

Image classification of sugarcane aphid density using deep convolutional neural networks

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ARTICLE INFO

Keywords:

Sorghum
Integrated pest management
Sugarcane aphid
Automation
Classification

ABSTRACT

Sugarcane aphid, *Melanaphis sacchari* (Zehntner), has caused significant yield loss across the sorghum (*Sorghum bicolor* L. Moench) production region in the U.S. Adequate management of sugarcane aphid depends on pest monitoring and economic threshold levels to spray insecticides. However, scouting this pest under field conditions is time-consuming and inefficient. To assist pest monitoring, we propose the use of deep learning models to automatically classify sugarcane aphid infestation on leaves according to different density levels in images. We used a total of 5,048 images collected during field scouting events and evaluated the performance of four deep learning classification models: Inception v3, DenseNet 121, Resnet 50, and Xception. We trained the models to classify aphid densities into 6 classes based on established standard threshold levels for spraying: no aphids present (0 sugarcane aphids/leaf), no threat or below an action/treatment threshold (1–10, and 11–39 sugarcane aphids/leaf), and infested above an economic threshold where an insecticide should be applied (40–125, 126–500, and > 500 sugarcane aphids/leaf) to manage sugarcane aphid in field conditions. Among these models, Inception v3 and Xception performed best with an overall accuracy score of 86% and a lower number of misclassified images. Importantly, the models correctly classified aphids as above or below threshold spray density over 97% of the time. The methodology developed and the models tested in this study can be used in sampling protocols and further mobile applications or remote sensing technologies. These technologies can assist sorghum growers and researchers to scout and screen sugarcane aphid in susceptible and resistant sorghum varieties automatically and provide accurate recommendations on whether or not to apply pesticides.

1. Introduction

Since the beginning of agriculture development, insects have played an influential role in food production and the ecosystem services they provide to the environment [1]. Growers have historically competed with herbivorous and pathogen-transmitting insects, collectively called 'pests', and different strategies have been developed to control them in agriculture [2]. Most of these management options include chemical, cultural, biological, and mechanical activities that help manage agricultural pests. Collectively, these options are longer-term strategies as part of integrated pest management (IPM) program, which aims to provide sustainable agriculture management solutions in various agro-ecosystems. IPM tactics have been applied on many crops, including corn, soybeans, cotton, wheat, and sorghum. In the U.S., sorghum (*Sorghum bicolor* L. Moench) is an important economic crop that had a value over \$1 billion in 2020 and was planted on 5880 million acres [3]. Sorghum contributed approximately more than \$1 billion to the

economy in Kansas in 2020 and ranked as one of the top crops produced by the state [4]. Nevertheless, sorghum faces significant pest management challenges and yield losses during its production.

Sugarcane aphid, *Melanaphis sacchari* (Zehntner) (Hemiptera: Aphydidae), is considered an economically important pest in sorghum across much of the Southern Great Plains since its re-introduction in 2013 [5]. Different management strategies have been developed, including pest monitoring guides, insecticide treatment protocols, and the development of resistant or tolerant hybrids to reduce the impact of this pest [5]. Usually, treatment decisions for sugarcane aphid depend visually assessing sorghum leaves for aphids to determine an economic threshold for insecticide applications [6]. An economic threshold is defined as the pest density that management action must implement to prevent reaching economic injury level [7].

According to Gordy et al. [8], a suggested economic threshold for sugarcane aphids is 40 aphids per leaf. However, obtaining an accurate estimation of the number of sugarcane aphids on leaves is a

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time-consuming and challenging task due to the high reproduction rates, variety of growth stages, clustering behavior, and the need to inspect wider areas of fields [9,10]. In addition, sugarcane aphid populations can change quickly, requiring continuous monitoring of infested fields through the growing season. However, automating the scouting process can address several of these challenges using artificial intelligence (AI) and associated classification methods to quantify sugarcane aphid densities.

Currently, AI technology can efficiently detect and classify surrounding living organisms with the slightest use of labor and time to advance precision agriculture. Machine learning is a subfield of AI in which labeled image data can be used to train a model, which can subsequently make predictions on new unseen images without additional programmatic effort using deep learning [11]. Convolutional neural networks (CNNs), a technology in deep learning, can analyze visual imagery and perform tasks such as image classification and object detection with high performances [12]. Deep learning models can be designed in a user-friendly manner that can be applied to solve agricultural activities that are labor intensive, like pest monitoring [11].

However, deep learning models for the automatic classification of sugarcane aphid densities have not been researched in sorghum for pest monitoring protocols. Thus, a vision-based automated system for image processing using deep neural networks is needed for accurate classification of sugarcane aphid densities to standardized sampling for pest monitoring protocols in sorghum. In the present work, we trained four different deep learning models, including Inception v3, DenseNet 121, Resnet 50, and Xception, and evaluated their ability to classify different densities of sugarcane aphid that are used to determine treatment decisions based on the economic threshold management actions. Our main objective was to develop an effective deep learning model for classifying sugarcane aphid densities in images. The results of this research can be applied to current sampling protocols with further development in mobile applications or remote sensing technologies to automate the classification of other pests in different crops during pest monitoring.

2. Methods

2.1. Field image collection

Sugarcane aphid imagery was collected from commercial sorghum fields from southern Kansas in 2020 and 2021. The imagery included either an individual leaf from the upper or lower section of a sorghum plant. Each image consisted of a section of the leaf with and without sugarcane aphid. Images were taken using a Sony ILCE-6000 v 3.10 digital camera and photographed during field scouting events of commercial sorghum fields (average field size was 5 acres). Initially, each image had a dimension of 4000×6000 pixels and an RGB color representation. A total of 5048 images were collected and manually classified into 6 distinct categories based on the number of sugarcane aphid per leaf per image. Classification categories were based on pest monitoring parameters to determine economic threshold levels for sugarcane aphid [5,6,8]. The categories were no aphids present (0 sugarcane aphids/leaf), no threat or below an action/treatment threshold (1–10, and 11–39 sugarcane aphids/leaf), and infested above an economic threshold where an insecticide should be applied (40–125, 126–500, and > 500 sugarcane aphids/leaf).

2.2. Summary of classification deep learning models

Different deep learning models have been proposed to detect and classify various living organisms, including insects, plants, or diseases, to advance the field of precision agriculture. We selected four broadly used models for classification tasks to evaluate their performance in accuracy on sugarcane aphid density classification using images [13–15]. The four models were selected based on the different tasks for image classification of other agricultural issues and model size

(<100 MB), which can influence the training process and further development of applications. The four models differ in architecture; however, they were selected based on the different tasks for image classification of other agricultural issues and model size (<100 MB), which can influence the training process and further development of applications.

The models tested were Inception v3, DenseNet 121, Resnet 50, and Xception, which are models found in Keras applications [16]. Inception v3 is a deep learning model with small convolutions, accelerated training speed, and reduced computational cost [14]. DenseNet 121, another lightweight model tested, requires fewer parameters than traditional convolutional networks, making it easy to train [13]. Resnet 50 has smaller parameter size compared with other CNNs making it faster to train [15], and Xception was selected for its higher value of top-1 and top-5 accuracy and the overall model performance using the ImageNet validation dataset found in Keras applications.

2.3. Model training and description of hyperparameters

The four deep learning models used in this study are pre-trained on the ImageNet validation dataset [17]. We retrained those models for sugarcane aphid density classification using a manually labeled image dataset. The image dataset was divided into training (80%) and testing (20%) sets. Images within the 6 categories of sugarcane aphid densities were split and randomly combined through the 80:20 ratio to maintain this training and testing proportion. We resized all 4000×6000 pixel images to a standard 500×500 pixel size (Fig. 1) to independently train the four alternative deep learning models.

To reduce the overfitting of our models, we used an image augmentation procedure built into the deep learning models that included random rotation ($\leq 100^\circ$), sheer ($\leq 30\%$), zoom ($\leq 10\%$), and horizontal flip [18]. Due to the categorical imbalance in our data set, the predictions were weighted by category sample size to reduce bias in model testing. We used 100 epochs with a batch size of 10. Training was performed using an Nvidia GeForce GTX 1080 graphic processing unit. To evaluate the classification performance of the four deep learning models, we evaluated the confusion matrix and the overall and class-level precision, recall, and F1 scores.

3. Results

The four deep learning models provided similar accuracy scores when classifying sugarcane aphids (Table 1). Inception v3 and Xception deep learning models had the highest overall test accuracy score of 86%. Resnet 50 and DenseNet 121 had slightly lower test accuracy scores of 85%. The highest average precision was 81% for Inception v3 and Xception and only 1% lower for Resnet 50 and DenseNet 121 model. The average recall and F1 scores were $\geq 80\%$ for the four models tested. The Inception v3 and Xception models had the best accuracy, highest average precision, recall, and F1 scores. Therefore, we used the Inception v3 and Xception models for the remainder of the results due to their better classification of sugarcane aphid densities.

The Inception v3 and Xception models adequately categorized sugarcane aphid densities into distinct categories based on features from the model. By combining aphid density classes as above- or below-threshold, the models correctly classified infested leaves as above or below threshold density 97% of the time. Our Inception v3 model correctly classified 504 of 511 and 474 of 499 images as above or below threshold, respectively. The Xception model performed similarly to Inception v3, as it correctly classified 505 of 511 and 476 of 499 images above or below the threshold, respectively.

Overall, the image classification results in the confusion matrix of the Inception v3 model (Table 2) had similar number of misclassified images to the Xception model. The classification category of no aphids, for example, was correctly classified with 211 of 227 test images and only 35 of 317 test images were mislabeled leaves in the 126–500 aphids

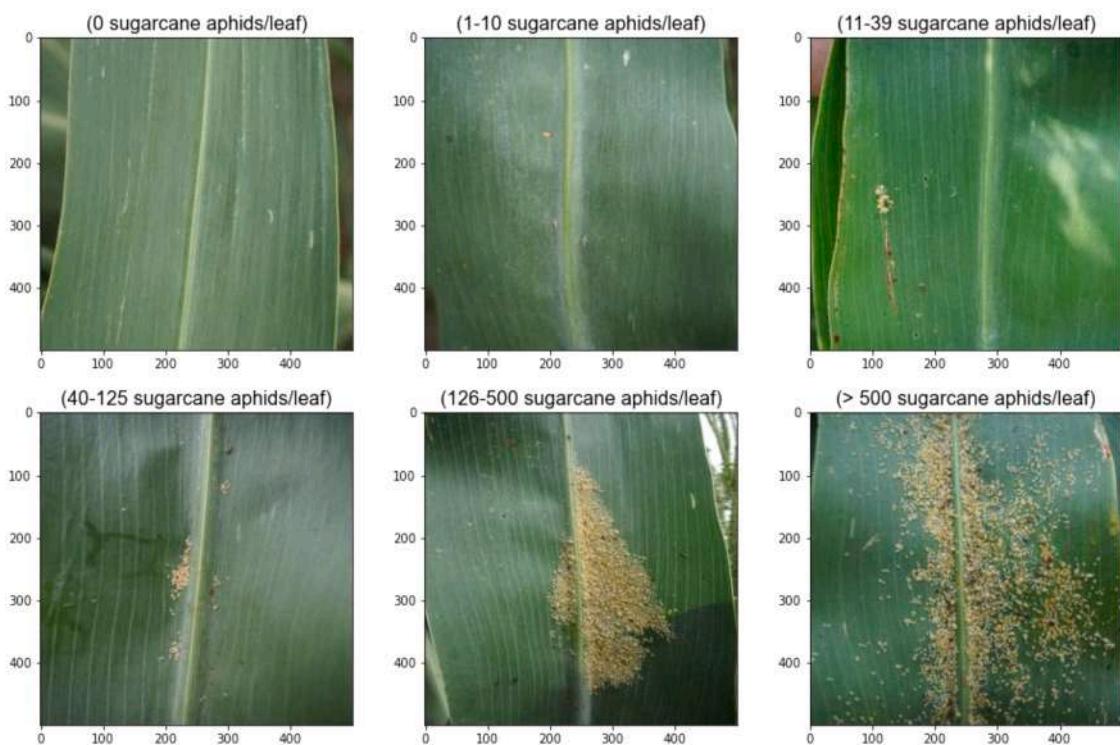


Fig. 1. Examples of training images for Inception v3, DenseNet 121, Resnet 50, and Xception models using 500 × 500-pixel images.

Table 1

Overall accuracy, precision, recall, and F1 scores of the classification models tested.

