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Deep Learning Technique with GUI for Detection of Various Stages of disease and Prevention Methods Based on Tomato and Grape Leaves

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Abstract:

In India, the main source of income for healthy lifestyle is agriculture and it is occupying 70% of rural population. Crop cultivation of India is highly miscellaneous. In India, the varieties crop is about 500 types. Even though there is advancement in technology, the practices of agriculture are still manually preceded and low automation level is involved as compared to the western countries. Plants are affected by many diseases and so the leaves are get damaged. From the images of leaves, the affected plant will be identified. This research proposes novel technique in detection of various plant disease stages using feature extraction and classification using deep learning techniques. here the input data has been collected from tomato and grape leafs. This data has been processed for noise removal, image resize and normalization. Then this image features have been extracted using graph Convolutional networks and classification of extracted features has been done using ResNet-50. Furthermore, from the experimental model for the public dataset of grape leaf diseases, this proposed method realizes better outcomes and 94% of average identification accuracy was obtained. This attention module is added and certified will be extracted accurately as complex features of various diseases with some parameters. The proposed model delivers a high-performance solution for diagnosing crop disease under the real agricultural environment.

Keywords: plant disease, tomato, grapes, feature extraction, classification, deep learning

1. Introduction:

In India, the main source of income for healthy lifestyle is agriculture and it is occupying 70% of rural population. The main population of country is indirectly or directly related with agricultural sector. Henceforth, the agricultural production is in high-quality and it is essential withstand the economic growth of country. For achieving the highest crop yield with higher productivity and quality, right products are decided by the farmers in order to decide the correct products to monitor and to control the essential temperature and requirements of humidity and light [1]. Moreover, the industry of agriculture is motivated towards the increment of food production in order to meet the growth of population, climatic changes and instability of political situation. The researchers are attracted towards exclusive, resourceful and consistent technologies used to increase the agricultural productivity. Some difficulties like initial plant disease identification where the farmers are struggling. For the disease type of observation, the type of the disease is not identified by the leaves of plant through the natural vision each and every time, therefore an automated expert system is utilized for the disease detection and are highly essential. The technical advancement with the combination of image processing and machine learning are utilized by farmers by means of plant disease in the initial stages [2]

Across the world, tomato is an important crop and 20 kg per year was consumed per year. Around 15% of tomato consumption are accounted. Nearly 170 million tons of fresh tomato are obtained as yearly yield. The US, India, Turkey, Egypt and China yields tomatoes in higher production rate [3]. As per the Food and Agriculture Organization survey data of UN, the production of tomato across the globe is affected mainly by the tomato disease with the rate of annual loss are in the range of 8%–10%. Though, most of the tomato disease begins from the leaves and it is spread across the whole plant. Diseases of tomato leaves are identified automatically is enhanced by managing the production of tomato and produces environmental growth. Conventional diagnosis expert on tomato leaf disease has higher cost and subjected towards the risk of misjudgement. Computer technology, computer vision, machine learning, and deep learning are developed rapidly by detecting the crop disease. Conventional methods of machine learning uses RGB image segmentation for crop disease and texture, shape features are also used in this machine learning methods. Though, various disease characteristics are same, so it is challenging task for the judgement towards the disease types, identification accuracy of disease is low in a complicated natural environment.

Deep learning network called Convolutional Neural Network (CNN) produces higher performance; this deserves a complicated image pre-processing and the operation of feature extraction and assumes an end-to-end structure in which the process of recognition is simplified as compared to its learning. Today, the recognition of crop disease is proceeded by CNN for real agriculture environments, in which tomato leaf disease is automatically detected and improve the diagnose accuracy and labor costs are reduced [4].

Molecular immunology and biology are used in this techniques for the crop disease detection at earlier stage. Still, human experts, enormous resources are needed in these techniques. As per FOA, areas of cultivation are insignificant and proceeded by the people in the undeveloped countries with lower income. Thus, exclusive solution are unreasonable for them and well-organized and effective techniques are proposed and it is made available to each and every farmers [5]. Now, machine learning (ML) depending on hand-coded techniques are established in the agricultural field for enhancing decision-making power. Because of the development of digital approaches, enormous amount of data is gathered by means of machine learning techniques and are used for making an optimized decision. These approaches such as decision trees (DT), support vector machines (SVM), K-nearest neighbours (KNN), and Gaussian frameworks, etc. are highly tested to detect the crop disease. The methods of Hand-coded keypoints are easily applied and didn't require enormous amount of training data like some time-consuming approaches are requires human expertise. Moreover, traditional ML computation models, there is a compromise between computational complexity and robustness of detection. Because larger keypoints are computed and improves the economic burden whereas the small feature-set are utilized that decreases the system's localization efficiency. Thus, performance improvements are required, that is specifically takes the frameworks of decision-support which can contributes thx`e enormous amount of data into appreciated recommendations [6]. Higher performance has been achieved by the proposed model for the crop disease diagnosis in the agricultural environment.

