

DISCRIMINATIVE MARGINALIZED CONVOLUTION NEURAL NETWORK FOR CLIMATE AND FUNGUS DISEASE SPECIFIC CROP DISEASE CLASSIFICATION

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Abstract

Crop Disease due to viral, fungal and bacterial types impacts the yield potential of the crop and economic damage to the farmers. Especially Anthracnose is group of fungal diseases typically cause dark lesions on leaves. It is difficult to phytosanitary control and will easily spread through the air and abundant presence in various climates especially tropical and continental which causes the loss of numerous crops and thus leads to large economic damage to farmers. Classification of crop species may lead to misinterpretations. It is to develop an efficient Spectral Angle Mapper system for the detection of anthracnose and other fungal diseases in the crops using hyperspectral images. For this purpose, Discriminative Marginalized Convolution Neural Network has been employed as classification methods on spectral data. The control measures can be improved by mapping the occurrence of spectral signatures of fungal disease specific end members. In this paper, Crop Disease Classification is carried out with respect to fungal disease on various climatic conditions. Initially image preprocessing is carried out to eliminate the spectral noises. Preprocessed image is processed using independent Component analysis to extract the endmembers of the spectral band representing the various crop species in the different climate regions like tropical and continental. Extracted spectral band is processed for spatial correction and the extreme spectral variability detection through spectral purity index. Spectral member of various spatial regions is selected using genetic algorithm. Finally Discriminative Marginalized Convolution Neural Network is employed to generate the Spectral angle mapper to classify the spectral band of the specific crop species in various climates on aspect of Chlorophyll and Nitrogen spectral values of the end members. Proposed classifier uses the multiple layer of network to discriminate the crop diseases related to fungal disease as healthy, moderately infected, and severely infected plants on 14 crop species on. Finally utilization of the disease index represents the severity of crop. The experimental results of the proposed model are evaluated on employing real-time hyperspectral image data sets acquired from Indiana region in the North Karnataka on various climates. Performance of the proposed model is compared with conventional approaches with respect to precision, recall and f measure.

Keywords: Hyperspectral Image, Convolution Neural Network, Fungal Disease, Crop Classification, Genetic Algorithm, Independent Component Analysis, End Member, Vegetation Index

1. Introduction

Agricultural food crops consumption is increasing in all parts of the world due to several health benefits and natural ingredients. Various developments in agriculture place it as second

largest economy around the world[1]. Food Security has to be increasingly addressed to increase the food production as various bacterial, fungal and bacterial diseases are accelerating in the plant and crops due to climatic changes. Nowadays a large number of researches towards controlling and preventing the crop diseases is influencing among many researchers. Especially considerable research has been carried out to identify the severities of the crop disease as it highly influences the crop growth and yield on basis of the plant phenotype and plant pathology[2].

Plants are affected by disease causing pathogens and it is characterized on disease symptoms such as reduction of biomass, decrease in leaf index, lesion due to infection and destruction of the pigment system. Monitoring and early detection of the plant diseases is highly necessary to farmers. Compared to various detection approaches[3], Hyperspectral images acquired using remote sensing technologies has numerous advantages in monitoring the extensive regions as it is considered as non-invasive technique[4]. In particular, images identify the symptomatic and asymptomatic plant diseases based on the spectral signatures which are considered as endmembers which is mixed into the pixels.

The electromagnetic spectrum ranges of hyperspectral sensors mainly concentrate on VIS-NIR (400–1000 nm) and sometimes contain a short wave infrared range (SWIR, 1000–2500 nm). These sensors could acquire spectral information from hundreds of narrow spectral bands. These narrow wavebands have high sensitivity to the subtle plant changes caused by diseases and make it possible to distinguish different disease types and perform early asymptomatic detection. Specifically it is mandatory to develop an efficient Spectral Angle Mapper system for the detection of anthracnose and other fungal diseases in the crops using hyperspectral images[5]. For this purpose, Discriminative Marginalized Convolution Neural Network has been employed as classification methods on spectral data. The control measures can be improved by mapping the occurrence of spectral signatures of fungal disease specific endmembers[6].

