Co-occurrence Matrix(CCMs) on the segmented disease leaf segments [14]. Color Level Co-occurrence Matrix is texture based analysis which represents more information related to the diseased region. It produces the texture feature on procedure consists of primary mathematical processes such as Computation of Dependence Matrices and determining Haralick textual features. Dependence matrix of CCM is represented as

$$CCM_{m,n}(I,j) = \sum_x \sum_y^n x \begin{cases} 1 & m(x,y) = i(x,y) = j \\ 0 & otherwise \end{cases} \quad [4]$$

CCMs can be acquired from the collaborative discrete color components. In this article, feature parameter to assess the segmented texture complexity of the image based on CCMs has

been defined. Comprehensive texture based feature extraction technique with utilization of CCM is represented in the dependence matrix in Figure 5 as follows

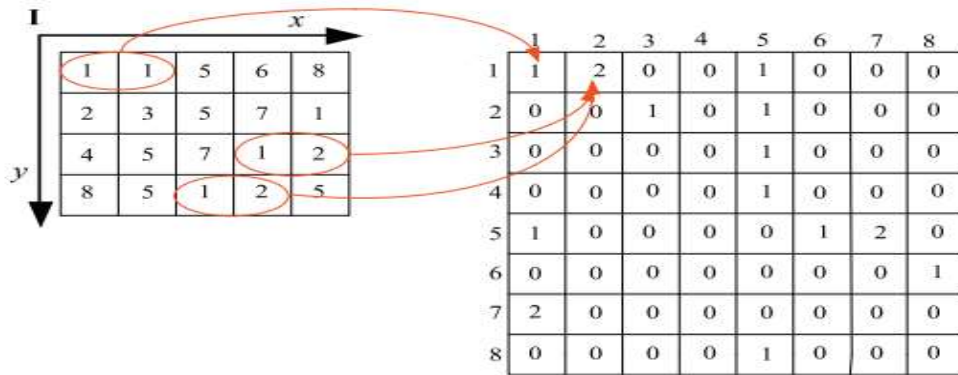


Figure 5: Color Level Co-occurrence Matrix Representation

The most salient features of the disease segment of the image is computed using pixel co-occurrence, however it is required to conform the pixel matrices to decrease the recall value (Every CCM is partitioned as addition of its matrix elements. The elements of the CCM are similar to Haralick features which are extracted on segmented images matrices. Feature considered as entropy, correlation, contrast, variance, inverse difference moment, etc.

4.3.1 Entropy

Entropy (ENT) is considered as computation of weight of the amount of image information. It returns the degree of image texture complexity or disorder. The image complex texture, the higher entropy, and vice versa. Entropy Feature calculation is as follows

$$ENT = \sum_{i=1}^L \sum_{j=1}^L p(i, j) \log \{p(i, j)\} \tag{5}$$

4.3.2 Inverse Difference Moment

Inverse difference moment (IDM) is a calculation of the local homogeneity of a segmented image. The larger value of inverse difference moment, the result is more homogenous to the input image, and vice versa. Inverse Difference Moment is calculated as follows

$$IDM = \sum_{i=1}^L \sum_{j=1}^L p(i, j) \frac{p(i, j) \log \{p(i, j)\}}{1+|i-j|} \tag{6}$$

4.3.3 Correlation

Pixel Correlation is the estimation of equal degree of CCM elements in a matrix row or matrix column portion. Correlation returns the image local texture correlation. When the matrix elements are same and equal, the correlation value is high and vice versa, when the matrix elements changes highly, it is low. Correlation is calculated as follows

$$\text{Correlation COR} = \frac{\sum_{k=0}^{L-1} \{ \sum_{|i-j|=k} p(i, j) \}}{\sigma_x \sigma_y} \tag{7}$$

4.3.4 Contrast

Contrast returns the representation of image and the depth degree of texture groove. The deeper the texture groove, the higher the contrast of the image and the visual effect is increased. Vice versa, the shallower the texture groove, the lower the contrast and the fuzzier the effect.

$$\text{Contrast C} = \sum_{k=0}^{L-1} \{ \sum_{|i-j|=k} p(i, j) \} \tag{8}$$

- **Variance**

Variance which returns image texture roughness considered as the quadratic addition of every element in the image co-occurrence. Rough texture energy represents higher energy, while fine texture energy represents lower energy. Variance is represented as

$$\text{Variance } V = \frac{1}{2} \sum_{k=0}^{L-1} \{ \sum_{|i-j|=k} p(i, j) \} \quad [9]$$

These texture features which consider the texture data of the segmented diseased region of leaf image is further processed using feature selection to generate the relevant feature for disease classification.

