A Deep Multi Scale Convolution Global Pooling Neural Network Modelfor Identification and Classification of maize Plant Diseases

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Abstract

Identification and classification of Maize plant diseases is an essential step in agricultural studies towards analyzing and extracting plant diseases. In existing, many automatic segmentation algorithms such as Region Based Segmentation and Boundary Based Segmentation has been applied to identify the diseases as it produces the higher accuracy and less mean squared error. Despite of several advantages, the model is time consuming and it generates less accuracy on the volumetric changes of the diverse dataset. Nevertheless, due to the occurrenceof artifacts imaging,functional variability, varying disparity properties, lesion changes and poor cataloging, most of these techniques do not give pleasing results. In order to resolve those issues, a novel framework named as Deep multiscaleConvolution Neural Network(CNN)Model has been proposed using K- means clustering, Sparse Principle component Analysis, Affinity propagation and Linear Convolution Neural Network to segment the maize Images. The model segments the leaf pest and disease into subfields on different growth stagesof maize plant disease images. Affinity Propagation identifies the changes of the leaf spots along plant pathologies and represented as features set. Sparse Principle component analysis extracts the sparse information and its interrelationship on the feature set which is represented in the form of max pooled data. Further Linear Convolution Neural Network has been employed to generate the class labels for the sparse information in the form of feature set. Linear CNN also helps tosmoothens edges of the class labels on the batch normalization to separate diseases of the plant. ReLu activation unit has used to generate the class label for the max pooled data. Experimental analysis using plant village dataset on the proposed model explains the performance in terms of dice similarity coefficient, Jacquard Coefficient and segmentation accuracy respectively towards disease identification.

Keywords: Leaf Disease, Linear Convolution Neural Network, Sparse Principle Component Analysis, Affinity Propagation

1. Introduction

Leaf disease identification is an imperative technique for the analysis of agricultural data for cultivation system. Generally, there are eight types of common leaf diseases, including dwarf mosaic,Curvularia leaf spot, northern leaf blight, gray leaf spot,round spot , brown spot, rust, and southern leaf blight[1][2]. It is important to perform pre-processing step toanalyze complex structure of the plant pathology. Many automatic approaches have been employed in existing to carry out automated disease segmentation [3]. Those techniques can be roughly distributed into three categories: region, boundary, and hybrid based approaches.

Region-based methods categorize connected regions based on intensity criteria, employing thresholding, clustering, and morphological filtering to identify the acknowledged volume. Boundary-based methods [4] primarily dependent on gradientevidence to locate the lesion surface of the plant, usually exhibited by an active contour [5][6]. Hybrid approach customspathological operations and active shape segmentation to identify the plantcomponents on basis of color and space characteristics of the disease [7]. Automatic plant disease identification is a challengingchore because of the doubtful boundaries, low contrast images, and nonexistence of intensity standardization. Moreover, entire leaf diseasewithdrawal becomes more perplexing when datasets with a obsessive disorder are used [8].DenseNet201 Model gives better results when compared with other Models without using data argumentation technique [9]. The architecture AlexNet along with Support Vector Machine (SVM) is one of the best Classification methods [10]. Hybrid Deep Convolution Neural Network (DCNN) with five convolution layers, five pooling layers and two associated layer gives good performance [11]. Inception model, a multiscale convolution global pooling added neural network connected with Softmax classifier .This improved model called as TCI-ALEXN helps to improve the precision of maize diseases identification [12]. Deep Convolutional Neural Network (CNN) with tuning parameters and combination of pooling values gives better results [13]

2. Related works

Deep learning approach is mainly used for solving complex problems. It overcomes the limitations of conventional machine learning approaches. Various Conventional Neural Network architecture includes Region-based Convolution Neural Network(R-CNN),Region-based Fully Convolution network(R-FCN), Single Shot Multibox Detector (SSD),Google Net ,Alex Net,VCC-16 AlexNet , MobileNetV2, InceptionRes NetV2, Dense Net 201 are used to enhance plant leaf Disease classification performance. The data augmentation features such as Zoom, rotation, brightness, cutout and Mix-up were collective and used in training process.