Crop Disease Classification is carried out with respect to fungal disease on various climatic conditions. Initially image preprocessing is carried out to eliminate the spectral noises. Preprocessed image is processed using independent Component analysis to extract the endmembers of the spectral band representing the various crop species in the different climate regions like tropical and continental. Extracted spectral band is processed for spatial correction and the extreme spectral variability detection through spectral purity index. Spectral member of various spatial regions is selected using genetic algorithm.

Finally Discriminative Marginalized Convolution Neural Network is employed to generate the Spectral angle mapper to classify the spectral band of the specific crop species in various climates on aspect of Chlorophyll and Nitrogen spectral values of the end members. Proposed classifier uses the multiple layer of network to discriminate the crop diseases related to fungal disease as healthy, moderately infected, and severely infected plants on 14 crop species. Finally utilization of the disease index represents the severity of crop.

The remaining part of the article is categorized into following sections; section 2 provides the detailed background analysis of the hyperspectral data classification architecture in terms of machine learning paradigms. Section 3 models the proposed deep learning architecture to generate the new spectral indices for crop diseases and it is formulated with various layers.

Experimental analysis and performance analysis of the proposed model is processed in the section 4. Finally section 5 concludes the research article.

2. Related work

In this part, numerous conventional models have been employed for hyperspectral data classification for crop disease on utilizing machine learning model to the spectral features of the data has been detailed as follows

2.1. Biologically Interpretable Two Stage Deep Neural Network for Crop Disease Classification

In this literature, Spectral–spatial-based deep learning models have been employed for hyperspectral image classification especially for vegetation recognition and classification. In Particular, Biologically interpretable two stage deep learning model is capable of classifying the hierarchical structures of the crop species based on the two stages of spatial and spectral features which is represented as low level and high level features and those extracted features are encapsulated to achieve the high classification accuracy and reduced complexity [7].

2.2. Crop Species Classification using restructured Convolution Neural Network

In this literature, a new crop disease spectral index has been constructed to classify the crop disease effectively. In Particular, restructured convolution neural network has constructed to determine the chlorophyll and nitrogen value of the crop region. Inclusion of Sparse Multinomial Logistic Regression and Joint Spectral distribution generate the crop disease index to the spectral signature of the crop with reference to biological properties of the pathogens in the plant. Further complexity of the disease analysis is reduced using the end member's extraction and selection techniques using particle swarm optimization [8].

3. Proposed Model

In this section, a new deep learning architecture named Discriminative Marginalized Convolution Neural Network has been designed for classifying the crop disease on processing of hyperspectral images. Proposed architecture has been modelled to detect the particular crop disease on basis of severity of the spectral signatures with respect to fungal type of the disease occurring on the various component of the crop. Figure 1 represents the architecture of the proposed methodology