Deep learning models	Accuracy score	Precision weighted average	Recall weighted average	F1 score weighted average
Inception v3	0.86	0.86	0.86	0.86
DenseNet 121	0.85	0.86	0.85	0.85
Resnet 50	0.85	0.86	0.85	0.85
Xception	0.86	0.87	0.86	0.86

category. The highest precision values were observed for categories of no aphids and 126–500 aphids with 92% and 93%, respectively. The next two categories, 11–39 aphids and 40–125 aphids, had slightly lower precision score of 86% and 80%, respectively. The lowest precision scores of 75% and 61% corresponded to categories of 1–10 aphids and > 500 aphids, respectively, on sorghum leaves.

For the image classification results in the Xception model confusion matrix (Table 3), the classification category of no aphids was correctly

classified for 198 of 227 test images resulting in a 93% precision. Lower precision scores were found in the classification categories of 1–10 aphids and > 500 aphids, which was similar to the classification results of the Inception v3 model. The highest precision values were observed in categories of no aphids and 126–500 aphids with 93% and 95%, respectively. Lastly, the 11–39 aphids and 40–125 aphid categories had precision scores of 86% and 80%, respectively. Sugarcane aphid categories with a higher number of trained images had a lower percentage of misclassified images

Table 2

Confusion matrix of Inception v3 model. Numbers in bold correspond to correct predicted image classification in each density category. The green boxes show the number of correct predictions below threshold level, and yellow denotes the number of correct predictions above threshold.

		Predicted (sugarcane aphids/leaf)						Total number of tested images
Categories (sugarcane aphids/leaf)		0	1-10	11-39	40-125	126-500	> 500	
True (sugarcane aphids/leaf)	0	211	15	1	0	0	0	227
	1-10	19	77	13	1	0	0	110
	11-39	0	11	127	23	1	0	162
	40-125	0	0	6	128	15	0	149
	126-500	0	0	1	8	282	26	317
	> 500	0	0	0	0	4	41	45

Table 3

Confusion matrix of Xception model. Numbers in bold correspond to correct predicted image classification in each density category. The green boxes show the number of correct predictions below threshold level, and yellow denotes the number of correct predictions above threshold level.

Categories (sugarcane aphids/leaf)	Predicted (sugarcane aphids/leaf)						Total number of tested images
	0	1-10	11- 39	40- 125	126- 500	> 500	
True (sugarcane aphids/leaf)	0	198	29	0	0	0	227
	1-10	13	81	15	0	1	110
	11-39	1	12	127	21	1	162
	40-125	0	0	6	134	9	149
	126-500	0	0	0	13	285	19
	> 500	0	0	0	4	41	45

but higher precision scores compared to sugarcane aphid categories with a lower number of trained images. However, from a pest management perspective, the Inception v3 and Xception model can correctly classify aphids as “above or below threshold density” 97% of the time.

4. Discussion

4.1. Overall models performance and applications

The current study demonstrates that two deep learning models can classify images of infested sorghum leaves into different aphid densities categories with an overall accuracy of 86% and correctly classified aphids as above or below threshold density 97% of the time. To date, estimates are performed using visual assessments, but accuracy can vary based on sampler experience and training history increasing bias during sampling [6,8]. Current sampling protocols suggest collecting 40–60 two-leaf samples and treating when 20–30% of plants are infested with an estimate of 25–125 sugarcane aphids/leaf [19].

During sampling, a visual assessment consists of manually evaluating the whole sorghum leaf to provide an estimated number of sugarcane aphids, which is a time-consuming task. We suggest applying these models to current sampling protocols by taking images with different sugarcane aphid infestation levels on leaves, which can be added and used as inputs for our models to provide a standardized estimate of the number of sugarcane aphids present. Our approach can reduce leaf evaluation time and decrease human error in estimates that usually occurs when sampling protocols for pests are deployed in the field. Thus, this could potentially result in more reliable and consistent data to inform treatment decisions for sugarcane aphid management in sorghum.

The Inception v3 or Xception models are adequate candidates for automatically classifying sugarcane aphid densities without manual counting and produced error rates within acceptable levels compared to standard measurements. Consequently, standardized, and automated aphid density estimates can be used to monitor changes in aphid population size in real-time using images of infested leaves that can be used to develop agile mobile applications, integrated in remote sensing systems for onboard, automatic pest monitoring, screening resistant sorghum varieties, and used to model the population dynamics of sugarcane aphid in sorghum.

4.2. Models performance within categories

At the categorical level of sugarcane aphid densities classification, Inception v3 had similar number of misclassified images to Xception based on the confusion matrices. However, both models can

differentiate between categories of sugarcane aphid densities accurately. The purpose of having an automatic categorical classifier of sugarcane aphid densities is to reduce time spent counting and sampler bias. In addition, to categorize sugarcane aphid densities because, to our best knowledge, sugarcane aphid counting is challenging when aphids start to cluster, making it difficult for visually assess aphid densities on leaves. We decided to combine the categories as “below threshold” including the first three categories of sugarcane aphid densities (0, 1–10, and 11–39 sugarcane aphids/leaf) since any management strategy that is warranted manage sugarcane aphid will not affect the development of the crop and therefore not reduce sorghum yield. On the other hand, the higher density categories (40–125, 126–500, and > 500 sugarcane aphids/leaf) were combined because current best management practices suggest applying an insecticide manage sugarcane aphid populations above 40 aphids per leaf. The results of our study have shown that the Inception v3 and Xception models can distinguish above or below these treatment categories 97% of the time, making these models candidates for pest monitoring in sorghum.

4.3. Models improvement

Collecting more images, especially of sugarcane aphid categories where we observed a higher number of misclassified images, will improve the classification accuracy of our models. However, for an IPM perspective, distinguishing between the below (11–39 aphids) and above (40–125 aphids) pest threshold level is sufficient and useful for making pest management decisions. Consequently, incorporating more images will reduce the current imbalance among categories resulting in more balance data for training future models, as observed in other systems [18]. Making these trained models trained accessible to other researchers makes it easier for other developers to continue increasing the accuracy score and overall performance of these models to classify sugarcane aphid densities, which is another benefit of CNNs in general [20].

4.4. Limitations and future work

This study provided a framework for how deep learning models can classify pests for pest monitoring in sorghum. The results were promising, however, collecting more images for the categories with the lower number of images for training will improve the accuracy scores of these models. We presume our models can significantly enhance the scouting of agronomic pests for sampling protocols and serve as valuable information for further sensor systems on unmanned vehicles to improve crop management decisions. The rise of unmanned aircraft systems, including unmanned aerial and ground vehicles (UAV and UGV), continue

progressing and helping growers manage their agricultural fields [21]. In the near future, drone technology will give the agriculture industry a high-technology renovation. Consequently, using UAV and UGV with our framework can provide real-time detection and mapping areas of sugarcane aphid infestation for economic management decisions.

5. Conclusion

More than 50 years have passed since the development of IPM, and pest monitoring continues to be time-consuming and laboriously expensive. Entomologists and growers continuously monitor pests using traditional methods that are time consuming. This study developed a framework and two models that can automatically categorize leaf-level sugarcane aphid infestation using digital images to renovate pest monitoring. The Inception v3 and Xception models were tested to evaluate their performance in classifying sugarcane aphid densities at 6 infestation levels, including no aphids (0 sugarcane aphids/leaf) and (1–10, 11–39, 40–125, 126–500, and > 500 sugarcane aphids/leaf) with a classification accuracy of 86%. More image samples can be added to the current models within sugarcane aphid categories to increase their accuracy scores and model performances. Ideally, these two models can be used in sampling protocols and further mobile applications or remote sensor systems that would detect and categorize sugarcane aphid densities, resulting in a reliable pest control strategy based on the economic threshold in sorghum. Ultimately, our study wants to project a new growth mindset to renovate pest monitoring, computer vision, and unmanned vehicles to improve the current IPM strategies to enhance sustainability and food production.

Funding

This project was partially supported by the National Robotic Initiative grant no. 2019-67021-28995. This is contribution no. 22-227-J from the Kansas Agricultural Experiment Station.

Credit authorship contribution statement

Ivan Grijalva: Investigation, Data curation, Resources, Conceptualization, Methodology, Software, Formal analysis, Writing – original draft. **Brian J. Spiesman:** Conceptualization, Methodology, Software, Formal analysis, Writing – original draft. **Brian McCornack:** Investigation, Writing – original draft.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data Availability Statement

The image dataset and codes used in this study will be made available on Mendeley Data.

Acknowledgments

We want to thank the research members of the Field Crops IPM Lab,

including Kent Hampton, Nick Clark, and Max Dunlap, for their support, data collection and manual classification of images.

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Received June 26, 2021, accepted July 11, 2021, date of publication July 14, 2021, date of current version July 21, 2021.

Digital Object Identifier 10.1109/ACCESS.2021.3097050

Grape Leaf Spot Identification Under Limited Samples by Fine Grained-GAN

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This work was supported in part by the 2021 Project of the 14th Five-Year Plan of Educational Science in Heilongjiang Province under Grant GJB1421224 and GJB1421226, and in part by the 2021 Smart Campus Project of Agricultural College Branch of China Association of Educational Technology under Grant C21ZD02.

ABSTRACT In practice, early detection of disease is of high importance to practical value, corresponding measures can be taken at the early stage of plant disease. However, in the early stage of disease or when a rare disease occurs, there are limited training samples in practice, which makes machine learning especially deep learning models hardly work well while the stronger representative ability needs large-scale training data. To solve this problem, a fine grained-GAN based grape leaf spot identification method was proposed for local spot area image data augmentation to the generated local spot area images which were added and fed them into deep learning models for training to further strengthen the generalization ability of the classification models, which can effectively improve the accuracy and robustness of the prediction. Including 500 early-stage grape leaf spot images every category were fed into the proposed fine grained-GAN for local spot area data augmentation, 1000 local spot area sub images every category were generated in this study. The improved faster R-CNN was integrated in fine grained-GAN as local spot area detector. After that, the segmented sub-images and generated sub-images were mixed as training data input into the deep learning models, while the original segmented sub-images were used for testing. Experimental results showed that the proposed method had achieved higher identification accuracy on five state-of-art deep learning models; especially ResNet-50 had got 96.27% accuracy, which obtained significant improvements than other data augmentation methods and verified its satisfactory performance. This is of great practical significance for rare diseases or limited training samples.

INDEX TERMS Fine grained-GAN, grape leaf spot identification, deep learning, few-shot learning, agricultural engineering.

I. INTRODUCTION

When enjoying the most luscious grape wine such as *Lafite* or *Latour*, we may not realize that the grape planting industry may have a disastrous threat by various diseases. The grape planting industry and even the planting industry are suffering from plant diseases, according to FAO (Food and Agriculture Organization of the United Nations); plant diseases cost around \$220 billion of global economy every year [1]. How to accurately identify early symptoms of disease and prevent plant from further intrusion is one of the most important

The associate editor coordinating the review of this manuscript and approving it for publication was Liandong Zhu.

problems for agricultural growers. Since the symptoms of grape diseases mainly appear visually on the leaves, computer vision and image processing is an effective and rapid method to identify it. The traditional computer vision approaches have been carried out for grape disease recognition task.

In recent years, researchers have made unremitting efforts to identify grape diseases and achieved a lot of meaningful results. A. Bharate, *et al.* [2] proposed a computer vision based method to classify grape leaves into healthy and non-healthy ones, grape leaf features such as texture and color were extracted and input into K-nearest neighbor and support vector machine classifiers. The experimental results showed that the best performance of the two classifiers was 90%

and 96.6% respectively. J. Zhu, *et al.* [3] proposed an automatic grape leaf disease detection method using image analysis and back-propagation neural network. According to the lesion region, the authors extracted five features of it such as shape complexity, circularity, perimeter, rectangularity, and area. Based on the five features, the back-propagation neural network was introduced in this work to identify grape leaf diseases with high classification accuracy; the proposed method can identify five grape leaf diseases: *round spot*, *sphaceloma ampelinum debary*, *leaf spot*, *downy mildew*, and *anthracnose*. M. Shantkumari, *et al.* [4] proposed an adaptive snake approach in grape leaf disease segmentation method. They used the plant level dataset and precision and recall as the model metrics for evaluating the proposed model, the proposed methodology outperforms the existing grape leaf segmentation model. S. Jaisakthi, *et al.* [5] proposed an automatic grape leaf disease detection system based on image processing and machine learning technique. The authors segmented region of interest of grape leaf from the background image by grabbing cut segmentation, and the diseased region was segmented by global thresholding and semi-supervised method. Finally, the support vector machine, *adaboost* and random forest tree were selected for extracting features and classifying grape leaf disease into four categories such as leaf blight, rot, esca, and healthy. Experiment results showed that the Support Vector Machine classifier had achieved the best performance as high as 93%. Kirti, *et al.* [6] proposed a new method based on support vector machine to identify the color difference between the black rot area of grape leaves and the surrounding healthy leaves. The color technology HSV and the L*a*b* color model were used to segment the discolor-spot area, and the highest classification accuracy could reach 94.1%. A. Sinha, *et al.* [7] proposed two ways to separate disinfected leaf areas. First, L*a*b* color model was used to segment leaf color thresholds; then, K-means was used to segment color in RGB color model; after that, machine vision recognition method was used to verify the quantization of the ratio between the segmented area and the whole leaf area. C. Khithuk, *et al.* [8] proposed an unsupervised simplified fuzzy ArtMap neural network method for the detection of plant diseases.