4.4 Feature Selection -Improved Gaussian Behaved Particle Swarm Optimization

Feature Selection is to select the optimal features for disease classification using Improved Gaussian behaved Particle Swarm Optimization. It is a metaheuristic optimization algorithm [15]. Gaussian Contributions in PSO is to determine the normal distribution of the extracted features and to remove abnormal features in the data distribution on basis of fitness computation. Fitness computation is carried out along with the calculation of the pbest and gbest on position and velocity of the feature vectors

Algorithm 1: Improved Gaussian Behaved Particle Swarm Optimization

```

For each feature Vector
  Initialize
Do
  For each feature value of crop
    Calculate fitness value of the feature on basis of criteria's
    if the fitness value is good than its region best
      set present value as the new pBest of the feature vector
    Else
      Select the vector with the best fitness value of all as gBest
  For each feature vector
    Calculate velocity of the changes of particular feature with other segmented feature vector
    Update position according correlation
  While large iterations or less error criteria is not attained
  Compute fitness
    
```

The feature selection methods produce the optimal weighted features through gaussian distributions. Those features are employed for effective recognition and classification of the various bacterial, viral, fungal and worm disease using CNN optimization along with PReLU activation function.

4.5 Feature Classification: Optimized Convolution Neural Network

Optimized Convolution Neural Network is utilized to classify the feature of the segmented infected regions into various classes of diseases. In order to perform classification using Convolution Neural Network, optimization is carried out in activation layer of GoogLeNet model with PReLU function. In this work, more parallel convolutional layers of the segment with a size of 2×2 and 5×5 and max pooling layer for the acquiring of dissimilar features continuously has been included.

Specifically, the proposed deep learning incorporates two fully connected layers, two Convolutional layers, Activation layer, Soft max layer and a loss layer. Next, every model

composed of Convolutional layer, pooling layer and a activation layer with *PReLU* operation. The correlation among the various pooling layers will be combined to yield high recognition accuracy. A dropout operation with an high probability output can reduce overfitting issues of CNNs. The *PReLU* function will employ the network to learn similar sparse features.

4.5.1 Convolution Layer

Convolution layer is the vital operation of the Neural Network. The convolution layer computes the kernel to be mapped to segmented pixel for the continuous sliding convolution window. In proposed architecture, feature group is convoluted by many input feature graphs. For input x of the i th Convolutional layer, Feature Map is calculated as

$$H_{ic} = f(w_i * x) \quad [10]$$

Where H_{ic} convolution operation considers the convolution layer kernels, and f considers the activation function.

$$W = [W_i^1, W_i^1, W_i^1, \dots, W_i^k] \quad [11]$$

K is the number of convolution kernels.

Particular kernel W_i^k is an $M * M * N$ weight matrix with M region is the window size and N is the number of channels input.

4.5.2 Activation Layer

Activation layer uses the *PReLU* is an activation function. It is non linear function which uses sigmoid and tanh function to compute the activate class for the disease types with fungal, viral and bacterial categories.

4.5.3 Pooling Layer

On increase of the Convolutional layers for the feature processing, the network parameters will enhanced the model for classification. The pooling operation can minimize the number of network parameters to classification in all regions by computing the statistical characteristics of a region in order to consider the whole region's characteristics.

4.5.4 Drop Out layer

Dropout layer is to reduce the training images in the neural networks by intercept the synergies of definite elements. For each input image sample, the illustrating network representation is dissimilar, but every dissimilar network structures allocate the latent nodes weight at the similar time, so that dissimilar samples represents to dissimilar models. It intercepts overfitting issues and enhances the model generalization through a dropout process and it attached to the Google net structure in testing phase.