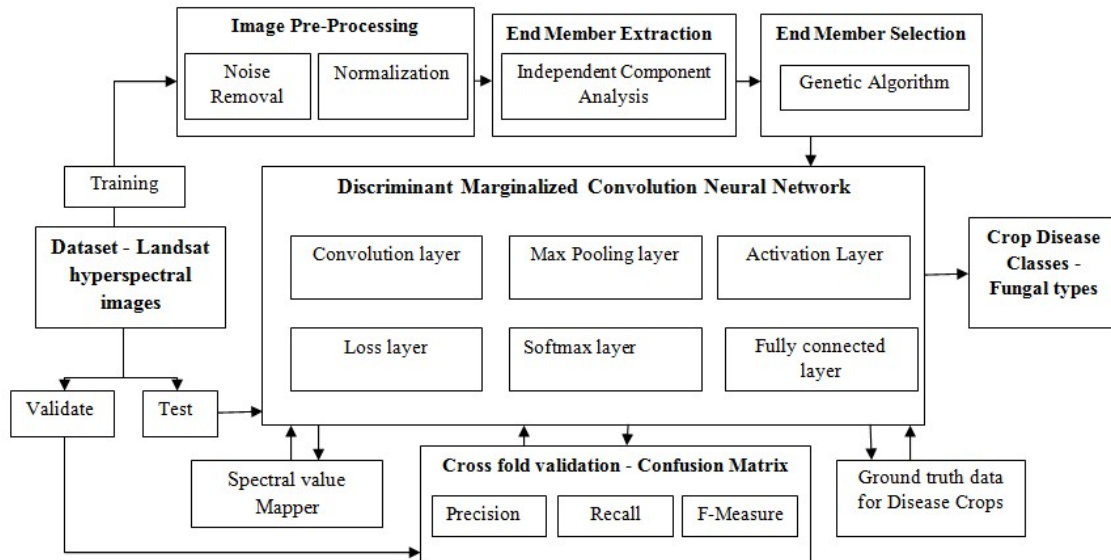


Figure 1: Architecture of the proposed methodology

3.1. Image Pre-Processing technique

Hyperspectral image pre-processing is carried out to increase the contrast and to reduce the noise of the image. Atmospheric calibration, geometric correction, and spectral calibration are important contrast enhancing techniques to reduce the geometric distortion and the surface reflectivity error caused by atmospheric scattering and absorption along spectral normalization. Hyperspectral Image is represented as

$$HS = \sum_{p=1}^P x_{ip} s_p + w$$

Where p is the number of endmembers in the image, x_{ip} is the abundance fraction and s_p is the pure spectral signature w is noise. Hyperspectral images usually represented as three dimensional images in that two dimensions represent the spatial information and third dimension represents the spectral information. In spatial domain, there exists large number of local and global redundancy [9]. Degradation model of removing noise is represented as

$$\{x, s\} = \arg_{x, s} \min_{\frac{1}{2}} \|HS - w\| + \lambda j_1(w)$$

In this λ is the parameter to balance the noise on regularization $j_1(w)$. Finally all patches are summarized and averaged to create the restored HSI.

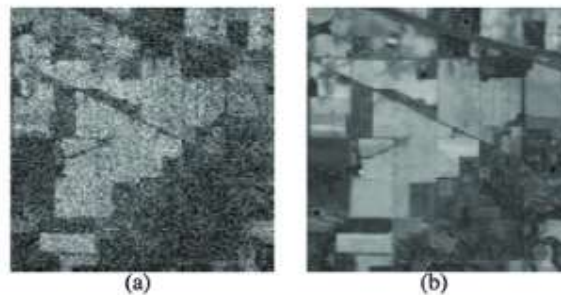


Figure 2: Noise Filtered Hyperspectral Image

3.2. End Member Extraction – Independent Component Analysis

Retrieving of the pure plant disease spectral signatures and their abundance fraction with minimum prior knowledge is termed as hyperspectral unmixing. N finder is the fast iterative pixel purity index. Nonnegative Matrix factorization estimates the abundance fractions and the endmembers in each pixel by iteratively minimizing a cost function[16]. It uses the constraints to force the abundance fraction to achieve abundance sparsity or spectra to achieve the spectral smoothness on each pixel. Further homogeneity based end member extraction is to compute the pure pixel spectra in the hyperspectral images on employing the criteria and clustering is applied to gather the similar spectral signatures.

Homogenous criteria $h_{ij} = \max(A_{ij}) - \min(A_{ij})$

It is mandatory to compute the pure pixel instead of computing the abundance fraction. Let consider A_{ij} as sub pixel to the y_{ij} hyperspectral pixel.

If (A_{ij} contains homogenous grey level)

y_{ij} is pure pixel

else it is considered as normal pixel

Spectra set L_h is the set of the similar sub images A_{ij}

Spectral Angle is to extract the several pure pixels that represent particular crop or diseases. Spectral angle extract the all the spectra corresponding the particular crop or disease.

Spectra Angle threshold is given as T_{sa}

First Cluster contain as first spectra of the list L_h on the condition that spectral angle value SA is less than spectral angle threshold T_{sa} . Spectral angle value is computed between the first spectra and other spectra in the list L_h . It is generated on sorting the spectra set L_h . Each spectra in the list is added to various separate cluster on the condition that spectra in the list is less than spectral angle threshold T_{sa} and list become empty. Cluster containing spectra is considered as crops are represented as pure pixels in the image.

Endmember matrix S_h is constructed with spectra of each cluster having best homogeneity criterion value.

Abundance matrix X_h is estimated with Non Negative Constrained least Square Algorithm

3.3. End Member Selection on basis of Spectral characteristics –Genetic Algorithm

Extracted spectral band is processed for spatial correction and the extreme spectral variability detection through spectral purity index. Spectral member of various spatial regions is selected using genetic algorithm. Spatial correction is to estimate the changes of the spatial reflectance value on the particular spatial location. Further spectral variability of the endmembers on the particular endmember determines the changes of the object. In order to construct the spectral purity index, genetic algorithm is employed to select the appropriate endmember for construction.