These methods above had made the state-of-the-art performance in grape leaf disease identification. However, in nature environment, these methods are hard to cope with the situation of large amount of test data. The deep learning method was introduced in plant disease identification area in recent years, which are good at processing large scale data and it can automatically learn feature representations from giving data [9], [10]. X. Xie, *et al.* [11] proposed a real-time grape leaf diseases detection system based on improved deep convolutional neural networks. Experimental results show that the proposed method obtained the precision of 81.1% map on GLDD and the detection speed reaches 15.01 FPS. This method provided a feasible solution for the identification of grape leaf diseases and guidance for the detection of other plant leaf diseases. K. Thet, *et al.* [12] proposed an improved

VGG16 method to improve the classification accuracy of five grape leaf diseases, which mainly adopted the full connection layer and support vector machine, had achieved a satisfactory performance. B. Liu, *et al.* [13] proposed a novel model based on Leaf GAN to generate four classes of different grape leaf diseases images for training. The authors first designed a generator model with digressive channels; instance normalization was introduced to identify real and fake disease images, and the deep regret gradient penalty method was adopted to stabilize the training process. A total of 8,124 images were generated, experimental results showed that the proposed model can achieve 98.70% accuracy on test data based on Xception, which demonstrated it could overcome overfitting problem and improve identification accuracy.

In addition to grape disease identification, in the field of plant disease identification, there are also many excellent research results that can be used for reference. X. Liu, *et al.* [14] proposed a plant disease identification method based on the dataset including 220,592 images with 271 categories, Experimental results showed that the proposed method had achieved a better performance than the exiting start-of-art models. L. Kouhalvandi, *et al.* [15] proposed a method to optimize the neural network using the S-metric selective college global optimization and DIRECT multi-objective Bayesian optimization techniques for detecting plant disease. S. Chouhan, *et al.* [16] proposed a bacterial foraging optimization algorithm based on radial basis function neural network, which could automatically classify and identify plant leaf diseases. A variety of fungal diseases have been studied with high identification accuracy. M. Chanda *et al.* [17] proposed a particle swarm optimization algorithm (PSO) which was used to optimize the weight of the neural network of the back propagation algorithm to solve the overfitting problem of the neural network. C. Senthilkumar, *et al.* [18] proposed a segmentation method for detecting citrus diseases based on classification model. In this model, reverse neural network was used to classify citrus diseases. A. Förster, *et al.* [19] proposed a method using hyperspectral learning models which included color and spot characteristics of various diseases, and adopted generative adversarial networks and time series to predict the transmission cycle of the diseases. S. Militante, *et al.* [20] proposed an improved deep learning model to capture plant leaf diseases using a large number of training data, which had achieved high identification accuracy. X. Guan, *et al.* [21] proposed a new classification model for detecting plant leaf diseases which combined four CNNs. X. Guo, *et al.* [22] proposed an improved traditional PCNN method of image segmentation technology to complete the image segmentation task of plant diseases. C. Zhou, *et al.* [23] proposed a restructured deep residual dense network for tomato leaf disease identification, which had achieved a satisfactory result.

These studies above had shown good results but few researches focus on the early stage of plant diseases [24]. Compared with the traditional machine learning and computer vision methods, deep learning models exhibit more

representative ability by inputting training dataset through optimize functions to produce robust descriptive features and perform recognition tasks based on those features. However, in natural environment of agricultural cultivation, there are not enough training data to train a machine learning model. In this paper, we proposed a fine grained-GAN based grape leaf spot identification model under limited training samples, which can take advantage of the strong representative ability of deep learning models and not be limited by the lack of training data. The main contributions of this work can be stated as follows.

1) A fine grained-GAN was proposed for local spot area data augmentation; the hierarchical mask generation method made the ability of spot feature representation stronger than the exiting GANs in grape leaf spot data augmentation, which makes it significantly improve the identification accuracy of grape leaf spot.

2) An annotated grape leaf disease spot image dataset was built up in this work.

II. RELATED WORK

Generative Adversarial Networks (GANs) [25] had made great success in image generation which can leverage the practically unlimited amount of unlabeled images and learn good intermediate representations. The state-of-arts models such as DCGAN [26], infoGAN [27], WGAN [28], LRGAN [29] were introduced in this study for grape leaf spot data augmentation.

A. DCGAN

Compared with other GANs, DCGAN (Deep Convolutional Generative Adversarial Networks) [26] uses step convolution layers in discriminator and fractional step convolution layers in generator instead of all the pooling layers, and the batch normalization operations are used in generators and discriminators. In DCGAN, the dense layers are removed and the global pooling layer instead, the *Tanh* activation function was used in output layer of the generator and the *ReLU* activation functions are used in other layers, and the *LeakyReLU* activation functions were used in discriminators. The DCGAN has proved that strong feature representation ability in unsupervised learning, which has shown the convincing evidence of DCGAN learned a hierarchy of representations from object parts to scenes in both the generator and discriminator, the applicability of learning features for novel tasks-demonstrating has been proved feasible.

B. InfoGAN

InfoGAN [27] was called one of the breakthroughs of NIPS 2016; it aimed to get the decomposable feature representation through unsupervised learning. Different from the traditional generation adversarial networks, it used random noise in a highly entangled mode, and each dimension of random noise cannot explicitly represented the attributes or features in the real data space. The proposed InfoGAN used unsupervised learning method to learn disentangled representation in the

hidden space. The InfoGAN can maximize mutual information between generated images and input implicit coding; it can be expressed in a random way without additional computing resource.

C. WGAN

Suffering from the training instability of GANs, WGAN [28] used an alternative to clip weights: penalize the norm of gradient of the critic with respect to its input. WGAN uses EM distance instead of JS and KL divergence to solve the distance measurement between generation and real distribution, which has improved the two kinds of problems existing in the original GANs, it performs better than standard GANs and enabled stable training of a wide variety of GANs architectures with almost no hyper-parameter tuning.

D. LRGAN

LRGAN (Layered Recursive Generative Adversarial Networks) [29] can generate images layer by layer recursively. Firstly, the background image is generated, and then the foreground image, pose and shape are generated one by one. After that, LRGAN put the foreground on the corresponding background in a context related way to generate a complete natural image. The whole model is unsupervised and trained end-to-end by gradient descent. In this way, LRGAN can significantly reduce the mixing between background and foreground. Furthermore, both qualitative and quantitative comparisons show that LRGAN can generate better and clearer images than the DCGAN.

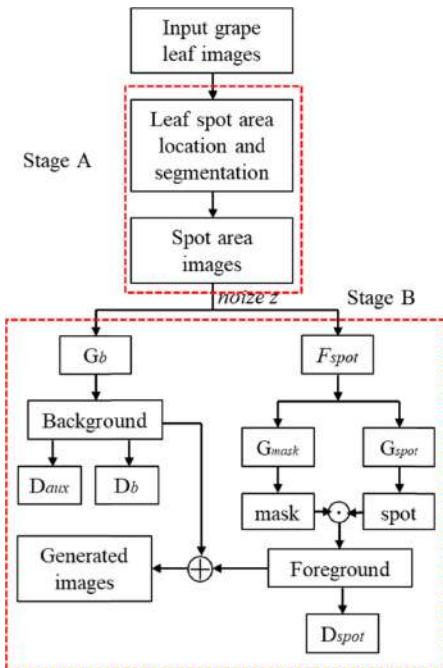
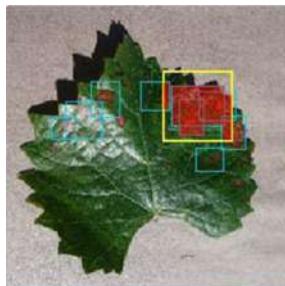
III. PROPOSED METHOD

In this study, a local grape leaf spot area data augmentation method named fine grained-GAN was proposed. The novel method integrated object detection, image segmentation and generative adversarial networks. Since the leaf background is almost the same, in order to improve the representation ability of leaf spot features and reduce the background noise interference, the improved faster R-CNN [30] was used for grape leaf spot detection and segmentation. As shown in FIGURE 1, the proposed fine grained-GAN can be divided into two stages: leaf spot location and segmentation stage, and local spot area data augmentation stage.

A. THE SIZE OF DETECTION BOUNDING BOX

To reduce the computational complexity and increase the network efficiency, a constant detection bounding box size was adopted in this study. The selection rule of the size of detection bounding box was depicted as follows.

- 1) 1000 grape leaves were randomly selected as samples, and 4 bounding boxes of different sizes were used as candidate bounding boxes. In this study, the size of 32*32, 64*64, 96*96, and 128*128 were selected.
- 2) The grape leaves were input into Faster R-CNN for spot detection with the adaptive size detection box.
- 3) The candidate bounding boxes were used to traverse each adaptive detection box and calculated the ratio

**FIGURE 1.** The flowchart of fine grained-GAN.**FIGURE 2.** The area of intersection.

of the area of intersection and the area of candidate bounding boxes, as shown in (1) and FIGURE 2.

$$Ratio = \frac{A_{Intersection}}{A_{candidate\ bounding\ box}} \quad (1)$$

where $A_{Intersection}$ denotes the area of intersection in adaptive detection boxes and the candidate bounding box, and $A_{candidate\ bounding\ box}$ denotes the area of candidate bounding box.

- 4) Count the number of candidate bounding boxes with the largest ratio, and selected the size of the bounding box with the largest number as the final bounding box size. In this study, the distribution of candidate bounding boxes were detailed in TABLE 1.

As can be seen from TABLE 1, the 64*64 size was selected as bounding box size in this study, and when the camera used for sampling changes, the constant sized should be recalculated under the same rule.

B. LEAF SPOT AREA LOCATION AND SEGMENTATION

In this study, the improved faster R-CNN was introduced for grape leaf spot area location and segmentation, faster

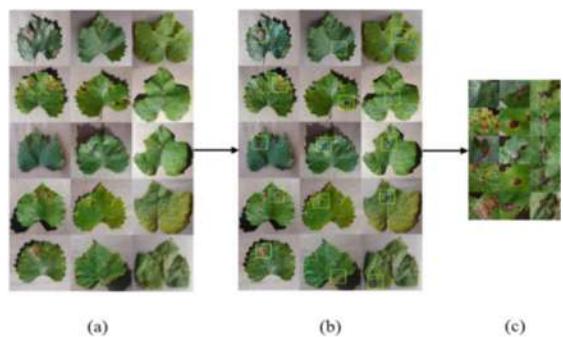
TABLE 1. The number of candidate bounding box with the largest ratio.

Candidate size	32*32	64*64	96*96	128*128
The number of largest ratio samples	12	961	18	9

R-CNN [30] enabled nearly cost-free region proposals by introducing a region proposal network that shares full-image convolutional features of the detection network. The region proposal network was used for detection though it was trained end-to-end to generate high-quality region proposals. Different from the traditional faster R-CNN method, the proposed fine grained-GAN aimed to segment the same size of significant spot area bounding box as input into generators. After experimental verification, the bounding box with 64*64 size had a better performance in leaf spot area saliency representation in this study. The bounding box was selected as follows.

- 1) In descending order of confidence and take top 50%, if the spot area size is greater than bounding box, output the bounding box with maximum size of spot area.
- 2) When the size of all lesion area is smaller than the bounding box, output the bounding box which contains the most number of spots.

FIGURE 3 shows the detection bounding boxes and the selected bounding box, where (a) denotes the original grape leaves; (b) denotes the detection bounding boxes and the selected bounding boxes; (c) denotes the segmented spot area. This approach can capture the significant disease spots in the segmented images.