2.1Robust leaf disease Extraction – Hybrid Approach

It is a well-known learning-based algorithm uses tree structured classifier capable of extracting and classifying the texture and intensity-based features of the image dataset that combines a discriminative random forest and a generative model with the graph cuts for image classification. It generates the training model to learn the unusual features to exactlyidentify diseases [14].

2.2D U-Net- Deep Network Architecture

It is a well-known semantic segmentation model uses the deep network architecture for plant disease identification in the maize crop. The architecture of 3D-UNet encompasses a diminishing path, amounting path, and detailed localization for the moral use of features. 3D-UNet also uses concatenation to syndicate the features at high resolution with the non-sampled output to find local characteristics [15].

3. Review of literatures

In this segment, literature related to the objective of the research has been analyzed to model the effective structure for maize crop disease segmentation on various layers of the deep learning architectures is as follows

Mingjie[16] et.al proposed a model that uses feature extraction function to extract the features under the complex illumination, blur and noise. The model uses the robust Alex-net architecture of the CNN to prevent the over fitting and to improve the convergence and accuracy on the difference perspective of the diseases of the maize plant.

Jahid Hasan[17] et.al proposed a model that uses classification model for detecting various pathogenetic diseases of the crop. Classification model employed in the literature can capture all important features of the plant related diseases. It especially classifies nine different disease of the maize plant. It is used to accelerate the recognition accuracy of the model.

Ronnie ConcepCion[18] et.al proposed a model that uses surface calculation of the Cercospora leaf spot of maize plant disease type using gaussian quantum behaved particle swarm optimization as phenotyping technique to understand pathogen interaction. It uses visual detection through graph cut segmentation technique. Segmentation results are leaf signatures to identify the maize leaf status.

Dan Joas M. Bonifacio[19] et.al proposed a model that uses zea mays disease detection of the maize crop using gray level segmentation and edge detection techniques. Further segmented model has been processed by classifier process to identify the maize disease in the corn plant.

4. Proposed Model

Deep Multiscale CNN Model on plant village dataset to segment the leaf diseases using Sparse Principle component Analysis, Affinity propagation and Multiscale Convolution Neural Network using various processing steps can be employed.