Spectral purity index of the plant image is computed using fitness computation. Initially the population of the spectral endmembers extracted is represented as population. Population is employed to operations like selection, crossover, mutation operation. Operation

iterates until the termination condition. Fitness function is constructed to select the suitable spectral end member to the spatial features. Optimal endmember is used to construct the spectral purity index.

Initialize the endmember as population P

Fitness function modelling using roulette wheel selection

Compute the Spectral Reflectance of the endmember S_R

Threshold = High Reflectance value of end member S_r^t

Fitness function (Select Endmember $E >$ specified threshold S_t)

$$\text{End member Fitness } F(t) = \sum_{k=0}^n \binom{S_r}{S_t} E^k P^{S_r}$$

High Spectral reflectance Endmember of the particular spatial location is selected and selected spectral reflectance value of the spatial endmembers of various climate changes is obtained. Spectral purity index is generated with spectral endmember of the plant on changes of the climate .

Spectral Angle Mapper – Spectral value Change Detection

Spectral angle mapper considered as change detection network which aimsto map the spatial correlated endmembers and identify the changes of the spectral changes of the endmembers on basis of temporal changes. Spectral correlated endmember of the spatial endmembers of the extracted endmembers of the training images. Spectral angle mapper create a index to the spectral endmember of the plant disease on the specified climate. Spectral angle mapper helps to assign the disease to the particular endmember to the particular climate effectively. It acts efficient discriminator of the hyper spectral images.

3.4. Crop Disease Classification – Discriminative Marginalized Convolution Neural Network

Crop Disease classification on various climate on geographical location is classified using the discriminative convolution neural network to the fungus disease. Discriminative marginalized convolution neural network is modelled with spectral angle mapper along the activation function of the fully connected layer. However the convolution and pooling layer reduce the endmember and generate the feature map. Those feature map is classified using softmax classifier and activation function in fully connected layer with reference to spectral angle mapper.

- **Convolution Layer**

Convolution layer reduces the spectral endmember of the images using filter and kernel. It generates the optimal endmembers on processing the end member matrix with kernel matrix to produce the feature map on the spatial correlated end members. Further it is considered as activation map to the fully connected layer. Representation of the convolution operation is illustrated with spectral signatures of the endmember on the matrix form

1	1	1	0	0
0	1	1	1	0
0	0	1	1	1
0	0	1	1	0
0	1	1	0	0

1	0	1
0	1	0
1	0	1

=

4	3	4
2	4	3
2	3	4

Endmembers Matrix

Kernel Matrix

Feature Map

Spectral Endmembers is converge into spectral map to the spatial and temporal changes of the spectral values to seasonal and climatic variations. Map correlates the spatial endmembers to the spectral endmembers. Convergence map is generated using epoch value fixed to end members and map is normalize the endmembers using the ReLu activation function to contain the linear end members for classification.

- **Pooling layer**

In this layer , max pooling is employed to further reduce the spatial dimension of the endmember. It is considered as spatial pooling which contains the spatial endmembers. In this layer, spatial endmembers are down sampled by retaining only the highly weighted endmembers which contains the high reflectance value. Further it connect the spatial endmembers with spectral endmembers as feature map to increase the model generalization. Pooling operation is represented as

4	3	4
2	4	3
2	3	4

=

4	3
3	4

Convolved feature

Max pool Features

Fully Connected Layer

Fully connected layer contains the spectral angle mapper, feature map, softmax layer, activation layer and loss layers to discriminate the feature map into discriminate plant classes as healthy and non healthy classes. Softmax layer contains multiple decision making strategies and constraints to classify the plant classes[17]. Spectral angel mapper integrated with softmax operation to discriminate the feature map effectively. Generated classes eliminates the over fitting issues on incorporation of the flattening layer. Fully connected representation of the endmember classification is as follows