The contribution of the work is as follows:

- To detect and classify the plant diseases using GUI in the ReSNeT architecture.
- To compare the performance of the proposed method with the state-of-art methods.

2. Related works:

Many methods are used for using the technology of dep learning in [7] for improving the vegetable's survival rate, field crops and fruits by the detection of early disease and suceeding management of disease. Transfer learning is applied in the original Alex Net network, average rate of recognition has 10 types of better tomato leaves. The original AlexNet, called VGG16 structure of network is used with the combination of migration learning in [8] for obtaining 97% of accuracy on 7 diseased tomato leaves which is segmented. The The belongings of deviation, weight and rate of learning on the accuracy and speediness of detecting disease are analyzed. Different highly resulted cameras are used in [9] for capturing images of 9 diseases in tomato and pests and Faster RCNN, R-FCN, and SSD are used for training. By the properties of transfer learning AlexNet and GoogleNet networks were trained in [10] for the identification of camellia oleifers. Pre-trained ResNet network was used in [11] for the classification of seven types of tomato diseases with 98.8% as rate of accuracy. The structure of deep detection model was designed in [12] for the optimization and the improvement of tomato leaf diseases in the residual network and the classification features of the diseases are obtained by using transfer learning. Though better results are achieved by the transfer learning, original VGG16 architecture and AlexNet has complicated structures and enormous parameter are used for its application and model deployment. Depending on the prior researches, as compared in [13] with the conventional feature extraction techniques, CNNs have greater potential. The method of detecting diseases are trained by improved CNN from the open source disease dataset and it is contrasted with conventional systems like SVM, LBP, and GIST and it is proved that this method is greater than the some other methods of classification. Saliency analysis was used in [14] for the pest location in ta gardens, to decrease the number of layers in the network and AlexNet with reduced convolutional kernels and it is fused with the algorithm of Dropout

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model optimization for improving accuracy. This algorithm is efficient to identify 23 pests in tea gardens and achieved 88.1% as the rate of accuracy. The convolutional kernel size is reduced by Alex Net in [15] to enhance the accuracy of disease detection and number of parameters for the analysis is reduced by this method. Four diseases in apple leaves are detected by AlexNet was presented in [16] and 97.62% of recognition accuracy is achieved. An influential NN was developed in [17] to successfully identify three various disease depending on the leaf's morphological patterns. This research gives enormous references for the tomato leaf disease diagnosis in the real time agricultural environment. Discriminative features are extracted with its characteristics in recent years, and the network is started to use the machine translation, generative adversarial networks etc. [18]. Even though there were many techniques available in agricultural field, still it is exploratory. ShuffleNet, attention module was added by [19] that enhances the grape disease rate of recognition with the PlantVillage dataset to 99.14%. The recognition and segmentation of grape leaf diseases was presented in [20]. In the fusion featuring process, irrelevant and redundant features are added with noise and it is detached by Neighborhood Component Analysis (NCA). An accuracy of segmentation with 90% was achieved and the accuracy of classification was 92% was achieved. For the disease detection, radial basis function (RBF) kernel-based support vector machine (SVM) learning algorithm was used in [22]. The classification techniques based on efficient machine learning for disease identification and detection was met in this field. The identification model of plant leaf disease depend on a deep convolutional neural network (Deep CNN) was presented in [23]. This method was trained utilizing various training epochs, batch dropouts and sizes. The performance of this system is better as compared to the other machine learning techniques. Reliability and consistency of this method is high. In the identification of plant disease based on random forest was used in [24]. Implementation at different phases called creation of dataset, extraction of features, classifier training and classification. It is suitable for the disease detection.

3. System model:

Proposed model possess several steps, in that the step1 is the process of dataset selection, in which the pre-trained weights for transfer learning is obtained from the larger dataset and the next step was associated with relation between various disease classes on plant leaves. The last step is to build and train the deep learning architectures based on the online available tool called Label Img. This architecture is defined in figure 1.