4.5.5 Loss Function

The loss function is compute the discrepancy among the determined results is computed using stochastic gradient descent (SGD) algorithm.

$$L(f) = \frac{1}{n} \sum_{k=0}^{L-1} \{ \sum_x [y \log(p(i, j)) + (1-y) \log(1-P(i, j))] \} \quad [12]$$

Where W represents the weighting matrixes of the Convolutional layer and fully connected layers, n represents the dataset training samples, i is the rank of training images, and k is the class index. Network training determine the output of W that reduces the loss method E where W is iteratively iterated as which is represented as

$$W_k = W_{k-1} - \partial(\partial E(w)/\partial w) \quad [13]$$

Where W is the image learning rate is a considered as vital parameter which computes the step size of the learning model. The k is the class index

4.5.6 Hyper Parameter Tuning

In this part, GoogLeNet models' hyper parameters are tuned to obtain the high recognition accuracy. It changes the base learning rate. Model optimization is carried out using stochastic gradient descent technique. Further batch training method will partition the training set and the testing set into numerous batches. Each batch composed of training 10 images.

Table 1: Hyper parameter Tuning of the Convolution Neural Network

Parameter	Value
Hyper Tuning type	Gradient Descent
Learning rate	0.01
Weight decay	0.002
Momentum	[0,1]
Batch size	10

Algorithm 2: Optimized Convolution Neural Network

Input: Optimal feature set $F = \{x_1, x_2, \dots, x_N\}$
Output: Target Disease Label $T = \{T_1, T_2, \dots, T_N\}$
Process
 For ($J = \text{Feature Vector}[i], J++$, $j < \text{threshold}$)
 Compute Convolution () for segmented feature as 3×3 layers for $H_{ic} = f(w_i * x)$
 Convolution value = Convolution Window (F)
 Compute Max pooling () for Convolutions
 Reduce (convolution Value)
 Max pooling value = Reduced Convolution Window containing Feature (F)
 Dropout () for overfitting
 Eliminate the feature with hidden segments
 Loss function ()
 Employ stochastic gradient descent (SGD) algorithm for sliding window of convolutions
 $L(f) =$ Weighted matrix of the convolution on eliminating error
 Hyperparameter tuning ()
 Softmax () to generate the classes with batch size and learning rate

 Class Labels = disease region of the plant and Disease type of maize Plant- Viral / Fungal

5 Experimental Results

Experimental assessment is explored using village plant dataset to classify the maize plant disease into three different classes based on test images. The proposed model is simulated in MATLAB (version 2018 b). In this processing, dataset of 27000 images are partitioned into train and test. Validate partitions such that 60 percent of the data used for training, 20 percent of the data used for validation and rest of 20 percentages of data used for testing. For experimental validation, 10 fold validations is employed as confusion matrix to enhance the performance of classification and segmentation of the disease region as shown in Figure 6 and Figure 7.