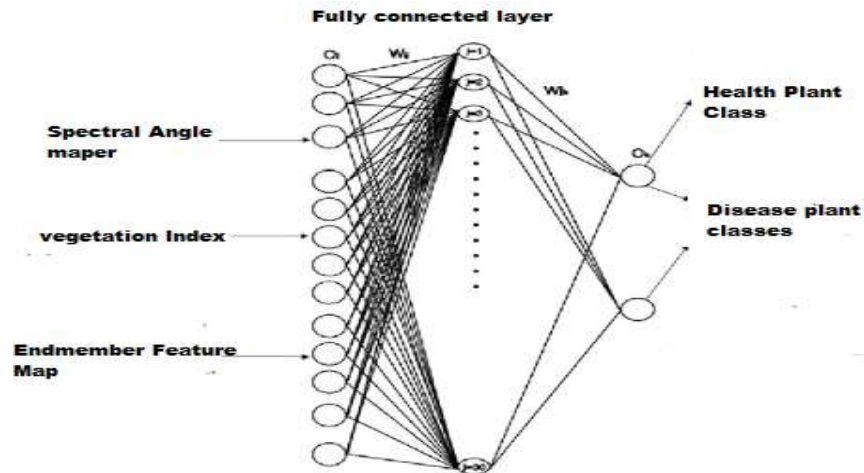


Figure 3: Fully connected layer of the DCNN

Fully connected layers also validate the model reliability. Further loss layer is integrated in fully connected layer to reduce the spatial variance on the classes of the endmembers. The closest approximation of the testing endmembers may be from various classes, which illustrates that the minimal residual may be obtained from numerous classes. The final classification result is generated by integrating the results based on the voting rule represented in the figure 3.

Algorithm 1: Discriminative marginalized Convolution Neural Network

Input: Spectral angle Mapper, Spectral Endmembers and Spatial Endmembers

Output: Plant classes { Healthy and Fungal Plant disease)

Process

Convolution layer ()

Generate the feature map on processing Spectral Endmembers with spatial endmembers using kernel

Normalized Endmembers as feature map

Max Pooling Layer ()

Reduce Feature map on the spatial features

Fully Connected layer ()

Discriminate(endmembers or feature map)

Activation function (Spectral angle Mapper)

Flatten layer () normalizes the Spectral features on over fitting issues

Softmax layer()

Classification Strategies (Spectral angle Mapper | Spectral Endmember

Loss layer ()

reduces the spatial and spectral variance on the classes

Output layer ()

Classify (Spectral map of Endmembers)

Class = (Anthracnose, Leafspot, Rust, Canker, Mildew)

Finally, proposed model based on the convolution neural network has been generated to plant classification with respect to the spectral angle mapper.

4. Experimental Results

In this section, performance analysis of the proposed architecture results has been evaluated using Indian Pines dataset on the various climatic conditions [14]. In this work, optimal hyper parametersto the current architecture have been set for the crop disease classification on basis of leaf spectral reflectance value of the crop. The model is simulated in matlab software on partitioning the dataset into training data containing 80% and testing data containing 20% to validate the proposed architecture.

In this model, 5 fold cross validation is carried out to enhance the accuracy of the model [15]. The hyper spectral images is processed to identify thefungal disease occurrence in the various agriculture crop on basis of the spectral values of the endmembers extracted on particular spatial location.Discriminative Marginalized Convolution Neural Network hyper parametersetting has been represented in the table 1

Table 1: Hyper parameter Setting of the model

Parameter	Value
Activation Function	ReLu
Learning rate	10^{-6}
Kernel Size	3
Loss function	Cross Entropy
Batch size	14
Max epoch	50

Spectral angle mapper[18] has been used to identify the endmember variations on the specified spatial location and specified climate. It is generated as mapper to discriminate the endmember in the fully connected layer of the proposed architecture. Softmax layer incorporates the spectral angle mapper towards efficient discrimination of the fungal disease on the various climate. Figure 3 represents the performance of the proposed architecture against conventional approach with respect to precision [15].