**FIGURE 3.** The flowchart of lesion area detection and segmentation.

C. LOCAL SPOT AREA DATA AUGMENTATION

As we know, the advantage of deep learning models can automatically learn feature representations from large scale training data. However, in practice, when a rare disease occurred or there is not enough training data in actual planting environment, the limited training samples cannot effectively exert the recognition ability of deep learning. Furthermore, the models with limited training samples often suffer from overfitting, and the diagnostic performance is drastically decreased on test data sets from new environments [31].

Therefore, a data augmentation method which can prevent model overfitting and increase the generalization ability is necessary when lack of training data. In this study, a fine grained-GAN method with strong local feature representation ability was proposed for local spot area data augmentation; compare to traditional data augmentation methods (such as scale, flip, translation and rotation, etc.), Generative Adversarial Networks [25] had been introduced for generating synthetic images with the similar features as the given training dataset and proved its representational power in image-to-image translation. In this study, the proposed fine grained-GAN focuses on the grape disease spot feature representation, inspired from LRGAN, which had proved a more natural images can be generated than DCGAN and different from LRGAN, the proposed fine grained-GAN paid more attention to foreground images information and minimize background interference. The details of proposed fine grained-GAN are as follows.

- 1) Select the segmented sub images which the background does not contains leaf edge background information as the unlabeled sub-images X . Let $X = \{x_1, x_2, x_3 \dots x_n\}$ as a dataset containing the leaf spot object categories. The objective function L can be demonstrated as:

$$L = \alpha L_b + \beta L_{spot} \quad (2)$$

where L_b and L_{spot} denote the background objectives and the spot objectives respectively, α and β denote the weights of generated background and spot objectives respectively. The random noise z and the induction vector b and s were introduced in the proposed method, which were expressed as $z \sim N(0, 1)$, $b \sim Cat(K = N_b, p = 1/N_b)$, $s \sim Cat(K = N_s, p = 1/N_s)$, where Cat denotes multiple distribution in this study.

- 2) Background generation stage. The purpose of background stage was to synthesize background images, which act as a canvas for the foreground leaf spots. To reduce the background interference, it shared a common feature pipeline and strengthened the feature expression of leaf spot, this stage contained of one generator G_b and two discriminators D_b and D_{aux} , G_b was a conditioned on latent background, D_b was used to judge whether the generated background image was real or fake, and the D_{aux} was a binary classifier with *cross-entropy* loss, which judged whether the generated image contains spot and helped G_b generate background images without spots. In this study, we set the 3 classes of background images, to generate the background, we used the images which separated from foreground to train G_b and D_b , and D_{aux} was used to correct the training process. The two objectives loss functions L_{b_adv} and L_{b_aux} were used in this method, which were demonstrated as:

$$L_b = L_{b_adv} + L_{b_aux} \quad (3)$$

where L_{b_adv} was the adversarial loss [23], [37], and L_{b_aux} was the auxiliary background classification loss.

The adversarial loss and background classification loss can be showed in (4) and (5).

$$\begin{aligned} L_{b_adv} &= \min_{G_b} \cdot \max_{D_b} E_x [\log(D_b(x))] \\ &\quad + E_{z,b} [\log(1 - D_b(G_b(z, b)))] \end{aligned} \quad (4)$$

$$L_{b_aux} = \min_{G_b} E_{z,b} [\log(1 - D_{aux}(G_b(z, b)))] \quad (5)$$

where the L_{b_adv} loss function aimed to generate images to predict images with the real or fake score for the corresponding patch in the input images on patch level. The L_{b_aux} loss function aimed to help the background generation task and the binary classifier D_{aux} used for weakening the texture differences to distinguish between foreground and background images.

- 3) Spot generation stage. In this stage, the proposed method automatically identified the location of spots. This stage was only to generate the foreground spot information, and independent from background. Two generators G_{mask} and G_{spot} transform from sub-images feature F_{spot} into foreground image Y_s and mask image Y_{mask} respectively, so that the foreground spot image $Y_{s,mask}$ can be obtained as follows:

$$Y_{s,mask} = Y_s \odot Y_{msak} \quad (6)$$

In the discriminator D_{spot} stage, the induction vector s was introduced, unlike the other GANs, the proposed method focused on capturing the leaf spot hierarchical concepts such as shape, texture, color and so on. Inspired from infoGAN [27], the random noise z and the induction vector s were used to approximate the posterior $P(z, s|Y_{s,mask})$:

$$L_{spot} = \max_{D_{spot}, G_{spot}, G_{mask}} E_{z,s} [\log D_{spot}(z, s|Y_{s,mask})] \quad (7)$$

where $Y_{s,mask}$ was used to make the decision of D_{spot} focus on spot features and not be influenced by the background information. The final generated images which were demonstrated as follows.

$$Y = Y_{s,mask} + (1 - Y_{msak}) \odot B \quad (8)$$

where B denotes the background images which were generated from stage 2), $(1 - Y_{msak}) \odot B$ denotes inverse masked background images.

FIGURE 4 shows the processing of fine grained-GAN based grape spot local image generation in this study.

D. COMPARED WITH OTHER GANS

In this study, the Fréchet Inception Distance (*Fid*) [32] was used for evaluating various GAN models. As we know, we can get the distribution of the real images and the generated images by GANs, the goal of GANs is to make the two distributions as same as possible. Thus, the value of *Fid* is the smaller the better. We set x and g denote the feature

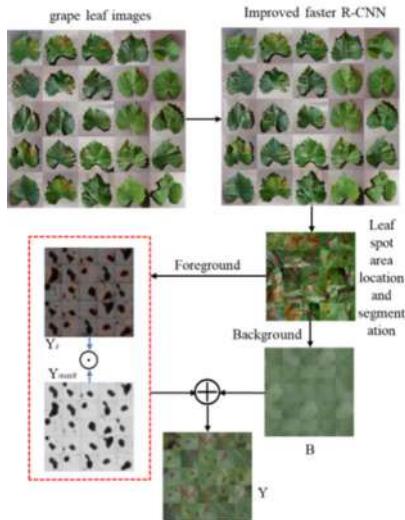


FIGURE 4. Fine grained-GAN based grape spot local image generation.

vectors of original images and generated images, the *Fid* can be described as follows.

$$Fid(x, g) = \|\mu_x - \mu_g\|^2 + Tr \left(M_x + M_g - 2(M_x \cdot M_g)^{\frac{1}{2}} \right) \quad (9)$$

where μ_x, μ_g denote the mean value of x and g respectively, and M_x, M_g denote the covariance matrix of x and g respectively, Tr denotes the trace of matrix.

A lower *Fid* means the two distributions are closer, which means that the quality and diversity of the generated images are better, and it is more sensitive to model collapse, compared with *IS* (inception score) [33], *Fid* has better robustness, because if there is only one class images, the *Fid* will be much higher. Therefore, *Fid* is more suitable to describe the diversity of GANs network. In this study, we select 1000 images in one class and 3000 images in total, the *Fid* of various GANs can be shown in TABLE 2.

TABLE 2. The fid of various GANs.

GANs	<i>Fid</i>
DCGAN	309.37648944577
InfoGAN	178.13124112312
WGAN	121.31231231244
LRGAN	128.23423413213
Fine grained-GAN (ours)	72.728907955885

As can be seen from TABLE 2, the proposed method had achieved the lowest score, which proved it a better performance of generating images.

IV. EXPERIMENT AND DISCUSSION

A. EXPERIMENTAL ENVIRONMENT

In this work, the high performance computing platform of Northeast Agricultural University is available for training and testing; the computing resources are shown in TABLE 3.

TABLE 3. Computing resources.

Hardware and Software	Specifications
OS	Cent OS 7.5
CPU	8*Intel(R) Xeon(R) Silver 4216 CPU @ 2.10GHz
Language	Python 3.8
GPU	2*NVIDIA GeForce RTX 2080 Ti (11G)
RAM	6*16G
Disk	320G
Framework	Pytorch 1.3.0, Cuda 10.1

B. DATA ACQUISITION

Including 1,500 early stage of grape leaf spot disease images with 3 categories were obtained from AI Challenger 2018 [34]. According to the obtained unlabeled data, we built up an annotated grape leaf spot images dataset by annotating the training images manually. From the dataset, every 500 images each category, the grape diseases in this work are outlined as follows.

1) BLACK MEASLES

Black measles [35] is caused by several species fungi. The main symptom of black measles is an interveinal “striping”, the “stripes” start out as yellow in white cultivars and dark red in red cultivars, as time grows it becomes dry and necrotic. The foliar symptoms may occur at any time during the growing cycle, during July and August is the most prevalent. Some of the grape leaf black measles images can be shown in FIGURE 5.



FIGURE 5. Black measles.

2) BLACK ROT

Grape black rot [36] is a fungal disease, which is caused by *Guignardia bidwellii* and occurs in Asia, South America, and Europe. In humid and warm climates it can cause grape loss completely. The symptoms of grape leaf black rot is on infected leaves, the small, brown circular lesions are developed within days, if not intervened, the shoot infection results in large black elliptical lesions. Some of the grape leaf black rot images can be shown in FIGURE 6.

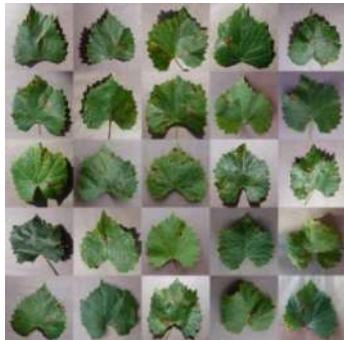


FIGURE 6. Black rot.



FIGURE 7. Leaf blight.

3) LEAF BLIGHT

Leaf blight is caused by *exserohilum turcicum*, which develops on grape leaves under warm and humid conditions [37]. This disease can produce tan spots or reddish-purple and coalesce to form large lesions, which can attack grape new leaves and cause huge loss. Some of the grape leaf black rot images can be shown in FIGURE 7.

C. EXPERIMENTAL DESIGN

In this work, we had trained five state-of-art classification models such as AlexNet [38], [39], DenseNet-121 [40], ResNet-50 [41], VGG-16 [42], and X-ception [43]. Nine groups of data were carried out by all of these models for training models: the original sub images of no data augmentation; data augmentation by DCGAN; data augmentation by InfoGAN; data augmentation by WGAN; data augmentation by LRGAN; and the recently published data enhancement methods such as LeafGAN [31], WGAN-GP [44], CAVE-GAN [45], and data augmentation by Fine grained-GAN (ours).

In order to verify the performance of these models, it is necessary to divide data set reasonably, in this work; there are three groups of datasets, to ensure the preciseness of the test, the original sub images were randomly divided into 3 parts separately, 60% for training, 20% for the validation set, and 20% for the test set. In (2) to (6) the generated images were used for training only, all of the models used the same test set of group (1).

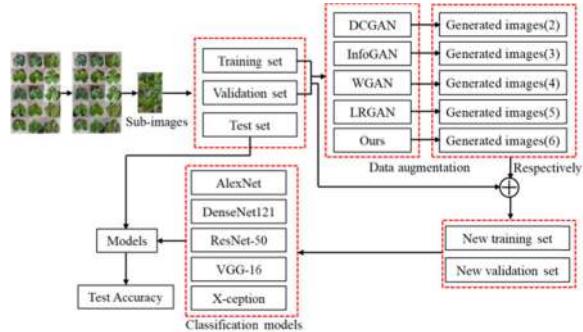


FIGURE 8. The flowchart in proposed work.

As can be seen from FIGURE 8, in order to ensure fairness, we only used the stage B of proposed fine grained GAN for comparison. In this work, in total of 1,500 saliency sub-images with 3 categories were segmented, to improve the ability of deep learning classification model and increase recognition accuracy, another 3,000 images with 3 categories were generated, and added to the original training sub-images respectively according to the category as input into classifier to train the classification models, after trained, the original test set was used for test respectively.

D. TRAINING DETAILS

The hyperparameters of the fine grained-GAN and classification models training process are shown in TABLE 4 and TABLE 5 respectively.

TABLE 4. The hyperparameters of fine grained-GAN.

Parameter	Value
Dimension of z	100
Optimizer function	<i>Adam</i>
Initial learning rate	$2e^{-4}$
Batch_size	16
Activation function	<i>LeakyReLU</i>
epochs	300
α	10
β	1

TABLE 5. The hyperparameters of classification models.

Parameter	Value
Input_size	64*64*3
Batch_size	32
Initial learning rate	0.0001
Optimizer function	<i>Adadelta</i>
Activation function	<i>ReLU, LeakyReLU</i>
epochs	200
Loss function	<i>Cross-entropy</i>

The loss function is one of the important tools to measure the gap between network output and targets. To deal with the

TABLE 6. The results of leaf spot identification accuracy.