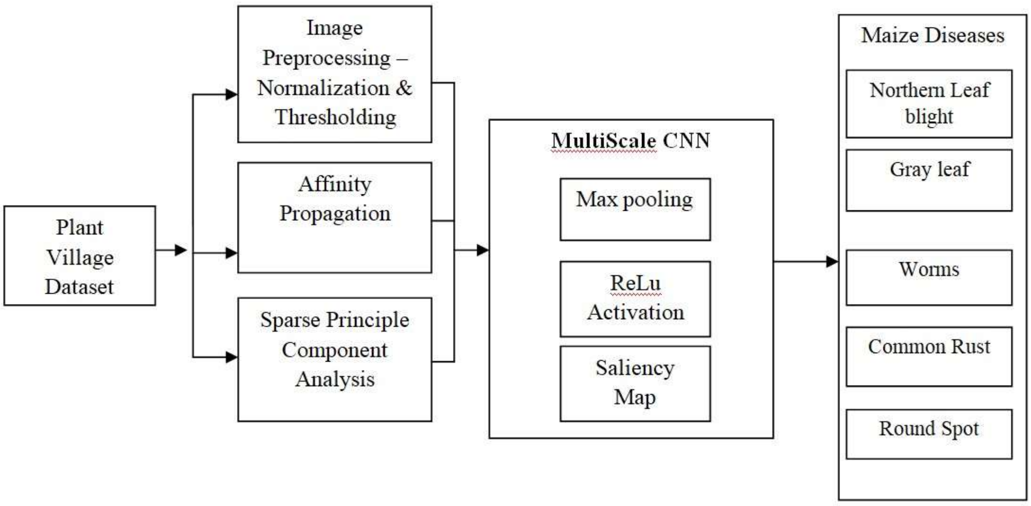


Figure 2: Proposed Architecture

4.1 Image Pre-processing

Pre-processing is used to figure out set of parameters for succeeding processing of the plant using extraction tool [20]. The parameter includes an higher bound on the intensity of the plant and other parameter of the images dataset. This initial estimate is used to normalize the input image and its format through normalization technique. Further noise and blur reduction, Contrast enhancementare employed in parallel using image Thresholding techniques to enhance the image details which contains the important factor for further processing steps.

4.2 Affinity Propagation

Affinity Propagation (AP) approach is first applied to cluster images pixels represented by exemplars. It considers of many data points as possible exemplars donethrough the minimization of an energy function toobtain the optimum set of exemplars and their equivalent clusters.Identify a subcategory of data points as paradigms and assigns all other data points to one of those standards [21]. Exemplars uses the soft max function to discriminate between the different lesions in the plan .Affinity Propagation identifies the lesion and its pathologically altered regions in the clusters which can be represented as features set.

Affinity Propagation attempts to find exemplars that maximize net similarity, i.e. the overall sum of similarities between all exemplars and their member data points. Responsibility, r[i, j], is a communication from data point i to j that replicates the accrued evidence of how well-matched data point j is to serve as the pattern for data point i. Availability, a[i, j], is a dispatch from data point j to i that redirects the accumulated evidence for how appropriate it would be for data point i to indicate data point j as its exemplar. All accountabilities and availabilities are set to 0 primarily, and their values are iteratively restructured as follows to compute conjunction values.

Algorithm 1: Affinity Propagation

- Input: A set of real-valued pairwise comparisons , $\{s(i,k)\}$, among data points and the number of exemplars (K) or a real-valued exemplar cost of the region

- Output: A subdivision of exemplar data points and an obligation of every other point to an exemplar to represent the plant pathology
- **Process**

❖ A set of pair sensiblesimilarities, $\{s(i,k)\}$, where $s(i,k)$ is a real number representing how well-matched data point k is as an exemplar for data point i mentioning legion of the disease part

$$s(i,k) = -\|x_i - x_k\|^2,\ i \neq k \text{ ---- Responsibility}$$

For lesion cluster

$$\rho[i, j]= s[i, j] - maxk=j\{a[i, k] + s[i, k]\}$$

For every data point k, a real number, $s(k,k)$, representing the *a priori*inclination that it be chosen as an exemplar

$$s[i, j] - maxk=j\{s[i, k]\}$$

$$s(k,k) = p\ \forall k \text{ ----Availability}$$

It can be derived as belief propagation (max-product) on a completely-connected factor graphto make best use of the sum of similarities between data points and their exemplars, minus the costof exemplars to generate the available feature set which contain the lesion regions. Lesions are complex and variable.

4.3 Sparse Principle Component Analysis

Sparse Principle component analysis extracts the sparse information and its interrelationship on the feature set which is represented in the form of max pooled data.Such sparse information can be extracted from maize plants affected with northern leaf blight, gray leaf spots, common rust and worm and round spot pathogens. In this, sparse information of the clustered feature set has been extracted [22]. Clustered feature set symbolized by a reduced number of "effective" features and however retain most of the essential information contained in the cluster. Figure 1 represents lesion region types of the maize plant.

(a) (b) (c) (d) (e)

Figure 1 : Maize Disease Categories (a) Leaf Blight (b)Gray Leaf Spot (c) Common Rust (d)Worms (f) round spot

Suppose that **x** of dimension m has to be transfer it using l numbers, where $l<m$. If the vector x has beentruncated, a mean square error identical to the sum of the differences of the elements has been generated and it will be eliminated from **x.** Further, there exists an invertible linear transformation T such that the truncation of Tx is optimum in the mean-squared since transformation T should have the possessions that some of its constituents can have low difference. Sparse Principal Component Analysis maximizes the rate anddecline of variance of the maize crop diseases segments.