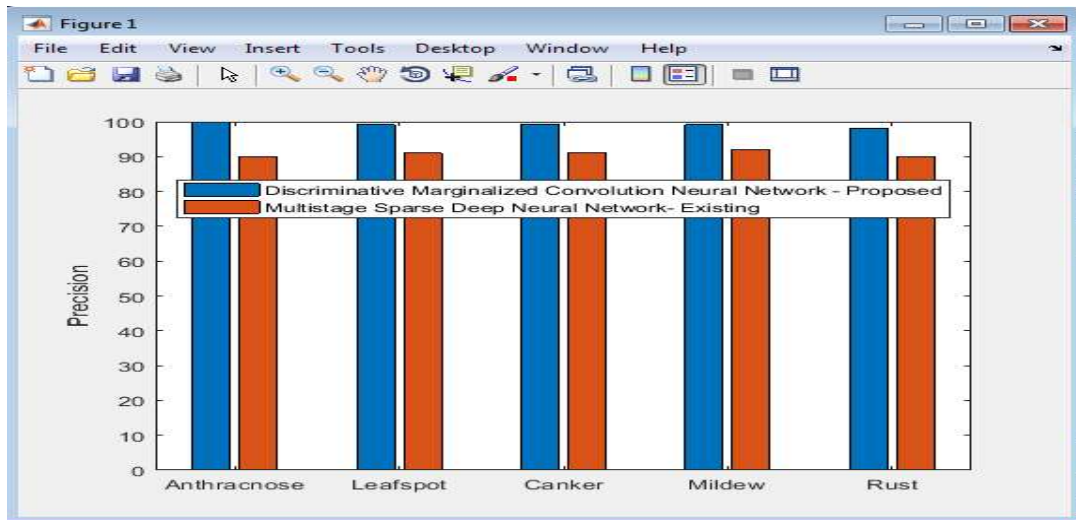


Figure 4: Performance Evaluation of the proposed model on precision

The precision, recall, Measure has be calculated using confusion matrix with parameters like true positive, false positive, false negative and true negative. Those values have been extracted from on various instances of classes to compute the performance accuracy on the spectral indices at various wavelength of the pixel of proposed architecture and it is compared with classified pixels of the spectral images.

Further it have been processed to identify the fungal disease in various type of crop with respect to correlation of the spectral signatures

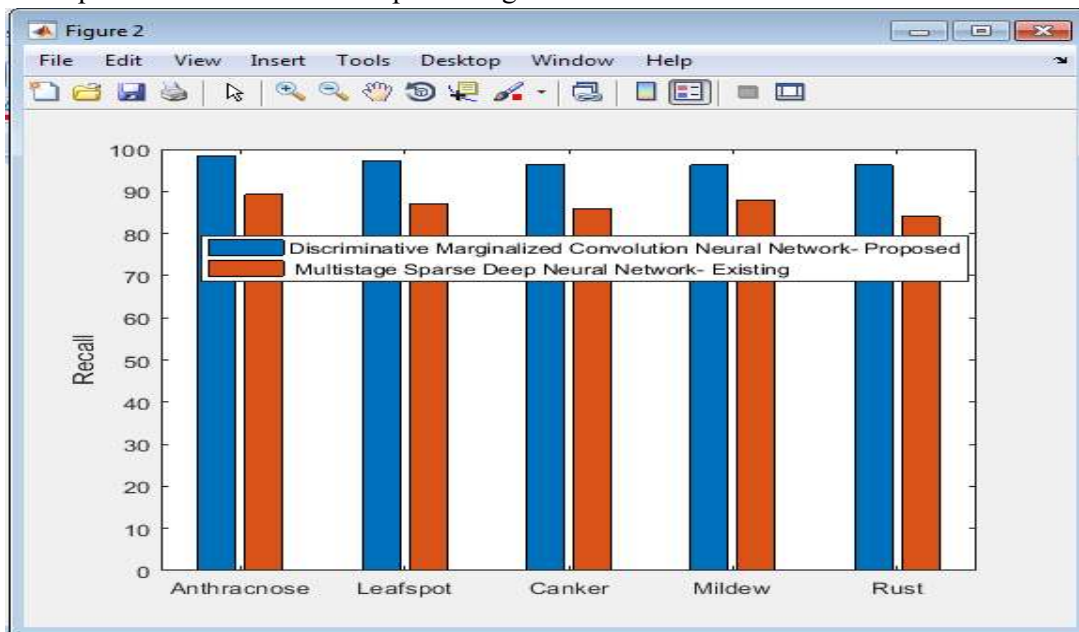


Figure 5 : Performance Evaluation of Proposed architecture against Conventional model on Recall

Figure 5 depicts the performance of the proposed architecture towards classification of the hyper spectral images in terms of recall on the classes of crop fungal disease on the various climate. On analysis, it yields effective results on true positive values computation.