	Original	DCGAN	InfoGAN	WGAN	LRGAN	Leaf GAN [31]	WGAN-GP [44]	CAVE-GAN [45]	Fine grained-GAN(ours)
AlexNet	83.72	86.88	84.72	85.8	89.62	84.57	86.19	88.63	89.67
DenseNet-121	85.33	86.06	86.17	85.8	88.62	85.75	87.18	87.19	89.67
ResNet-50	90.56	93.22	93.33	94.78	95.12	93.21	95.45	92.37	96.27
VGG-16	82.83	82.83	89.17	88.67	94.23	91.23	90.95	92.78	95
Xception	80.33	79	81	83	91.12	89.01	86.10	89.35	91.93

multi-classification problem more conveniently, the *cross-entropy* loss function was used in the loss layer and the *softmax* activation function in the output layer.

E. RESULTS ANALYSIS AND DISCUSSION

The performance of no data augmentation and eight GANs for data augmentation as training data for the five state-of-art deep learning models can be shown in TABLE 6. From this table, when no data augmentation used, almost all of these models cannot give satisfactory results, Xception can only achieve 80%, the main reason is that the limited training data made these models suffer from overfitting such as ResNet-50, VGG-16 and Xception, which could not get the ability of model feature representation and these models were not work well.

When the data augmentation methods were used by GANs, the accuracy of all of the eight GANs data augmentation methods had a higher accuracy than none data augmentation method. However, some models had got a worse performance such as Xception by data augmentation with DCGAN, the main reason for this phenomenon was that the images generated by DCGAN. Unable to adapt to the models. Besides this, the proposed method had achieved satisfactory results on above models, which proved that the proposed method had stronger feature representation ability than other GANs in making the spot features more obvious and the background noises were relatively reduced.

Compare with the traditional data augmentation methods, the proposed method integrated local-based object detection and local spot area image generation algorithm, which made the fine grained-based small target identification more effective, especially in the sparse distribution of small target. To highlight the expression ability of the features of leaf spots, the two generators G_{mask} and G_{spot} were adopted to make the generated images more representative and the two discriminators D_b and D_{aux} were introduced to make background more universal, therefore, the interference of background information was reduced as much as possible. As the identification experiment of grape leaf disease spots, the generated local spot area images were added to the original images for training made it further strengthen the generalization ability of the classification models, which can effectively improve the accuracy and robustness of the prediction.

Compare with the other GANs mentioned above, the proposed fine grained-GAN had a more ability with spot location and image segmentation, besides that, the hierarchical mask generation made the ability of spot feature representation stronger. However, the proposed method has its own limitation that it is only applicable to the case of leaf spot, when the plant leaf disease is not visually by spots, the effect of this method will be greatly reduced. In the future work, we will continue commit to the study of various phenomics in plant disease identification.

This study selected the significant spot area as the main grape leaf disease category; this is a single label multi classification problem. However, when there are multiple lesions appear on a grape leaf, which as multi labels multi classification problem, this method can only identify the main disease and there is the possibility of ignoring other unobvious diseases, in the future, multiple diseases on the same leaf should be considered.

V. CONCLUSION

This study presented a novel grape leaf spot identification method with local based fine grained data augmentation. In actual planting environment, fruit farmers always suffer from plant diseases, one of the most visual representations of the plant diseases on leaves. Different from the changes of leaf color or texture, in early stage of leaf spot, it is very hard to be found with the naked eye before the disease broke out on a large scale; therefore, early detection of plant disease is a challenging and meaningful work in agriculture planting.

The proposed method focused on the features of leaf spot, which integrated the improved faster R-CNN object detection algorithm with a fixed size bounding box, this significance detection box can not only reduce the amount of calculation, but also avoid the scale change caused by classifier. In local spot area image data augmentation, the idea of hierarchical mask generation was adopted, which was mainly divided into two stages, background generation and local spot generation. In background generation stage, the two discriminators D_b and D_{aux} were introduced, where D_b was used for judging whether the generated images were real or fake, and D_{aux} was used for judging whether the generated images contained spots, which aimed to generate background images without spot information. In local spot generation stage, the two

generators G_{mask} and G_{spot} were adopted to generate spot images and mask images. Finally, the foreground spot images were synthesized and added on the background images as the generated local spot area images. The experimental results showed that the proposed method outperformed the existing state-of-art models. In the future, this method can be combined with hardware, which can provide model and algorithm support for production practice.

ACKNOWLEDGMENT

The authors would like to thank the High Performance Computing Platform of Northeast Agricultural University for providing computing resources and technical support.

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Disease Detection for Grapes: A Review

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Abstract. A review of various Grapes disease detection techniques and further directions for the research in this field are presented in this paper.

The crops are affected by diseases because of the variation in the climatic conditions, bacteria, viruses and fungi. Grape is one of the cost effective and profit crops which gets affected by diseases on leaves, stem and fruit. Diseases on crop reduce the growth of the plant causing reduction in yield so there is a need for disease detection at the early stage that will help to take the appropriate measures. The recent advances in the field of Artificial Intelligence (AI), Machine learning (ML), and Internet of Things etc. technologies will enable the development of accurate disease detection systems.

Keywords: Artificial Intelligence (AI), Machine Learning (ML), Deep Learning (DL), Disease Detection

1 Introduction

As the world population is growing, there is a huge demand for the supply of food. To satisfy this demand, agricultural productivity needs to be increased, yield needs to be increased. This is possible when the crops grown are healthy. But because of pathogens present in the environment, the crops get various diseases and these unhealthy crops tend to reduce productivity. It is therefore necessary to monitor the crop health and its growth progress and detect the disease at the early stage and provide the future prediction of the disease spread so that farmers can take necessary actions like spraying herbicides/pesticides to prevent the crop from severe disease.

In the earlier time of crop disease detection, manual inspection by the farmers was used and accordingly decisions were taken to spray the chemicals. From the last decade the advanced and state of art technologies like Artificial Intelligence, Machine Learning, Internet of Things, Computer Vision and Image processing techniques are being used in the field of crop disease detection by the researchers.

Grapes are one of the profitable and cost-effective crops. Grape fruits are being used for the preparation of Wine, Juices, jams and jellies. Million tons of grapes are exported and imported in the world. However, the grape crop is affected by many diseases which reduce the yield of the crop. The diseases with which grape crops are

affected are Powdery mildew, , Anthracnose, Greenaria bitter rot, Bacterial leaf spot, Alternaria blight, Black rot, Blue mould rot, Botrytis bunch rot, Downy mildew, Black mould rot, Green mould rot, Rhizopus rot, Rust, Foot rot, IPM for Grapes. There is a need to detect the disease, predict the severity and suggest pesticide use so that farmers can take the required actions.

This paper has five sections. Section 2 presents survey of methods for plant disease detection. Section 3 presents survey of methods for Grapes disease detection. Section 4 presents summary of survey in tabular format. Section 5 discusses challenges and future directions and section 6 is the conclusion section.

2 Survey of methods for plants disease detection

Image processing and Convolutional Neural Networks based elaborated review for plant disease detection is presented in [1]. According to the survey, it is observed that when CNNs are applied on the data captured on real time environments, the accuracy tends to drop by 30% to 40% and results tend to vary significantly because of the diversity of pests, diseases, crops and environment. When applied the same model on Plant Village Dataset, there is enhancement in accuracy. Some diseases are also caused by abiotic factors which have similar characteristics as that of biotic diseases and therefore can result in false diagnosis of the disease. From the survey it has been observed that amongst the researches carried out in plant disease detection 65.28% use the datasets created in controlled environments and 37.19% of studies involve datasets from PlantVillage. It is also found that rice, Corn, Cucumbers, Tomatoes, Wheat, Bananas, and Grapes are the most investigated plants. Onsite survey also highlights that Multispectral and Hyperspectral imaging can be used with CNN which contain more information compared to RGB imaging in further scope of plant disease detection. The Authors also suggest use of Undammed Aerial Vehicle (UAV) technology for capturing high resolution images.

[2] Presents a CNN technique to identify plant disease for 10 crops with 27 diseases with Inception (ResNet-v2 backend) model for training. It used an AI challenger competition public dataset. Python, Tensor flow deep learning framework, Windows OS were used for implementation. The model achieved accuracy of 86.1% AP, and assisted farmers in identifying the disease. Surveys of various CNNs widely used like LeNet, AlexNet, Inception, Deep Residual Network is provided. A crop disease recognition model and processes involved in it is also presented. The future work is directed toward creating more datasets and more crops covering a large variety of diseases. Crop image classification accuracy can further be enhanced by designing accurate network models

A review on detection and classification of plant diseases in [3] discusses various current trends and techniques for plant disease detection using the Image processing and Deep learning Techniques. It targets plant disease detection studies on plants of Apple, Tomato, Rice, and Cucumber. It is observed that the traditional image processing methods like Global Color Histogram(GCH), Color 3 Coherence Vector(CCV), Principal Component analysis(PCA) can give good accuracy but they still lack in some areas like the process is time consuming, It is difficult to test the perfor-

mance of the disease detection model in complex environments. So this calls for design of novel disease detection model which is more accurate, fast and intelligent. So the Author suggests development of new Deep Learning models. The author has also reviewed the machine learning models like Support Vector machine (SVM), KNN, K Means Clustering, Deep Learning models like CNN, GANs. Labeled datasets are difficult to obtain for early plant detection using HSltc Adversarial networks (for Data augmentation) techniques. Various research gaps are identified like there is a need for larger data sets for CNN training. For plant disease detection large and diverse datasets are not collected. If a large data set is not available then there is a need to implement Transfer learning with deep learning with limited dataset. It is found that early detection of diseases with limited sample set is still under research and more research can be directed towards it. There is a need to build a large dataset of plant diseases in actual real conditions, for the experimentation purpose the data set from PlantVillage is most commonly used but the data in PlantVillage data is created under laboratory conditions.

A review on advanced techniques for agricultural disease detection is presented in [4]. It compares the merits and demerits of machine learning methods with Deep learning and transfer learning methods. Traditional ML methods like SVM, Bayesian classifiers depend on the quality of data images. Also, the realization is complex and difficult when the number of training samples is large. It's concluded that Deep learning with CNN is best suitable for disease detection as compared to traditional machine learning methods, but still there is scope to improve the accuracy of CNN as the dataset is limited. Transfer learning can also be used over the deep learning methods as DL requires a huge amount of dataset and quality of deep learning models is more dependent on the datasets and in agriculture there is still scarcity of huge dataset. Also, Parameter Optimization is major concern in DL. The author explains the need for the construction of Image Dataset and expanding current datasets as presently lack of disease image labeled data determines the quality and accuracy of DL models. From this survey it is concluded that most of crop disease study is focused on Tomato, Rice and Cucumbers, Apples, Citrus, there is need to design a method to identify disease independent of specific crop. It suggests that DL can be integrated with current Smartphone technology. Along with disease detection it is necessary to find the severity of the disease and also need to relate disease with other factors like temperature, Humidity, Soil type. Diverse Image dataset construction in the actual cultivation environment is needed instead of the image datasets collected in a controlled laboratory environment that will help to improve the accuracy of the plant disease detection deep learning models. The Author suggests the use of a heterogeneous mode of transfer learning can be employed to predict the disease based on text, Image and video data instead of only image data.

A detailed survey about plant disease detection using Image Processing and ML techniques is presented in [5]. It gives a survey of various plant diseases for plants like Apple, Corn, Cherry, Grapes etc. It also discusses the steps involved in the plant disease detection process like image pre-processing, Feature Extraction and selection, image segmentation, disease classification; various classifiers for plant disease detection are also explored. It also summarizes the previous research work done by re-

searchers for various crops like profit crops, mixed culture, grains, etc. using image processing techniques in terms of percentage of papers. From this survey it is observed that a lot of research is being done on Rice, Tomato, Cucumber, Citrus and Wheat but less research is directed towards profit crops like sugarcane, groundnut. Further the gaps in research for plant disease detection like there is a need to detect the disease at a particular stage are discussed. It will be helpful to farmers if stage wise special precautions are suggested to him. Also, if precise estimation of infected area of the plant is done then it is possible to control and minimize the unmanaged use of pesticides by the farmers. Though a lot of researchers have provided solutions to this problem, there is less availability of the actual corresponding systems, so there is a need to develop mobile based applications and Website solutions for the farmers in the world. A Disease Analysis Report” can be generated for the farmers. There is a need to develop real time applications using real time conditions data rather than data obtained from the controlled environment in laboratory.