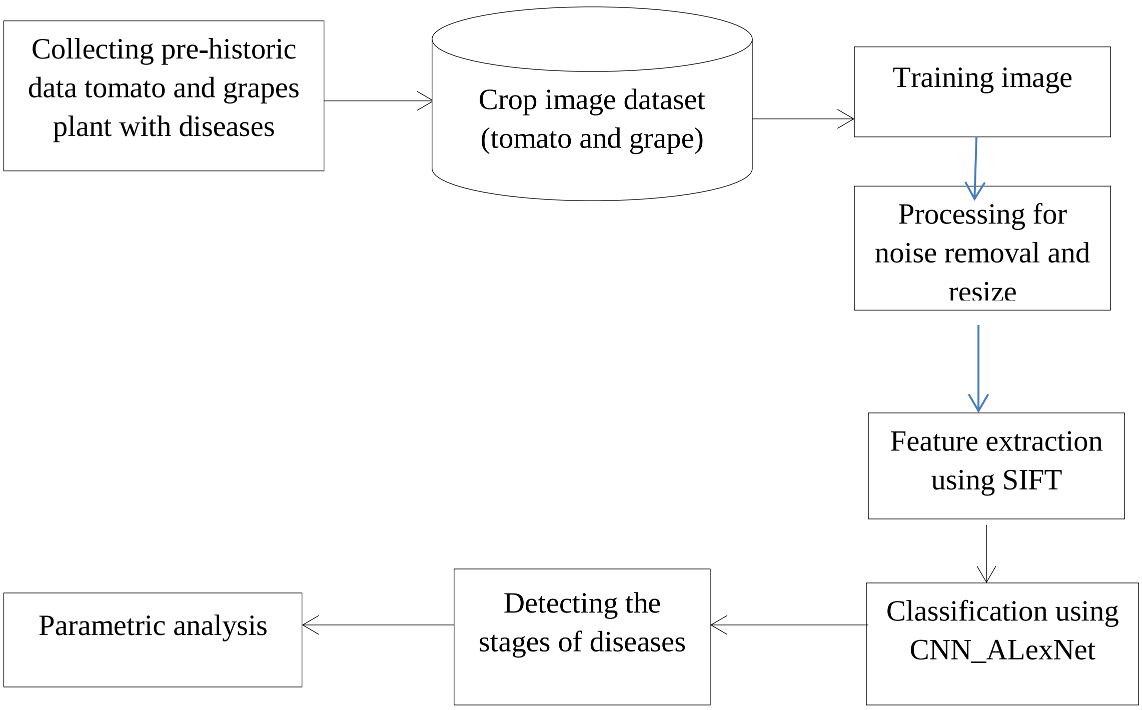

Figure- 1 Overall Proposed architecture

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An effective image classifiers are built by the process of image augmentation. Starting from 100s to 1000s of training samples are present in the dataset and this is not enough to construct an accurate method. Few in several options of image augmentation are used to tune the vertically/horizontally, rotated by several angles and image scaling. In the dataset, the relevant data is increased by these augmentations. Every image size in the dataset of plant village is in the size of 256x256 pixels. Keras deep-learning are used to process the data and augmenting images. The training procedure neds the following options of augmentation, they are: Rotation- The training images are randomly rotated over different angles, Brightness- Lighting variation are adapted in the process of image feeding at the time of training. Shear- Image's shearing angle is adjusted in the direction towards clockwise/counter-clockwise. Zoom- Input image is provided by scaling various factors. Vertical/Horizontal Flip – Random flipping of image towards the vertical/horizontal axis.

3.1 Dataset Selection

For several operations performed in real life, so many datasets are developed having enormous number of classes. E.g; in the research of object classification/detection, ImageNet dataset with extraordinary number of images are used. Likewise, MS COCO dataset dataset are used for the purpose of transfer learning and selection respectively. In this dataset, the number of plant varieties are 14 in number with 4 bacterial diseases, 17 fungal infections, 2 infectious diseases, 2 fungal illnesses and1 mite-induced disease. 12 species of plant represent the healthy images of leaves.

3.2 Annotation of the Training Dataset

The three sub-datasets of Plant Village dataset are as follows: for the purpose of training it has 70% of total images (38017 images), for the validating purpose it uses 10% of images (5431 images) and for the testing purpose remaining 20% of images (1517 images) are used. This training set annotation is the 1st step for identification of plant diseases by using meta=architectures of deep learning. LabelImg was used to annotate the training images, this application of annotation is in open-source graphic image representation. The coordinates of the bounding box like (Xmin, Ymin, Xmax, and Ymax) were constructed as a result. The intersection of the union (IoU) and the bounding box predicted have been intersected and its result are investigated by the ground truth in the bounding boxes. For saving the annotations, the format of XML files, the Pascal VOC have been utilized.