Algorithm 2: Sparse Principle Component Analysis

Input: Clustered Feature Set composed of varied maize crop disease features

Output: Max pooled Feature Set

Process

Let X be an m-dimensional random vector demonstrating region of interest in the particular cluster which represents the disease such as such as northern leaf blight, gray leaf spots, common rust and round spot

Assume vector X has zero mean

$E[X]=0$

Where E is the statistical expectation operator

If (X has not zero mean)

(X- Mean)

Let q denote a unit vector, also of measurement m, against which the vector X is to be estimated

A= inner product of the vectors X and q

$A=X^Tq=q^TX$

Where A is a random variable

Constraint

$||q||=(q^Tq)^{½}=1$

If (X has zero Mean)

$E[A]=q^TE[X]=0$

Variance of A= $\sigma^2=E[A^2]=E[(q^TX)(X^Tq)]=q^TE[XX^T]q=q^TR\ q$

Correlation Matrix $R=E[XX^T]$

Matrix has been transformed to m*1 vector a and b as follows

$$a^T R b = b^T R a$$

Variance σ^2 of A is a function of the unit vector q

$$\psi(q)= \sigma^{2=} q^T R\, q$$

Above mathematic notation is represented as a variance probe $\psi(q)$

Further feature set containing variance probe undergoes various constraints are follows

$\psi(q+ \delta q)= (q+ \delta q)^T R\, (q+ \delta q)$ – First order Constraint for northern leaf blight features

$\psi(q+ \delta q)=q^T Rq+2(\delta q)^T Rq+ (\delta q)^T R\, \delta q$ – Second order Constraint for gray leaf spots

On applying perturbation δq which is orthogonal to q

$$(\delta q)^T R\, q-\lambda(\delta q)^T q=0 \Rightarrow (\delta q)^{T(} R\, q-\lambda\, q)=0$$

From above constraint, q is an eigenvector and λ is an eigenvalue of R

Eigen Value R can be represented as $R=\sum_{i=1}^{m} \lambda_i \vec{q}_i \vec{q}_i^{\,T}$

Principle Component of the Cluster contain sparse information is given by $\alpha_j=q_j^T x= x^T q_j$, $j=1,2,\ldots,m$

In particular, analysis reduces the number of structures needed for operative data representation by leaving those linear combinations by retaining the features with large variance on the composition of maize diseases.

4.4 Linear Convolution Neural Network

CNN-based algorithms are trained with identifiedcharacterized data to learn the fundamental mathematical explanation required for object Classification and segmentation [23]. The network architecture involvesfour convolutional layers for the volume with kernels of 3 × 3 × 3 elements. The number of convolutional layers is absoluteand empirically based on the performance of the model on the confirmation set. The number of training iteration is decided inevitably based on the model presentation on the validation and training set. The figure 2 represents the proposed architecture of the work.

- **Max pooling Layer**

A 3*3*3max-pooling layer is used to compute the maximum value in the feature set as down sampling with stride of 2 in each dimension. It further increases the generalization capacity of the model and it also reduces the computational capacity and tallyingtoughness to noise. The number of feature channels is doubled after each down sampling with disease segment. Feature regularization is carried out to eliminate the over fitting issues of similar kind of diseases of the plant.

- **Cluster Normalization**

Cluster Normalization (CN) is used for faster convergence of feature processed through Sparse Principle Component Analysis with varied diseases segments with object characteristics and signatures. CN is the regularization of the activation function value .The output value of CN with filter processing helps to determine the stage of the disease. When CN is used, it is not inclined by a parameter scale but by weight propagation of the disease pathology. Thus, the learning rate that controls and adjusts the weights during increasing and enabling rapid learning of disease growing in the plant.