Deep Convolutional network with 9 layers methodology is presented in [6] for 39 different classes of plant leaf diseases. The 9 layer Deep CNN performance is compared with SVM, KNN, AlexNet, VGG16, InceptionV3 and ResNet. The image data set was taken from Plant Village. As the training model requires huge data the images are augmented to create many numbers of images. The models were trained and tested using Keras, OpenCV, and Pillow libraries with Python Programming. The developed model achieved 96.46% of accuracy as compared to SVM, KNN, Logistic Regression, and Decision tree. The further suggestion is that an improvement in accuracy can be achieved by creating the enhanced dataset. The new data set can be created by collecting the different images from different plants, cultivation, geographical areas, and image qualities. The research can be extended to fruits, flowers and stem parts of the plant. Also, the research can be extended to plant disease diagnosis.

A comparative study of various Deep Learning models for plant disease identification and classification is presented in [7]. It provides information about the image processing based disease detection techniques using deep Convolutional Neural networks. It used plant disease dataset from the ImageNet Dataset Library and implemented the deep learning architectures VGG 16, Inception V4, ResNet with 50,100, and 152 layers, DenseNet with 121 layers and compared their performance. It is found that DenseNet gives more accuracy as compared to others but some research can be still carried out to reduce the computational processing time.

Table 1 gives tabular summary of Plant disease detection methods and gaps identified in the literature.

Table 1. Plant disease detection methods

Reference No.	Methodology used	Limitations/Future Scope
André Abade Et.al[1]	Image processing and Convolutional Neural Networks	Use of CNN with Multispectral and Hyperspectral imaging with more information compared to RGB images. Use of Unmanned Aerial Vehicles (UAV) technology for capturing high resolution images Farmers use books and local networks and experts to manage crop disease
YONG AI Et.al [2]	CNN, Inception ResNetV2 Model with AI challenger competition public dataset Used Python, Tensor flow Deep learning framework,	Dataset can be extended for Rice and Wheat and their diseases and more crops can be considered Crop image classification accuracy can be enhanced further by designing another network models Supervised DL techniques present challenge in terms of large amount of data, Data labeling is a tedious process. Unlabeled data with unsupervised learning may be promising. Early Detection of diseases with limited sample set is still under research
LILI LI Et.al.[3]	Traditional Image processing GCH, PCA,SVM CNNS SVM,KNN,K-means GAN for Data augmentation Integration of Multiple CNN classifiers Multiscale ResNet Model Hyperspectral imaging	Need of intelligent, rapid and accurate plant disease recognition Need of larger data sets for CNN training. For plant disease detection large and diverse datasets are not collected Use of Transfer learning with DL for limited dataset Need to establish a large dataset of plant diseases in real conditions, Most of the datasets are taken from PlantVillage datasets but these datasets are obtained in a LAB

		Construction of Image Dataset where images are collected under actual cultivation conditions rather in controlled environments in the laboratory. Traditional ML methods depend on quality of data images. Difficult when no of training samples is large
		Most of crop disease study is focused on Tomato, Rice and cucumbers, Apples, Citrus
		Parameter Optimization is major concern in DL
		Can Integrate DL with current Smart phone technology
		Necessity to find the severity of the disease and relate disease with other factors like temperature, Humidity, Soil type.
Yuan Yuan Et.al.[4]	DL and Transfer Learning CNN for Image classification Homogeneous Transfer learning	Heterogeneous mode of transfer learning can be employed to predict the disease based on text, Image and video data instead of only image data
Vibhor Kumar Et.al. [5]	Image processing Unsupervised and supervised classifiers	Recognition stage of infection Accurate classification Development of Website Solution and Mobile App and reliability of detection systems
Geetharamani G Et.al.[6]	Image Processing Deep CNN	Need to increase Database Classes and size by capturing images in real environment. Research can be extended to other parts of plant like flower, fruits and stems
Edna Chebet Too Et.al.[7]	Deep CNN,VGG 16,Inception V4,ResNet with 50,100 and 152 layers, DenseNet with 121 layers Keras with Theano Backend for training	Computational time needs to be improved

3 Survey of methods for Grapes disease detection

A novel method of image processing and multiclass support vector machine was used in [8]. Grape diseases like leaf blight, black measles, black rot, and were detected. Authors used Gray-level co-occurrence matrix (GLCM) and Principle Component Analysis (PCA) for extracting features and reducing feature dimensions. An accuracy of 98.71% was obtained using GLCM method while PCA method achieved an accuracy of 98.97%. Deep Learning algorithms i.e. CNN and GoogleNet were also used and an accuracies of 86.82% and 94.05% were achieved respectively.

Authors in [9] proposed a deep convolutional network (DCNN) for identification and classification of grape leaf diseases. The Grape leaves RGB image dataset from PlantVillage was used. The developed model obtained an accuracy of 99.34%.

Ghost Convolution and Transformer Network for grape leaf disease detection and pest detection is proposed in [10]. Total of 8 grape diseases namely Black Rot, Leaf Blight, Esca, Downy Mildew, Brown Spot, Powdery Mildew, Nutrient Deficiency and viruses were identified. A dataset of 12615 images was collected. An accuracy of 98.14 percent was achieved using this model. One of the drawbacks listed is that the proposed model works only on labeled data. A suggestion to enhance the labeled data set is also given to enhance the accuracy. Further the research can be directed towards segmenting the legion area for severity grading.

Hyper spectral imaging and Machine learning approach for detecting Flavescense Doree Grapevine disease is used in [11]. The Auto encoders are used for reducing the dimensionality of hyper spectral images. The Dataset consisted of 35 Hyper spectral wine grape leaf images in 272 Bands. But for reduction in the computational complexity, the number of bands is reduced from 272 to 64. The proposed model achieved an accuracy of 83%. Further the authors suggest using all full band data of 272 bands to improve the accuracy.

A pre-trained Model AlexNet DL model is used in [12] for Mango and Grape Leaf Disease detection also called transfer learning. The grape diseases addressed are Black Rot, Black Measles and Leaf Blight. The model was trained and tested for 7222 grape leaf disease images taken from PlantVillage Dataset. An accuracy of 99% was achieved. The authors used RGB images captured in Single Background and Uniform lighting conditions. So a suggestion to use a large dataset with an uncontrolled environment to increase the accuracy is suggested.

In [13] A Machine Learning Model Fine grained Generative adversarial network (GAN) is used to Classify 5 grape diseases namely Leaf Spot, Round Spot, Downy Mildew, Anthracnose and Sphaceloma with limited training samples. The model achieved Accuracy of 96.27%. Authors used around 1500 images for the experimentation. The drawback of the system is that it can detect a single main disease on a multi diseased leaf.

The performance of AlexNet, GoogleNet and ResNet-18 for grape disease detection for 3 classes of grape diseases namely Black Rot, Black Measles, and Isariopsis is compared in [14]. The accuracy of 95.65 % was achieved on AlexNet, 92.29% on GoogleNet and 89.49% on ResNet-18. The authors used annotated image dataset from Kaggle.com. The dataset of around 1000 Images was used for the experimentation.

In [15], real time grape leaf disease detection using Deep CNNs using Inception ResNet-v2 and Inception V1 was implemented. The disease detection is done for 4 classes of grape disease namely Black Rot, Black Measles, Leaf Blight and Mites of grape. The authors created a Grape Leaf Disease dataset of total 4449 images in controlled environment and in grapery and used augmentation for enhancing the dataset to 62286 images. The model achieved an accuracy of 99.47%. It expresses a need to use a large dataset.

Multiple Convolutional Neural Networks United Model by integrating Google Net and ResNet was used in [16]. The research used an image dataset from PlantVillage with 1619 Images. The United Model achieved accuracy of 98.57%. The authors express the need to enhance the dataset in an uncontrolled environment in a complex background and extension of the model for other crops. The model classified three diseases namely Black Rot, Esca, and Isariopsis Leaf Spot.

Machine learning techniques like Support Vector Machine (SVM), Random Forest, and Adaboost with 5675 images of grape leaves disease from the Plant Village dataset for the identification of 3 grape diseases Black Rot, Esca, Leaf Blight along with image processing techniques were presented in [17]. The methodology used has achieved accuracy of 93%.

In [18] a grape disease detection technique using Back Propagation Neural Network (BPNN) and Image processing is presented. It used Wiener filtering along with wavelet transform. The research used a dataset of 300 images. Five types of grape diseases Leaf Spot, Anthracnose, Downy Mildew, Round Spot, Sphaceloma Ampelinum De Bary were detected with an accuracy of 80%.

A Grape disease detection using Random Forest based classification was presented in [19]. Back Propagation Neural Networks (BPNN), Probabilistic Neural Networks (PNN), Support Vector Machine (SVM) and Random Forest implementation was done with their performance comparison. The dataset of 900 images captured in an uncontrolled environment was used and the proposed model achieved accuracy of 86%. The research targeted three grape fungi diseases namely Anthracnose, Downy Mildew and Powdery Mildew.

4 Summary

A tabular summary of above Grape disease detection survey is given in Table 2

Table 2. Grape disease detection Methods

Reference No.	Methodology used and Diseases Detected	Accuracy	Limitations/Future Scope
Seyed Mohammad Javidan Et.al.[8]	Multiclass support vector machine, Gray-level co occurrence matrix (GLCM) and Principle Component Analysis (PCA), CNN, GoogleNet Black measles, Black rot,	98.71%, 98.97%, 86.82%, 94.05%	Experimentation carried out using limited dataset. Images in dataset are taken from PlantVillage dataset and not from the actual environment.

and Leaf blight			
Rajinder Kumar M. Math Et.al.[9]	Deep Convolutional Neural Network	99.34%	Images in dataset are taken from PlantVillage dataset and not from the actual environment.
Xiangyu Lu Et.al [10]	Ghost convolution and Transformer Network Black rot, Leaf Blight, Downy Mildew, Powdery Mildew, Brown Spot, ESCA , Nutrient deficiency	98.14%	Diagnosis of severity using legion area segmentation Use of data Augmentation for enhancing diversity of dataset
Diogo M.Silva Et.al [11]	Hyperspectral image and Machine Learning, Flavescense Doree– Grape wine disease	83.00 %	Experimentation with full 272 band high resolution image data
U.Sanath Rao Et.al.[12]	Deep CNN, Transfer Learning – AlexNet Black measles, Black rot, Leaf Blight	99.03%	Classify additional classes of disease & development of a recommendation system Preparing diverse dataset in real time with varying lighting conditions Method only applicable to leaf spot.
Changjian Zhou Et.al.[13]	Fine grained GAN Leaf Spot, Round spot identification, Downy Mildew, Anthracnose, Sphaceloma ampelinum de bary	96.27%	Inability with multi labels multiclass classification In future Multiple diseases on single leaf may be detected. Model implementation on hardware
Sandy Lau- guico Et.al. [14]	AlexNet, GoogleNet, ResNet 18 Blackrot, Black Measle Isariopsis	95.65%	Real time Dataset is not used.
Xiaoyue Xie Et.al.[15]	Deep CNN, inception V1, inception ResNetV2 Blackrot, leaf blight, Black measles, Mights of grapes	99.47%	Classify additional classes of disease and Improve accuracy
MiaomiaoJi Et.al.[16]	Multiple CNN(Integration) of GoogleNet & ResNet Blackrot, ESCA, Isariopsis	98.57%	Create a real time dataset. To do model compression to reduce computational resources
S.M. Jaisakthi Et.al.[17]	Image processing, Machine learning Algorithms, SVM., ADA boost, Random Forest	93.00%	Real time Dataset is not used

	Blackrot, ESCA leaf blight Image analysis(Wiener filter and Wavelet transform) and 3 stage BPNN		
Juanhua Zhu Et.al.[18]	Anthracnose, Downy Mildew, Round Spot, Leaf Spot, Sphaceloma ampelinum De bary	80.00%	Dataset size can be enlarged
Biswas Sandika Et.al.[19]	PNN, BPNN, SVM, Random Forest Anthracnose, Powdery Mildew, Downy Mildew	86.00%	Dataset size can be enlarged.

5 Challenges and Future Directions For Researchers

As far as the literature survey for the plant and grape disease detection is concerned, most of the disease detection is carried out using the dataset from PlantVillage, ImageNet dataset which is collected in a controlled environment. There is a need to design more accurate models to detect multiple diseases. For Grape plant disease detection systems to be more accurate there is a need to create a diverse dataset by considering the real environment and not the laboratory environment. To address this issue the data set can be created by taking images with the help high resolution Smart Phone RGB cameras, Multispectral Cameras and Hyper spectral Cameras. There is a need to detect the disease stage wise and inform farmers. Early detection of disease is important. It will be helpful to farmers if stage wise special precautions are suggested to him. Also, if precise estimation of infected area of the plant is done then it is possible to control and minimize the unmanaged use of pesticides by the farmer. It calls for the precision praying system to be implemented. According to the literature survey, most of the disease detection techniques work with data of diseases on the leaf section of plants. The research can be directed towards disease detection by considering other parts of the plants like stem, fruits etc.