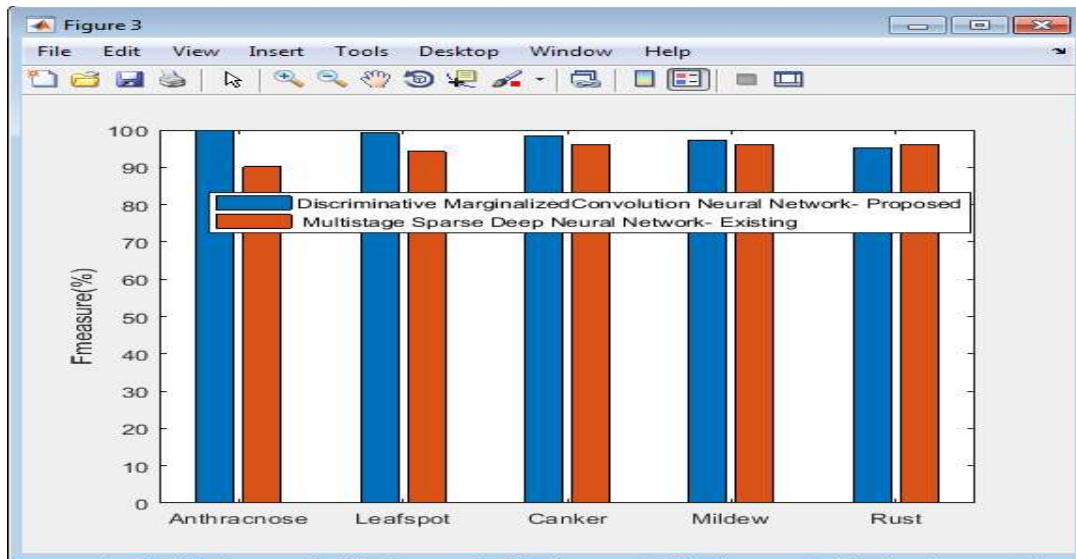


Figure 6 : Performance Evaluation of Proposed architecture against Conventional model on F measure

It is interesting that the accuracy values of the proposed model are high in the classification of hyper spectral images on multiobjective activation functions of the classifiers using spectral angler mapper. It classifies the discrete spectral values and spatial value of the soil and plant compositions containing reflectance value[19]. This paradigm can be applicable to any type dataset of hyper spectral images. Figure 6 provides the performance results of the f measure on outcomes of classes containing fungal disease. Table 2 represents the performance of the classification accuracy on proposed classifier against conventional approach.

Table 2: Performance computation of proposed architecture on Crop fungal Disease Classification

Techniques	Classes	Precision	Recall	F measure
Proposed Technique –Discriminative Marginalized Convolution Neural Network	Anthracnose	100	98	100
	Leaf spot	99	97	99
	Canker	99	96	98
	Mildew	99	96	97
	Rust	98	93	95
Existing Technique- Multistage Sparse Deep Neural Network	Anthracnose	90	89	90
	Leaf spot	91	87	90
	Canker	91	86	90
	Mildew	92	88	91
	Rust	91	84	90

Performance of the proposed approach produces the classification maps with high classification accuracy [10]. Proposed model can highly minimize the data redundancy and enhances classification efficiency on basis of the dataset

Conclusion

In this work, a discriminate marginalized convolution neural network for crop disease classification using the hyper spectral images has been designed and implemented. The proposed architecture employs non negative matrix factorization to extract the endmembers and genetic algorithm as feature selection technique to selects the optimal spectral endmembers related to the fungal disease. Optimal endmembers is processed further to generate the spectral angle mapper. Endmember and spectral angle mapper is projected to discriminative marginalized convolution neural network classifier. Proposed classifier classifies the fungal disease in the crop effectively and accurately with reference to the spectral angle mapper generated. Proposed model is capable of identifying the anthracnose, leaf spot, rust, canker, mildew type of fungal disease present in the crop plants. The experiment analysis was evaluated and tested on the Landset 8 OLI dataset to compute its effectiveness and efficiency in terms of accuracy.

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