- **Convolution Layer**

The Convolution layers capture the cluster normalized features through their inherent mechanism hierarchically from minimum level to more abstract features and acquire the discriminative features with stage of the disease varied object characteristics and signatures. It works in a approach that it makes zero-padding everywhere each pixel followed by convolution on the padded image to cluster it particular disease category. The final convolution filter size is 1 *1 * 1.

- **Activation Function**

The architecture uses the Rectified Linear Units (ReLU) activation function, which presents non-linearity to the system under feature maps without loss of the information. Each activation function is followed by cluster normalization, the over suitable helps to improve the system generalization by standardizing the output of the activation function to produce effective recognition rate with small variance of the object under particular disease type on basis of the signature and size. It avoids significant changes in the parameter.

- **Output Layer**

The output of the deepest convolutional layer is flattened and fed to fully connected layer, which serves as a classifier in the architecture and processes features extracted through convolutional layers with significant distinctions in different stages of the plant growth. The system learns the most discriminative features using soft max and cross entropy mechanism on various stage of the disease of the maize crop. These both mechanisms the compares the features with ground truth label collected or generated using manual segmentation process.

Algorithm 3: Linear Convolution Neural Network

Input: feature set F={x1,x2,…xN}

Output: Target LabelT={y1,y2..yN}

Process

```
 While feature set f: 1 → F do
    Compute the j activation function using Rectified Linear Unit (ReLU) capture various edges in the featureset of the respective field of the maize plant to represent a disease
        Generate Noise Vector n
Compute Error e
Apply Feed Forward Propagation to compute cross entropy Gradient E(θ)
cd= Convolution(F)
mp= Max_pooling(cd)
Cn =Cluster Normalization (mp)
fc= Fully Connected(Cn)
Update Network Parameter θ using gradient descent
```

- **Multi Scale Convolution**

The Multiscale convolution has been employed on output layer of Linear CNN towards identifying the discriminative segments of the fully connected features through weighted feature layer to determine the discriminative features processed in linear CNN with multi scale convolutions of different size to find the features with changed scales. The Saliency map has been derived to map the features on interpreting and rationalize the decision of the trained system towards the interrelationship feature between pixels to avoid the patch alignment issues.

$$x_{ij} = \frac{1}{K} \sum_{l=0}^{k} x(l)$$

In the above equation, K termed as weight factor and x is considered as feature. The system is to detect the various kinds of maize plant diseases on the varied period with changes in the size of the plant.

Algorithm 4: Automated Segmentation

Input: Saliency Map

Output: Segments

Process

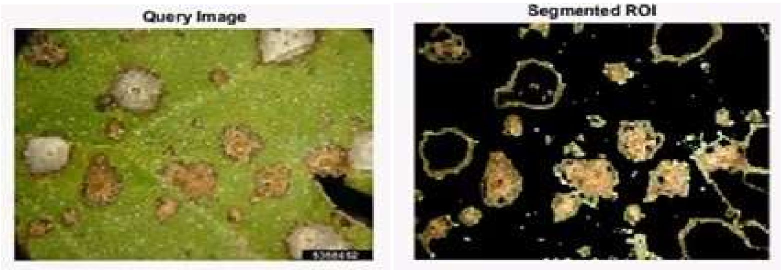
```
  For D = 1 to N do
      Generate a training data
For i = 1 to M do
          Calculate Class label
            Class label = Soft_Max (fc)
Class Labels = disease region of the plant
```

The system segments (localize) the pathological lesion changes into various categories such as worms, gray leaf spots, rust and northern leaf blight.