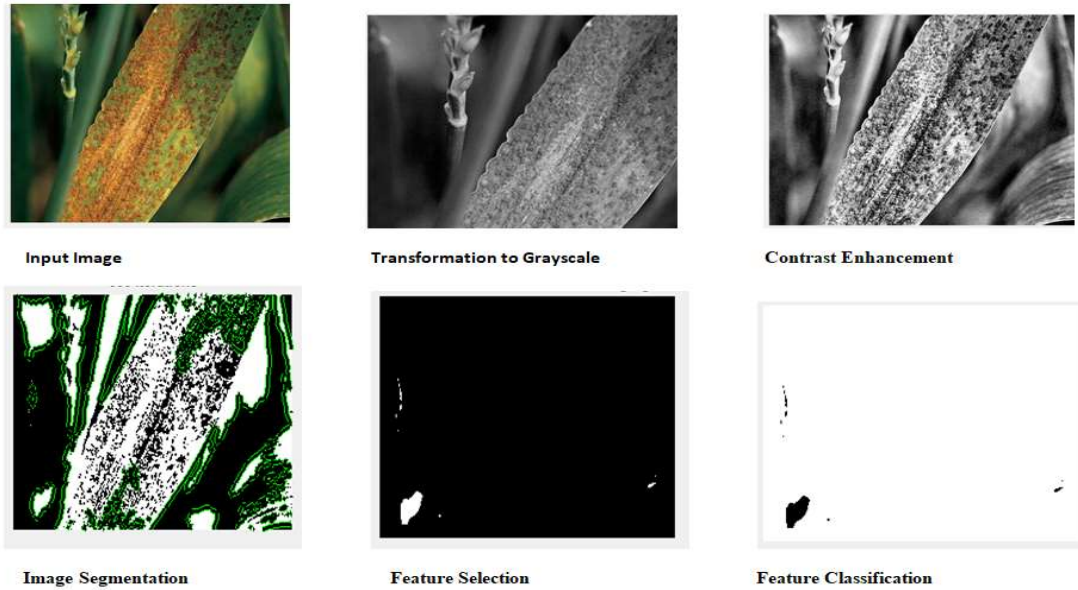


Figure 6: Maize Rust Disease Classification

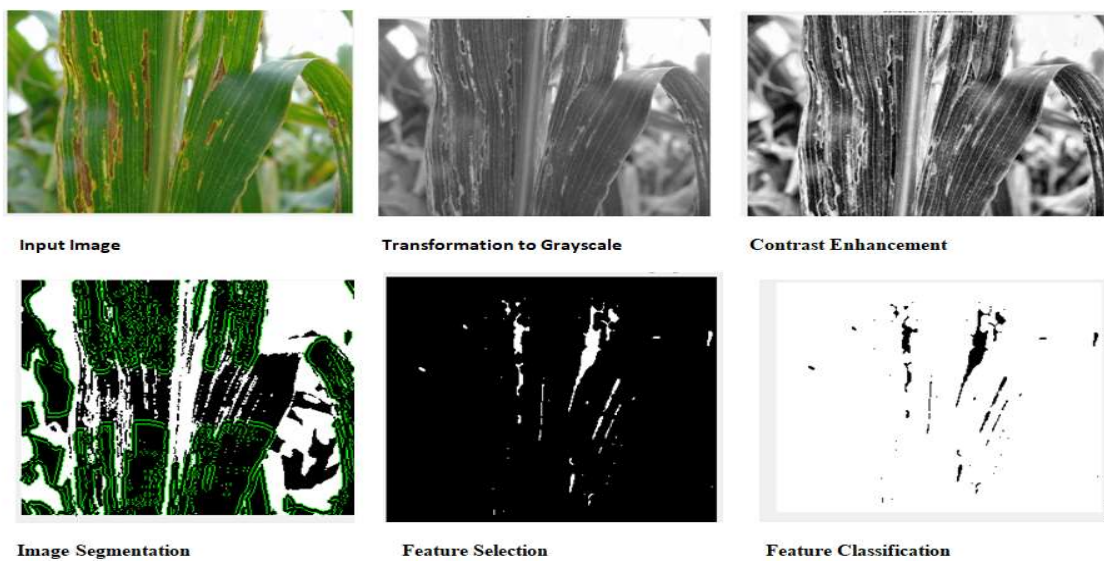


Figure 7: Maize Blight Disease Classification

In this work, Google Net architecture of CNN is used to achieve higher detection accuracy on recognition of maize plant disease. Segmented part of plant can be classified into viral, bacterial and fungal category. The model outcomes the good output on determining the varied size disease region using improved Gaussian distribution and its characteristics using Particle Swarm Optimization.

5.5 Performance Evaluation metrics

The performance of the model has been evaluated with Dice coefficient, sensitivity, and specificity against the state of art approaches for maize plant lesion detection with volumetric changes of the plant on various stages of the plant growth. The analysis on different test samples on plant village dataset on identifying the disease type using deep learning technique has been evaluated on dice coefficient, sensitivity and specificity in the Table 2.

Table 2: Performance Evaluation of Autonomous Segmentation Techniques

Technique	Diseases	Average Dice Coefficient (%)	Average Sensitivity (%)	Average Specificity (%)
Bacterial foraging optimized Recurrent Neural Network	Rust	92.72	94.87	93.78
	Brown spot	94.72	94.28	94.33
	Culvularia leaf spot	89.22	90.34	90.02
	Leaf Blight	93.51	93.46	93.48
	Mosaic	87.62	88.95	88.27
	Healthy	95.31	94.27	94.78
Improved Gaussian Particle Swarm Optimization on Convolution Neural Network	Rust	98.95	98.47	98.67
	Brown spot	98.03	98.6	98.01
	Culvularia leaf spot	99.16	97.17	97.07
	Leaf Blight	96.78	97.52	97.05
	Mosaic	91.14	95.12	96.25
	Healthy	99.2	98.44	98.08

It explains that presented architecture partitions plant disease segments accurately. Convolution neural Network with Particle Swarm Optimization provides high performance against Recurrent Neural Network. The proposed architecture outcomes the enhanced performance without using any parameter tuning. The values from table shows that Improved Gaussian particle Optimization gives results 99.2 %, 98.44 %, 98.08 % for Dice coefficient

measure, Sensitivity measure and Specificity measure respectively compared with Bacterial foraging Optimized Recurrent Network.