3.3 Graph Convolutional network based Feature extraction:

Convolutional layer: Neural network (NN) dependent on the spectral theory for the implementation of convolution operations on topology is called as graph convolutional network. In the graph theory, the spectral convolution is defined as the product of signal $x \epsilon \mathbb{R}^N$ (each nodal scalar) and filter$g^{\theta} = \mathrm{diag}(\theta)$; fourier domain $\theta \epsilon \mathbb{R}^N$ is used for parameterization and it is represented in equation (1) as shown below:

$$g\theta * x = Ug\theta(\Lambda)U^T x \qquad (1)$$

Where I given vector matrix of normalized graph is represented in a matrix form called U. $L = I_N - D^{-\frac{1}{2}} A D^{-\frac{1}{2}} = U\Lambda U^T$ is the Laplacian, which is diagonal matrix with Λ eigenvalues and U^T is defined as x's graph Fourier transform. For larger graphs, L which is the eigen decomposition, computed initially as the expensive prohibitive. For this problem avoidance, K-localized spectral filters are suitably controlled by utilizing the truncated expansion with respect to the Chebyshev polynomials for filter parameterization $g\theta$ in an efficient manner is represented in equation (2)

$$g\theta(\Lambda) = \sum_{k=0}^{K} \theta_k T_k(\Lambda) \qquad (2)$$

Where the Chebyshev coefficient's parameter vector is $\theta \epsilon \mathbb{R}^N$ and Chebyshev polynomial for k^{th} order is $T_K = (\Lambda') \epsilon \mathbb{R}^{n \times n}$ and $\Lambda' = \frac{2\Lambda}{\lambda_{max}} - I_N$ was evaluated as a diagonal matrix with scaled eigenvalues in the range of [-1, 1]. The polynomial of Chebyshev filter is $T_k(x)$ in the k^{th} order was calculated by the relation of stable recurrence $T_k(x) = 2xT_{k-1}(x) - T_{k-2}(x)$ having $T_0 = 1 \text{ and } T_1 = x$. The Chebyshev polynomial's truncated expansion is the experiment and it is capable for the filter estimation gθ efficiently. The convolution of a signal with gθ filter is given by the following equation(3) as follows:

$g\theta * x = \sum_{k=0}^{K} \theta_k T_k(L')x$ (3)

It is noted that $(U\Lambda U^T)^k = U\Lambda^k U^T$ by the verification of $L' = \frac{2}{\lambda_{max}} L - I_N$

Therefore, multi-layer Graph Convolutional Network was considered by the rule of layer-wise propagation as followed in the equation (4):

$H^{(l+1)} = \sigma(\sum_{k=0}^{K} T_k(L')H^{(l)}W^{(l)}$ (4)

Here, Layer-specific trainable weight matrix is given by $W^{(l)} = \theta_k, (k\epsilon[0, K]\Lambda k\epsilon\mathbb{Z})$. An activation function is defined by $\sigma(\cdot)$.the activation matrix in the l^{th} layer is denoted as $H^{(l)}\epsilon\mathbb{R}^{N\times D}$; $H^{(0)} = X$

Pooling layer: The graph scale is reduced by the graph signal's fast pooling whereas preservation of local geometry and original graph's connected information. The Metis graph partitioning algorithm with the coarsening phase produces graph's fast pooling principle. Smaller graph's set $G_i = (V_i, E_i)$ in the coarsening phase was obtained from $G_0 = (V_0, E_0)$ as the original graph through the nodal fusion, in which $|V_i| < |V_{i-1}|$. The combination of nodal set in the graph G_i in one node in the next-level roughening graphG_{i+1} is used in most of the process of coarsening. The set of nodes are given by V_i^v in the G_i graph that are fused by V_i node of G_{i+1} graph. The coarsened graph was made better by taking nodes and original graph's edge weights, the node's weight is given by v and it will be set to the sum of each and every nodes in V_i^v. If V_i^v with multiple nodes have connected edges for u vertex at the similar time, vertex v with edge weights are the edges weights sum.