5 Experimental analysis

Experimental analysis has been carried out in the kaggle (https://www.kaggle.com/smaranjitghose/corn-or-maize-leaf-disease-dataset). The model is simulated in Matlab (version 2017a). Processing of the image for training and validating the system is highly challenging. During processing, 60 percent of the data has been taken for training, 20 percent of the data has been utilized for validation and remaining 20 has been employed for testing. In this experimental analysis,10 fold validationshave been applied to improve the performance of the classification and segmentation of the diseased region.

In this work, Alex Net is used to perform iterations to achieve high accuracy of disease regions detection forrecognition of worms, rust and gray leaf spot etc. The model provides the better results for identifying lesion regions with varied size and characteristics compared with existing methods.Figure 3 represents the lesion regions identified using Multi-ScaleConvolution methods which extracts feature. This helps to accurately illustrate different diseases toincrease the accuracy of disease salutation at different stages of lesions found in rust and round spots of maize crops.



(a) (b)

Figure 3: Maize Lesion Detection (a) Query Image (b) Segmented Image with Worm and Round spot lesion

The routine 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

- **Dice similarity Coefficient**

It is computed by considering the difference between the segmented result and ground truth data. In addition it can be computed using true positive, false positive and false negative values of segmentation results. It is denoted as

$$\text{Dice Similarity Coefficient} = \frac{2\text{TP}}{2TP+FP+FN}$$

- **Sensitivity**

It is measure of percentage of True Positive which computes the skull correctly in terms of various features. It is given by

$$\text{Sensitivity} = \frac{\text{TP}}{TP+FN}$$

- **Specificity**

It is measure of percentage of True Negative which computes the non skull correctly in terms of features of the data. It is given by

$$\text{Specificity} = \frac{\text{TP}}{TP+FN}$$

Table 1: Performance Evaluation of Autonomous Segmentation Techniques

Samples	**Technique**	**Dice Coefficient**	**Sensitivity**	**Specificity**
Test 1 Samples	Deep Multiscale Model – Proposed model	0.9978	0.9412	0.9989
	3D- U Net- Existing Model	0.9851	0.9336	0.9853
Test 2 Samples	Deep Multiscale Model – Proposed model	0.9965	0.9514	0.9971
	3D- U Net- Existing Model	0.9842	0.9389	0.9889
Test 3 Samples	Deep Multiscale Model – Proposed model	0.9956	0.9615	0.9965
	3D- U Net- Existing Model	0.9836	0.9399	0.9841

The analysis on different test samples on various autonomous segmentation techniques has been evaluated on dice coefficient, Sensitivity and specificity in the Table 1. It proves that proposed model segments plant disease regions edges more accurately. Deep learning methods spectaclesadmirable performance compared to conventional methods. The proposed model provides the improved performance without any parameter tuning [24]. The deep learning model is consistent on various cross validation results. The performance is produces nearest results on validating with ground truth data.

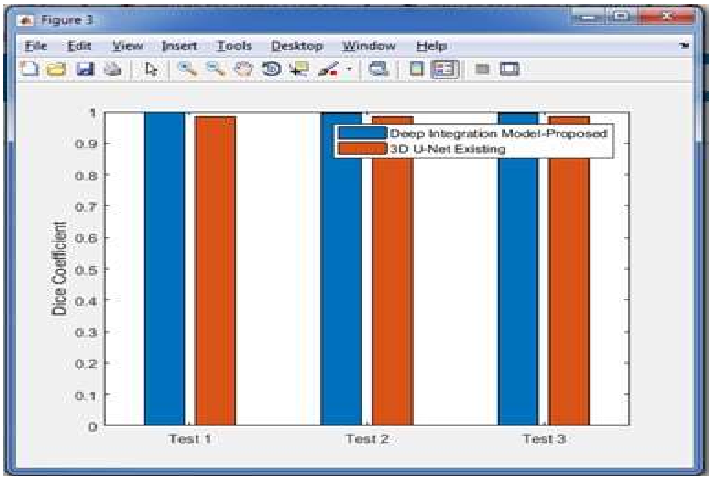


Figure 4: Performance Comparison ofproposed model in terms of Dice Coefficient

The Dice similarity Coefficient produces excellent results on evaluating with segmentation results in the figure 4. Concerning the sensitivity measure, it performedabove average level. However, varying the threshold when producingthe binary masks that can be used to refrain between sensitivity and specificity based on various cross validation of the results. Figure 5 represents the results the sensitivity on the disease identification.