6 Conclusion

The survey of various disease detection methods for Grapes diseases is presented in this paper. This paper provides a summary of existing methods and the challenges present. In the future a more accurate disease detection model can be developed using the dataset created by capturing images in real time scenarios and varying illumination conditions. The dataset can be created by capturing Multispectral and Hyperspectral images and developing a model for it. It is not only sufficient to classify the plant as diseased or non-diseased but also it is needed to identify the type of disease and severity of it and its future prediction of spread so that the quantity of pesticides can be decided. Additional classes of diseases can be considered for model

training and a recommendation system for the farmers can be developed to take appropriate action for getting rid of the disease.

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Review of various grape diseases

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Abstract

Grapevine is a foremost vegetative disseminated berry with high global socioeconomic prominence. It is vulnerable to numerous graft-transmitted agents that cause several diseases and extensive crop fatalities, decreasing fruit quality, plant strength, and also reduce the durability of vines. The vegetative transmission and frequent exchanges of propagative material within countries contribute to unfold these pathogens, esteeming the development of multifaceted diseases. Its lasting life cycle further accelerates the blending and introduction of numerous epidemiologic agents into a single plant. At present, almost 65 viruses belonging to different families have been reported infecting grapevines, however, all do not cause economically significant diseases. Regrettably, there are several breeds of vine diseases that prosper in all circumstances. Bacteria and fungi are a source of most common grapevine diseases. Insects can also propagate viruses and harm roots. Ecological circumstances can cause mold development that inflicts disorder on grapevines in vineyards. Here, we review the recent knowledge of these viruses, report advances in their diagnosis and prospection of new species, and give indications about the management of the associated grapevine diseases.

IndexTerms - Grapevine, Crop fatalities, grapevine diseases.

• Introduction

India is an agricultural country. More than seventy per cent of the population depends on agriculture. Our economy in major depends on agriculture. Thus, development in this field will highly contribute to the economic welfare. Irrigation/Water stress, Fertilizers, pesticides and quality of yield, disease monitoring and detection are the major factors of concern in agriculture. Major expertise is required to analyze the problems. Such problems are being time consuming and also costlier issues in the developing countries.

We are inflating in a new epoch of computing technology, i.e. Internet of Things (IoT). IoT is a kind of "wide-ranging universal neural structure" in the cloud which interfaces diverse things. The IoT is a cleverly associated gadgets and frameworks which encompassed savvy machines collaborating and communicating with further machines, surroundings, matters and groundworks.

In the Agricultural sector, endeavors are being made to improve the efficiency and lessen fatalities by utilizing the cutting edge innovation and gear. One such technology, such as, Internet of Things can come about into economical yet operative strategies for agribusiness, which subsequently will without a doubt, offer rise to greater quality production.

Grape farming has social and monetary significance in India. Maharashtra positions first in grape production[1]. In the due course, the quality of grapes has debased in light of many reasons. One of the essential causes is ailments on grapes. To avoid maladies, agriculturists sprig tremendous measure of pesticides, as the consequence of which the creation cost expands. Agriculturists are likewise incapable of distinguishing the infections physically. The illnesses are recognized simply after the disease, nevertheless it takes up a great deal of time and unfavorably affect the vineyard.

Grapes are a harvest that is vulnerable to numerous infections. The imperative grape maladies are anthracnose, downy mildew, powdery mildew and bacterial leaf spot, mealy bug, black rot and some more. It is prescribed that vineyards be efficiently examined all through the developing season to screen the appearance and improvement of infections. Also, at harvest and toward the finish of the season, it is recommended, to evaluate the occurrence of ailments like downy and powdery mildew or anthracnose on the leaves to assess the level of inoculum. Quick, precise distinguishing proof of ailments in the vineyard is vital to avert genuine flare-ups and misfortunes in yield and quality.

The trending and future technologies like IOT, digital image processing alongside sensor networks has demonstrated their evitable accomplishment in different applications individually, but the combination of these is so far non-existent.

An expert system based on the Internet of Things (IoT) can be used to collect and monitor the real time data. To further detect the grape leaf diseases, an image processing based approach can be applied. This will help to take proactive and preventive actions.

The trending and future advancements like IOT, digital image processing close by sensor systems have exhibited their evitable achievement in various applications separately, however the blend of these is so far non-existent.

We propose a specialist framework in light of the Internet of Things (IoT) to gather and monitor real continuous information. To additionally recognize the grape leaf maladies, an image processing based approach will be utilized. This will take proactive and preventive actions.

The objective is to detect, identify, accurately quantify and prevent disease occurring in order to minimize the losses and increase the economical profit.

This review endeavors to present a gritty record of grapevine diseases and their protection followed by a concise discourse on technological measures to determine them.

• LITERATURE REVIEW

Grape diseases arise due to many reasons , to name a few as Fungi, Bacteria, Virus, Pests.

Fungal Diseases :

Powdery Mildew, Downy Mildew, Rust, Phomopsis cane, Leaf Spot, Bortrys Bunch Rot

Bacterial Diseases :

Crown Gall of Grape

Viral :

Grapevine fan leaf, Arabic mosaic ,Rupestris stem pitting ,

Pests

Grape cane borer, Mealy bug, Spider Mites, Vine Girdler

Fungal Diseases

The vital grape diseases are anthracnose, downy mildew, powdery mildew and bacterial leaf spot. In current years, Alternaria is additionally turning into a genuine pathogen[2].

Powdery Mildew:

This is a fundamental disease caused by the parasite Uncinula necator, that can taint each and every tissue of the grapevine [3]. This has a fine white appearance and produces a whitish dim, dusty growth on grape leaves or shoots and fruits as presented in Fig.1.



Figure 1 a) Powdery Mildew on leaf b) Grapes with powdery mildew c) Powdery Mildew on shoots d) Disease on buds

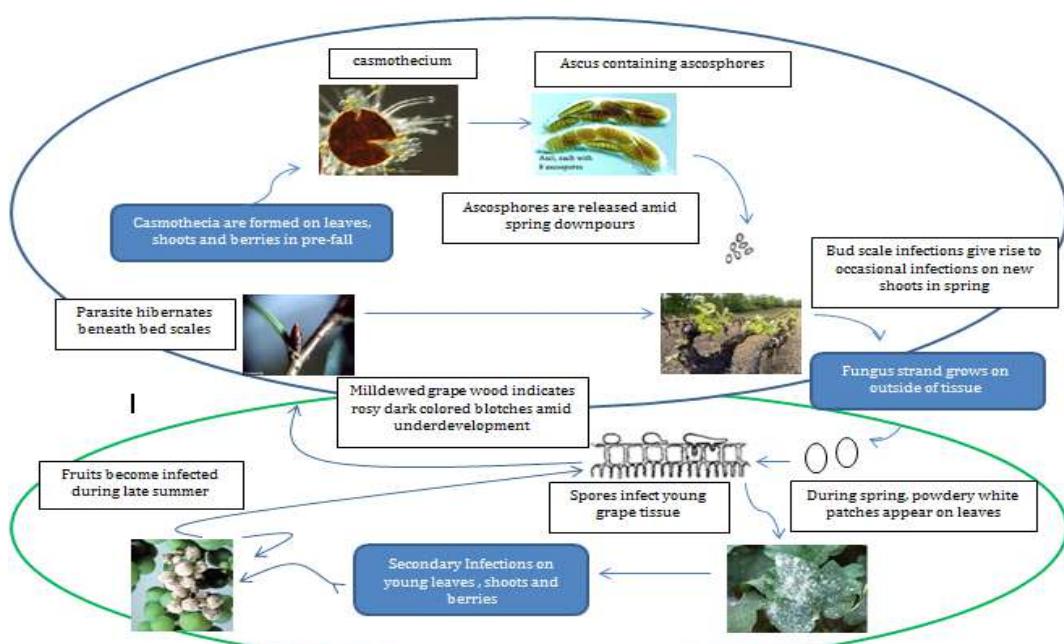


Figure.2 Powdery Mildew disease life cycle[4]

Due to this, the bunch stems and green shoots often seem to be twisted or hindered. Berries too can be contaminated, resulting in the reduction of the wine quality, even if the infection is insignificant. Berries are vulnerable to disease from early sprout through three in a month after blossom. The leaves infected due to powdery mildew may turn dim and tumble off.

As shown in Fig.2, the temperatures of 21°C to 31°C are ideal for contamination and disorder, in spite of the fact that the disease can ensue from 15°C to 32°C. Temperatures over 35°C restrain germination of conidia and exceeding 40°C they are thrashed. High relative humidity is helpful for creation of conidia. Climatic moisture in the 40 to 100 percent relative moistness extend is adequate for germination of conidia and contamination.

Free moisture, particularly rainfall, is adverse to existence of conidia. Low, diffuse light appears to support powdery mildew expansion. Under ideal conditions, the time from contamination to generation of conidia is around seven days. It is critical to recall that powdery mildew can be a major issue in drier emerging seasons when it is excessively dry for different diseases, for example, dark decay or downy mildew to raise.

Downy Mildew:

The grapes become highest prone to the Downy Mildew disease. It is responsible for the severe damages of the crops. The risk of infection is most common during the 'Adra lunar mansion' of rainy season i.e. the wet moist weather. Sticks and bunches of grapes also damage due to inefficiency cause of this disease.

Downy mildew [5] is caused by the parasite *Plasmoparaviticola*. The disease cycle of Downy Mildew is displayed in Fig 3. The parasite hibernates in contaminated leaves on the ground and conceivably in contaminated shoots. The overwintering spore (oospore) grows in the spring and develops an alternate sort of spore (sporangium). These sporangia are spread by wind and sprinkling precipitation. At the point when plant parts are secured with a flick of humidity, the sporangia discharge little swaying spores, called zoospores. Zoospores, which likewise are spread by splashing rain, sprout by developing a germ tube that enters the leaf through stomates (minor pores) on the lower leaf surface. The Fig.4 depicts the damages caused due to downy mildew. The ideal temperature for malady advancement is 18°C to 25°C.

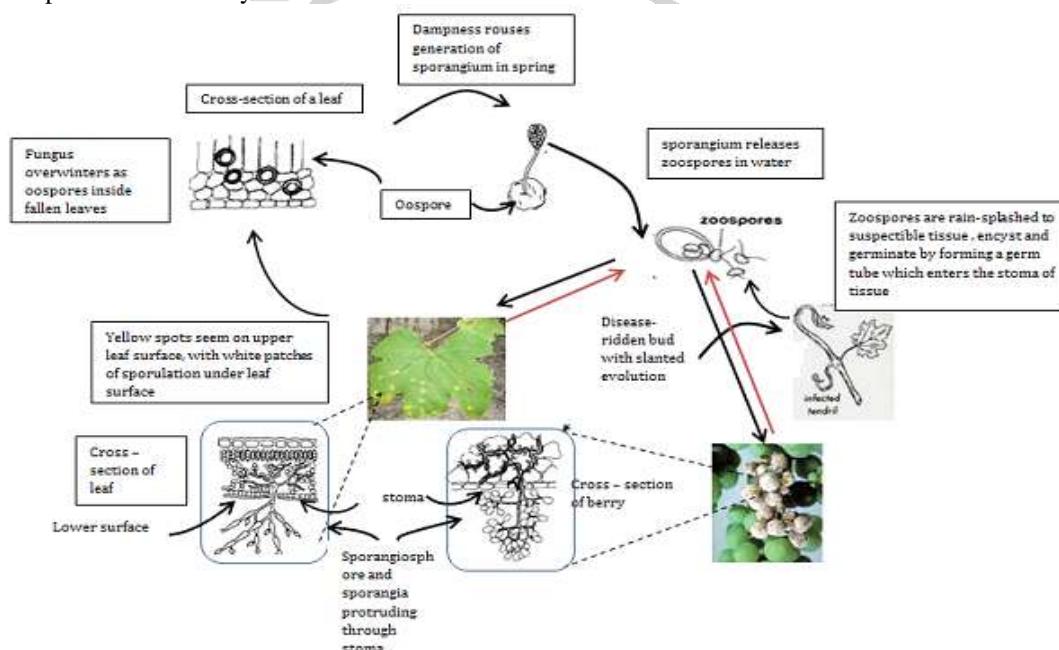


Figure.3: Downy Mildew disease life cycle [6]

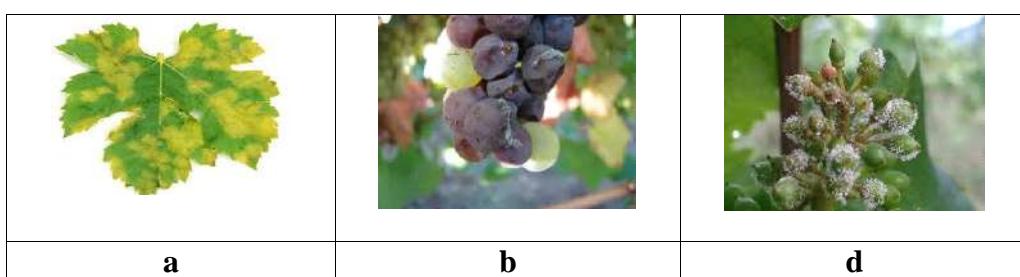


Figure.4 a) Downy Mildew on leaf b) Grapes with downy mildew c) Downy Mildew on buds

The infection can withstand a base temperature of 12°C to 13°C and a greatest temperature of around 30°C . Once inside the plant, the organism develops and spreads through tissues. Contaminations are generally noticeable as injuries in around 7– 12 days. During the evening amid times of high moistness and temperatures over 13°C , the organism becomes out through the stomates of contaminated tissue and creates infinitesimal, stretched, tree-like structures (sporangiophores) on the lower leaf surface. More spores (sporangia) are created on the tips of these tree-like structures. The little sporangiophores and sporangia make up the cottony, downy mildew development.