Single Shot MultiBox Detector (SSD): The SSD methods are simpler because of the region proposal's elimination and next pixel or features are resampled. This deep learning architecture incorporates each and every computation in a network, that is called single-shot detector. From the findings of experiments, the dataset MS COCO, ILSVRC, and PASCAL VOC are revealed and SSD is attained as better precision as compared to other deep learning methods like ResNet-50 with lesser time of computation whereas unified training and framework of inference was provided. The SSD key feature depends on the convolutional filters that are small like 4x4 and 8x8; category score with feature maps and the collection with box offset prediction for default bounding boxes.

ResNet-50 based Classification: Grape and tomato leaf disease image is provided as input ResNet-50 with the structure of network is provided in figure 2, convolutional layer is passed first, activation layer, BN layer and the feature map is obtained is maximized pooling. The Stage 1–4 is mainly included in this ResNet50 model every stage comprised of sampling module and numerous mapping modules are identified. The AVG pooling operation has proceeded by the output feature map and then flatten layer was passed for making the multi-dimensional feature's output and one-dimension and the output is obtained finally by the fully connected layer.

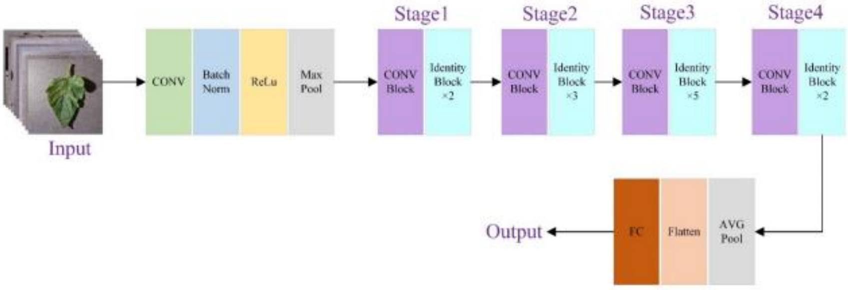

Figure 2 The structure of the ResNet-50

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As the number of network layeruoujpipu6y]t, o90s are deepened, when the network's internal characteristics have attained certain layer's optimal level, the next superimposed layer of the network doesn't alter the characteristics. ResNet-50's residual module will have utilized efficiently in the problem solving for the mapping identification and network parameters and computations are reduced.

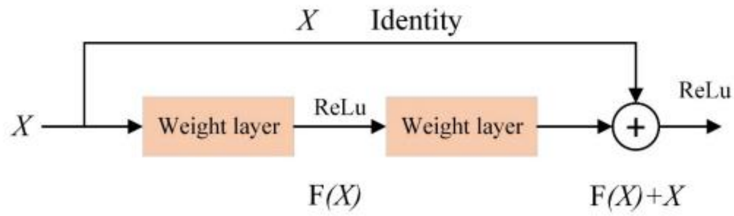

Figure 3. The residual block

Residual units form the basis for residual networks [25]. Every residual unit will be shown in equation (5) and (6):

$y_i = h(x_i) + F(x_i, w_i)$ (5)

$x_{i+1} = f(y_i)$ (6)

Where, the residual function is given by F, ReLU function is denoted by f, weight matrix is given by w_i and layer i with input and output is given by x_i and y_i respectively. The h function has a mapping identity expressed as

$h(x_i) = x_i$ (7)

The F as residual function is described in equation (8) is as follows:

$F(x_i, w_i) = w_i.\sigma(B(w_i').\sigma B(x_i)))$ (8)

Where, the batch normalization is given by $B(x_i)$ and convolution is denoted by "·" and σ(x) = max(x, 0). The necessary impression behind the residual learning in the path's branching for gradient propagation. Some similarities are shared in the residual networks having highway networks like residual blocks and shortcut connections. Every path's output in the highway network is measured by the function of and it is learnt in the phase of training. ResNet's residual units are not stacked together with convolutional layers in CNN. Rather every convolutional layer's input to its output is introduced by the shortcut connections. Shortcut connections with mapping identification reduces the residual network complexity in deep network which are trained faster. Many path's ensemble was used in ResNets rather than noticing DL architecture. Each and every network paths in the ResNets are with similar length. A single path goes off with each and every residual units. Furthermore, each and every signal path doesn't propagate the gradient that accounts for fast optimization and ResNet's training.

The 224×244×3 is the input image size. Five convolution blocks are present in this network, every block comprising convolutional layers and pooling layer with two FC hidden layer (4096 neurons with every layer), output layer is end with softmax activation with 1000 classes.

In between the deep layers, skip connection is present depending on the ResNet. More than one non-linear transformation layers have skipped by these skip connections. These connection's output and the network stacked layer's output are added.

In this final block output is given by H(x), the connected layer's output is given by x and the stacked network layer's output in the similar block is represented by F(x).