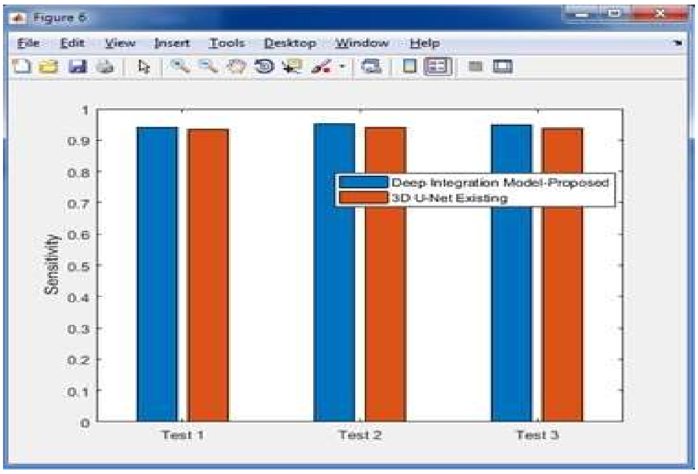


Figure 5: Performance Comparison of proposed model in terms of Sensitivity

The possibility of the performance on trained network has been adapted effectively with target domain as it results better with specificity value. The figure 6 represents the performance comparison of the specificity measure. Instead,suitable features for the given task arise during trainingautomatically.

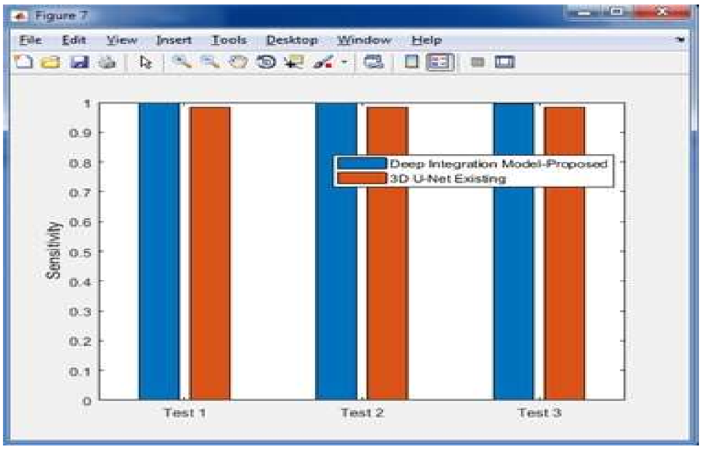


Figure 6: Performance Comparison of proposed model in terms of Specificity

Saliency map identifies the changes of the particular disease region in size and characteristics accurately on the segmented results. It is confirmed that this modified updateis definitely of great implication to speed up the training process. In accumulation, zero padding convolution layers are approved tomaintain the longitudinal dimension of the images and feature maps through each convolutionlayer. The model can even determine the larger through by pathological changes.

Conclusion

In this work, design and implementation of novel framework named as Deep multiscale CNN Model has been carried out on inclusion of the Sparse Principle component Analysis, Affinity propagation and Linear Convolution Neural Network in diseased maize plant images. Plantdiagnosis is an essential step in agricultural studies in order to exploit various information of the plant. Autonomous Segmentation technique based on deep learning produces the higher accuracy and less mean squared error with less time consumption. It produces the better results on volumetric changes, imaging artifacts, anatomical variability, varying contrast properties, and poor registration of the diverse dataset on analyzing the modalities and pathologically altered tissues.

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