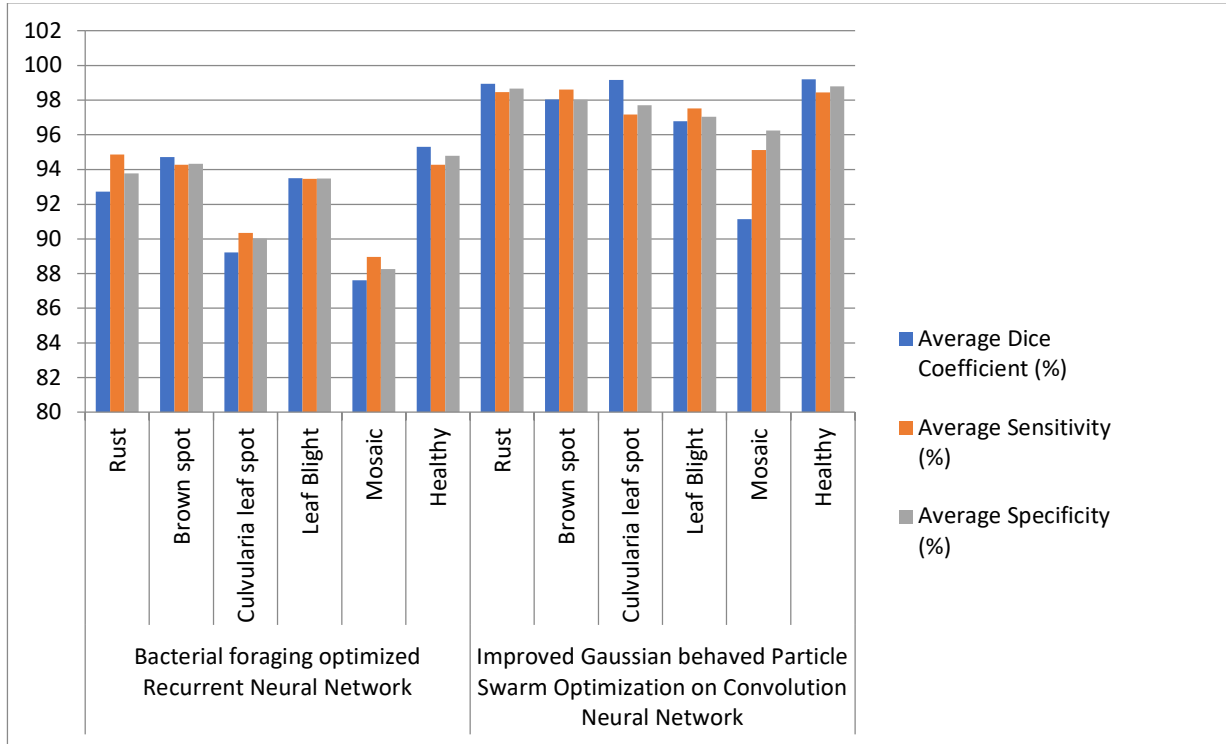


Figure 8: Performance Comparison

Improved Gaussian behaved Particle Swarm Optimization produces elevated Dice Coefficient measure, Sensitivity measure and Specificity outcome when compared with Bacterial foraging optimized Recurrent Neural Network with disease determination using deep learning architecture as illustrated in the Figure 8. On basis of the sensitivity measure, optimization of the feature extracted using the particle swarm optimization yields better classification outcomes. Performance of the architecture on training data results good with high specificity value. Hence for testing phase, improvement of the classification accuracy is carried out by changing the depth of the network and size of the kernel using hyper parameter tuning.

Conclusion

A new framework represented as Improved Gaussian Particle Swarm Optimization with convolution neural network for classifying the maize plant diseases is designed and implemented. Initially image is preprocessed using CLAHE and segmentation through the graph cut on disease lesion regions. Segmented region is employed for feature extraction and selection using Color level co-occurrence matrix and Particle Swarm Optimization to obtain the quality feature for classification. Proposed model is capable to determine the type of the plant disease with high recognition accuracy with less mean squared error. It outputs the quality outcomes on various size of the image, image defects and variation in plant anatomy and changing contrast of the image.

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