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3.4 Stochastic Gradient Descent (SGD) with Momentum

One of the Neural network's optimization algorithm is called as gradient descent. Ability of faster convergence are present in the momentum version than the standard algorithm. The

The elementary impression is used for the calculation that is weighted average of the gradients are weighted exponentially and the weights are updated by the gradient used. For the cost function optimization, minimum loss is obtained by the gradient descent, that slows the gradient descent and large rate of learning are avoided. Higher learning rate are utilized and the problems of overshooting and diverging are ended. SGD optimizer are contrasted with the calculation of weight's gradient and biases with calculated gradient, dw and db are th weighted averages are exponential a momentum algorithm is considered [26] by the following equation (9) and (10) as follows:

$$V_{dw} = \beta * V_{dw} + (1 - \beta) * dw \qquad (9)$$

$$V_{db} = \beta * V_{db} + (1 - \beta) * db \qquad (10)$$

4. Performance analysis:

Python tool is used for the implementation of proposed disease classification and PC with Ubuntu, 4GB RAM, and Intel i3 processor are the configurations of the system.

4.1 Dataset description:

Plant Village is an open dataset used for the experimental analysis. Grapevine leaf black rot with 1180 images are used for detecting disease. LabelImg are used for the disease annotation. The number of diseases are there in images that can detect about 17000 targets of detection in total. Previous to the training process, 1180 images are divided into training and test sets. The network training of 1072 was selected for network training and test set with 108 images are used for the network evaluation named as test_pv. Additionally, grape leaves with 108 images with spotted black rot in the orchard environment were gathered as an extra test set named test_orchard. Two parts of training set in the network training process is called as training set and validation set. The training and validation division ratio is 9:1.In CNN, the training set is utilized for fitting model and the validation set is a distinct sample set in the model training process, that was utilized towards the adjustment of super parameters in this method and the capability of the model is preliminarily evaluated.

4.2 Results:

The stages disease detection for tomato and grapes has been analysis based on the confusion matrix given in figure 4 (a) and (b). Here the disease has been detected from the true and false positive rate by actual and predicted class. It provides the efficiency of the proposed model in comparison with actual and predicted values. This evaluation depending on the estimating True Positive (TP), False Negative (FN), True Negative (TN), and False Positive (FP) as represented in equation (15)

$$\text{Confusion Matrix} = \begin{bmatrix} TP & FP \\ FN & TN \end{bmatrix} \qquad (15)$$

here, TP is the predicted value is predicted as positive. FP is the predicted value which is initially projected as negative and later as positive. TN is the value predicted as negative and expected as unfavourable. FN is the predicted value that is initially projected as positive and negative later.

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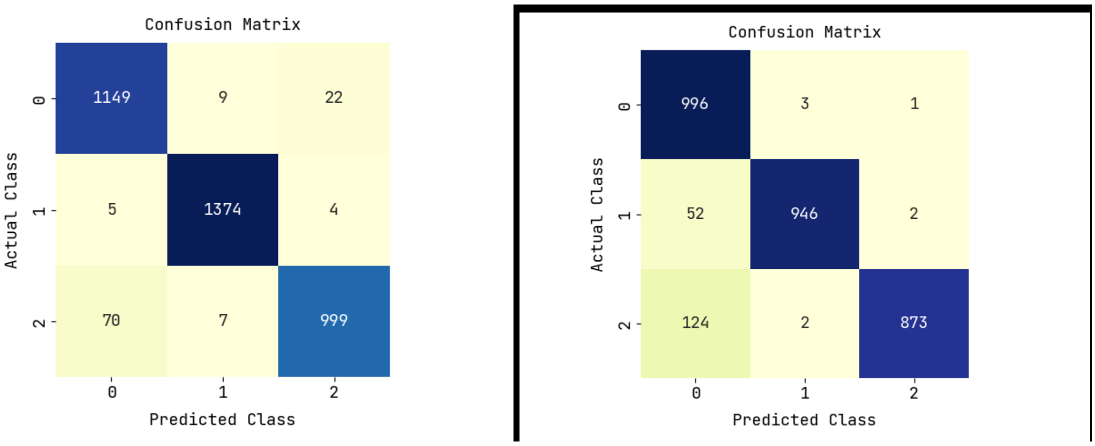
Result 1:

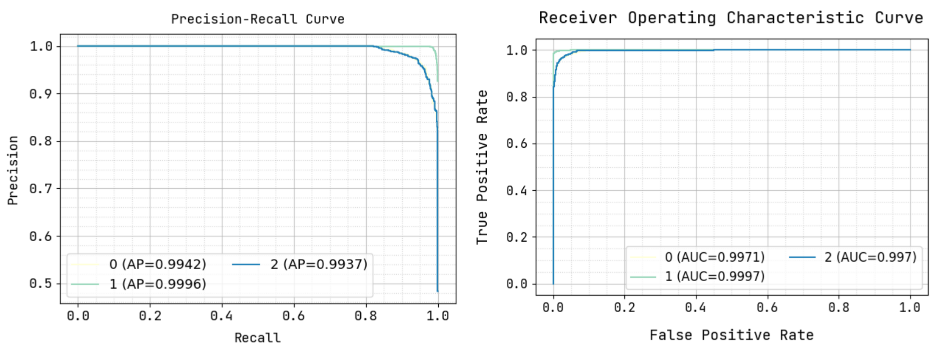


(a) (b)

Figure-4 Confusion matrix in stages of disease detection for tomato and grapes plant

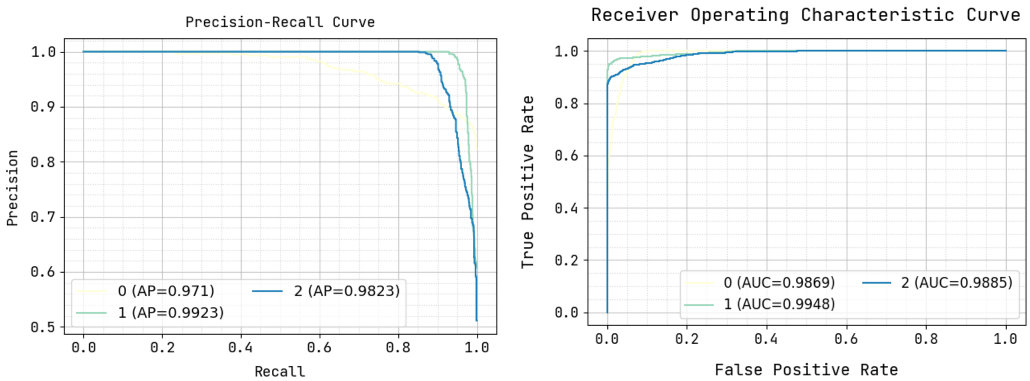
The below figure-5 (a), (b) shows the precision- recall (PR) and ROC curve for grape diseases detection using proposed feature extraction and classification techniques.

Result 2:



(a) (b)

Figure-5 PR and ROC curve for grape disease detection



(a) (b)

Figure-6 PR and ROC curve for tomato disease detection

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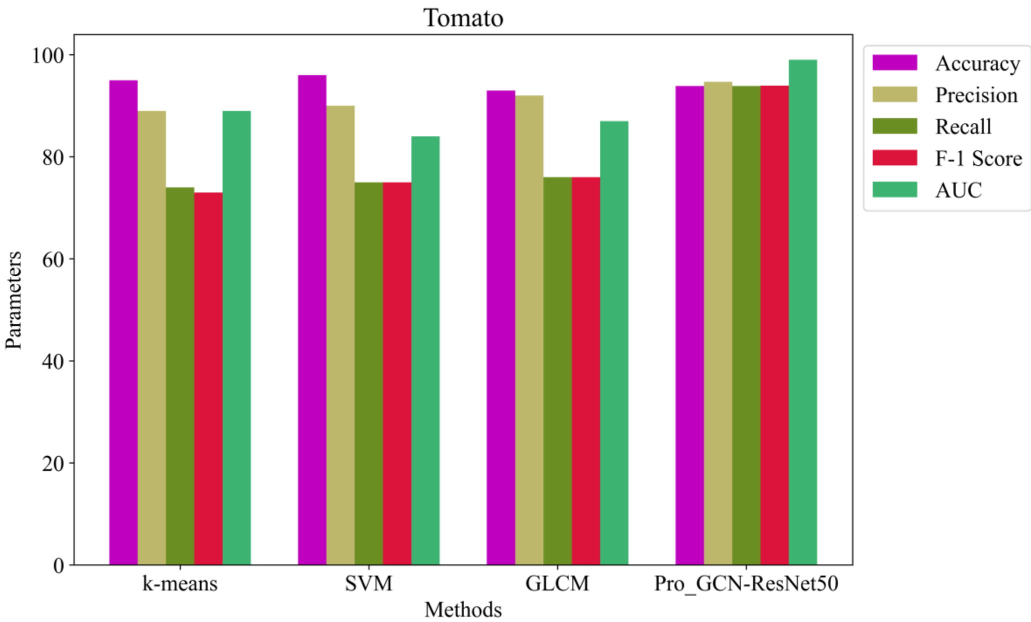
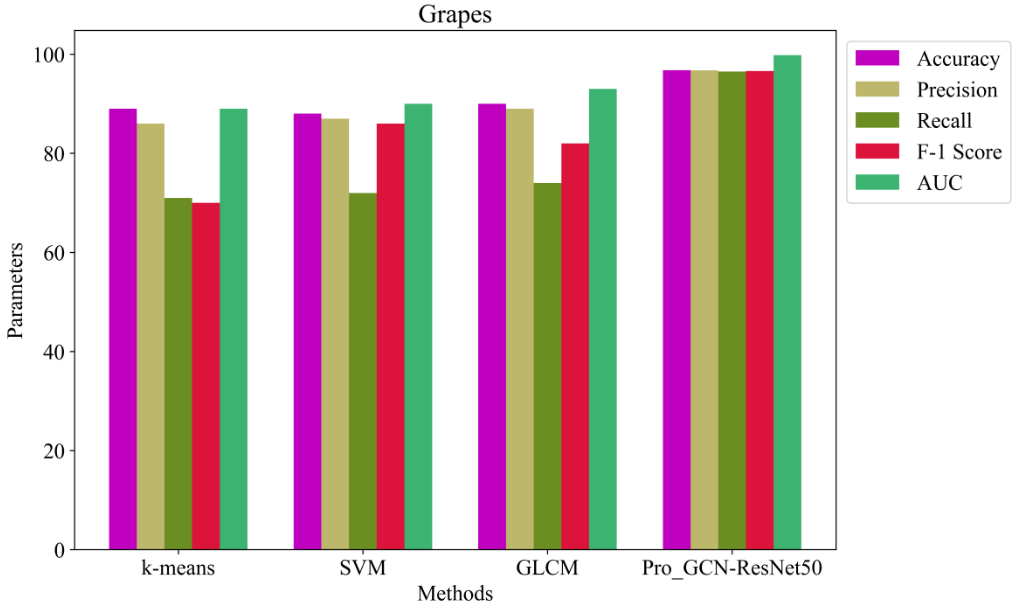
The above figure-6 (a), (b) shows the precision- recall (PR) and ROC curve for tomato diseases detection using proposed feature extraction and classification techniques. Hence from above confusion matrix the prediction class has been validated along with the parameters of precision and recall of a deep neural network classification method. The entire comparative analysis of proposed technique is represented in table-1 and figure-7 (a), (b).

Table-1 Comparative Analysis in crop disease detection

Crop	Parameter	k-means	SVM	GLCM	Pro_GCN-ResNet50
Tomato	Accuracy	95	96	93	93.86
	Precision	89	90	92	94.70
	Recall	74	75	76	93.86
	F-1 score	73	75	76	93.94
	AUC	89	84	87	99.01
Grapes	Accuracy	89	88	90	96.78
	Precision	86	87	89	96.73
	Recall	71	72	74	96.52
	F-1 score	70	86	82	96.60
	AUC				99.80



(a) Tomato stages of disease detection



(b) Grapes stages of disease detection

Figure-7 Comparative analysis of (a) Tomato and (b) Grapes stages of disease detection

5. Conclusion:

This research proposes novel technique in detection of various plant disease stages using feature extraction and classification using deep learning techniques. here the input data has been collected from tomato and grape leafs. This data has been processed for noise removal, image resize and normalization. Then this image features have been extracted using graph Convolutional networks and classification of extracted features has been done using ResNet-50. Seven disease classes are used for the identification of minimum layer's set are used in this technique. Plant Village dataset is used for training the neural network. This system is designed by using Graphical User Interface. The image dataset is chosen by the user with GUI permission. Any image from the dataset can be selected by the user and the images are loaded that is followed by the disease prediction and it is shown by the user interface. Identification and recognition of disease in the plant leaf is trained by ResNet-50 and it is used in the classification and prediction of correct disease for nearly with some anomalies. Furthermore, the experimental comparison of grape leaf diseases in the public dataset and better results are obtained with 94% of average identification accuracy. Attention module is added and it is certified there is an accurate complex feature extraction based on the disease variety and some parameters. Higher performance was achieved by the proposed model for the crop disease diagnosis in the agricultural environment.

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