Anthracnose:

This is also known as bird's-eye rot. Anthracnose of grape is caused by the organism *Elsinoe ampelina*[7]. The fungus overwinters in the vineyards as sclerotia (parasitic survival structures) on contaminated shoots. In the spring, sclerotia on contaminated shoots develop to yield ample spores (conidia) when they are wet for 24 hours or more, as well as the temperature is over 2°C . Conidia are spread by sprinkling precipitation to new developing tissues and are not carried by airstream. Another sort of spore, called an ascospore, is developed inside sexual fruiting bodies and may likewise shape on tainted sticks and berries left on the ground or in the trellis from the preceding year.

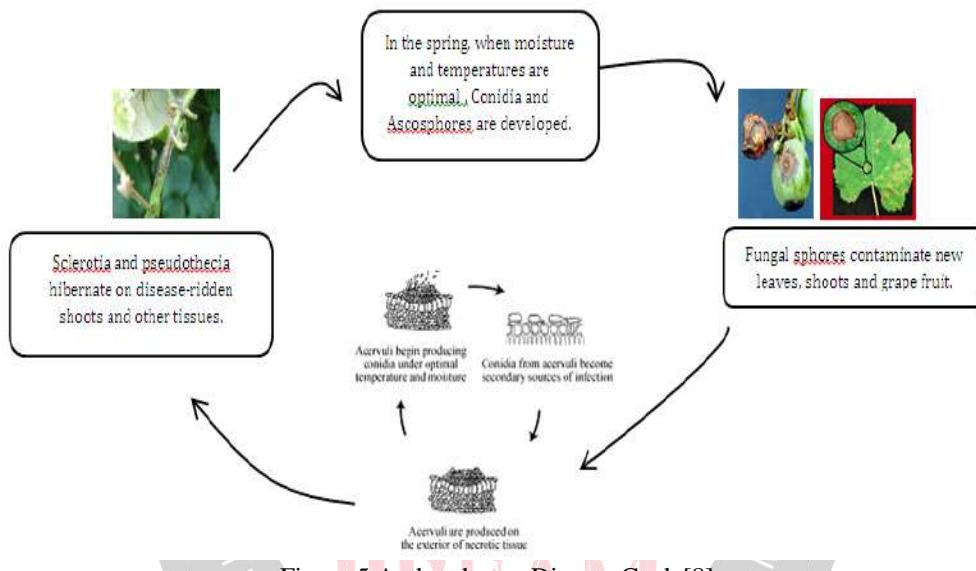


Figure.5 Anthracnose Disease Cycle[8]

Once the disease is built up, abiogenetic fruiting bodies called acervuli frame on the diseased ranges. These acervuli create conidia in the course of wet climate. These conidia are the optional cause of inoculum and are in charge of continuous spread of the organism and the disease all through the developing season. Damage due to Anthracnose is as shown in Fig.6.



Fig.6 a) Anthracnose on leaf b) Grapes with anthracnose c) Anthracnose on shoots d) Disease on buds

Bacterial Disease:

Crown Gall:

Crown gall is a plant ailment caused by the soil-inhabiting bacterium, *Agrobacterium tumefaciens*. The bacterium causes strange developments or lesions on roots, shoots, and branches. The bacterium encourages the speedy development of plant cells that outcomes in the lesions(galls). Notwithstanding being unattractive, the lesions weaken and stop the development of the plant. In spite of the fact that lesions can disturb the stream of water and supplements up the roots and branches, they do

not affect in complete plant loss. The malady can spread to other helpless plants through polluted soil and apparatuses. Most concoction medications are not successful.

Galls are usually found close to the ground level on the roots and lower branches of the plants. As the galls grow, they turn out to be timbered and rigid. Fig.8 shows the same. The external layer turns darker. The plant might be hampered and caught up with some branch or tip dieback. Indications may not grow instantly after contamination. Galls develop quickly amid the warm atmosphere.

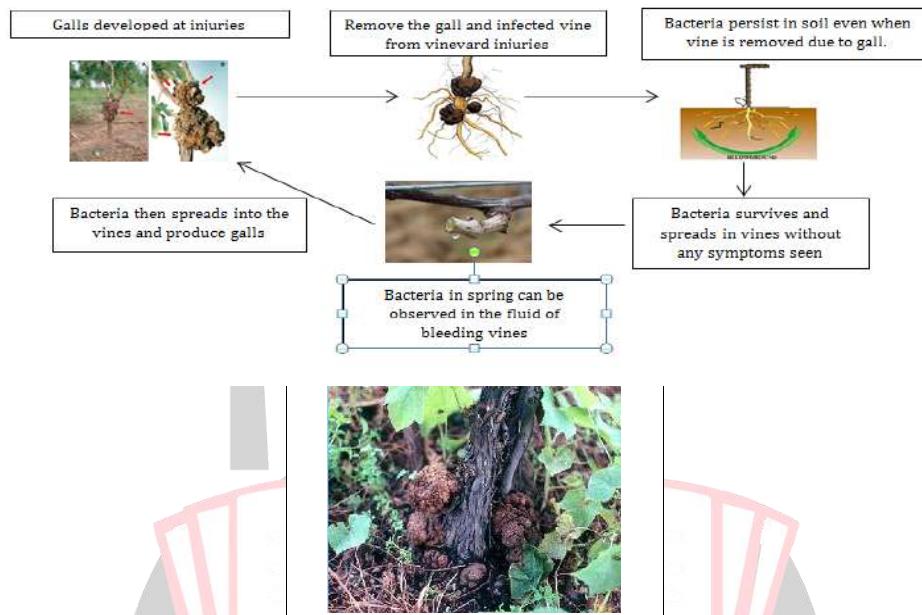


Fig 7. a. Crown Gall Disease Cycle[9] , b. Crown Gall Disease Damage

Viral Disease:

Grapevine fan leaf:

Grapevine fanleaf [10] degeneration is a typical grape infection transmitted by knife nematodes. With interpretations backtracking to 1841, it is the most established disease found and also extreme viral ailments of grapes. Any types of grape can be contaminated, yet Vitisvinifera, Vitisrupestris and their mixtures are the most susceptible. Contaminated plants frequently show a moderate decay and trouble setting fruit, however almost dependably bear a particular leaf deformation. Affected leaves display a fanlike shape due to the irregularities in vein development, and yellow tinge either in a mosaic pattern or in groups along significant veins. This yellow hue for the most part shows up in summer.

Pests Diseases:

The important pests of grapes in India are mealy bugs.

Mealy Bugs:

Mealybugs[11] are delicate bodied, wingless creepy crawlies that frequently show up as white cottony masses on the leaves, stems and fruit of plants. They sustain by embedding long sucking mouthparts, called stylets, into plants and drawing sap out of the tissue. Mealybugs create a foul, unattractive mess that can render your grapes unfit for sale. These pests excrete honeydew, a sweet, sticky substance that drops on leaves and fruit. Honeydew not only attracts ants, but also serves as a growth medium for damaging, unsightly sooty mold.

Mealybugs make a foul, ugly wreckage that can render your grapes unfit available to be purchased. These vermin discharge honeydew, a sweet, sticky substance that drops on leaves and natural product. Honeydew draws in ants, as well as fills in as a development medium for harming, unattractive dirty shape.

III FINDINGS

Table 1. Summarization of all Diseases

Disease	Development Reason	Development Time	Symptom s	Damages	Suggestio n
Powdery	• Dense diverse,	• After April	• Fine white	• Shoots,	• Keep capsules

Mildew[12]	<p>cloudy atmosphere, and windy air</p> <ul style="list-style-type: none"> Grows at optimal temperatures 22^0C– C 	<p>and October Pruning</p> <ul style="list-style-type: none"> Can be a serious problem in drier growing seasons 	<p>appearance</p> <ul style="list-style-type: none"> Small, white or grayish-white patches on leaves Dark-brown to black patches on shoots 	<p>leaves, flowers and fruit are all vulnerable</p> <ul style="list-style-type: none"> When the fruit is retained, there is a possibility of bloated white tissue on new cloves and possibility of fruit loss. The size of the growing fruit, irregularly, leads to dark hay feathers on the neck. 	<p>free from starting</p> <ul style="list-style-type: none"> Do not let the leaves to be crowded Start early-within 4-6 inches of shoot growth with an eradicant.
Downy Mildew [5]	<ul style="list-style-type: none"> Hot and Humid Climate Minimum temperature of 11^0C Grows at optimal temperatures 18^0C– C Heavy Rainfall is the principal factor 	<ul style="list-style-type: none"> After October Pruning From first leaf unfolded particularly during periods of rain, heavy dew and persistent fog at temperature above 11^0C. 	<ul style="list-style-type: none"> At young stage, very small, greenish-yellow, translucent spots that are difficult to see Cuts on leaves are angular, yellowish, sometimes oily, and found between the veins shoot tips [13], bend in a shepherds hook and become white with sporulation 	<ul style="list-style-type: none"> Extremely contaminate leaves will drop Infected shoot tips turn out to be thick, curl, and eventually turn brown and die. Disease-ridden white varieties will turn a dull gray-green whereas red varieties will turn pinkish red 	<ul style="list-style-type: none"> Cutting of the grapevines after the second week of October serves to limit the harm by this disease. Every influenced bit of the vine ought to be expelled at the season of cutting and devastated instantly. Downy mildew tainted leaves ought to be specifically gathered and thrown in the dung pit.
Anthracnose	<ul style="list-style-type: none"> Temperature and dampness are the key fragments in affecting ailment advancement 	<ul style="list-style-type: none"> In the spring when there is a wet period of 24 hours and temperatures above 2^0C Anthracnose can be very damaging during heavy rainfall and hail. 	<ul style="list-style-type: none"> Numerous small, circular, and reddish spots appear on shoots. Wounds with gray centers and curved or angular edges are produced further. 	<ul style="list-style-type: none"> Disease-ridden parts may crack, affecting shoots to be weak. Lesions may spread into the tissue and may crack the fruit. 	



ESTD - 1928

Crown Gall[14]	<ul style="list-style-type: none">• Chilly winter temperatures• Through Freezing, cutting, joining, hail damages, preparing vines, and from other mechanical gadgets utilized in keeping up the vineyard• <i>Vitis</i> dwelling in the dirt on root trash can specifically cause sores on creating roots and contaminate the plant through those wounds	<ul style="list-style-type: none">• First noticed in June-July• Galls can also sometimes be detected on ripening sticks and even on roots.• In the Spring when it is cold.	<ul style="list-style-type: none">• Dark reddish-brown to violet-black boundaries sooner or later frame the wounds• Abnormal development change in shape of the plants cells at the spot or close to the spot of disease• Close to the base of the trunk as small, smooth cankers• White plump tissue• Later, they become dry and cork-like subject to the stage of development.	<ul style="list-style-type: none">• When veins are affected, especially on young leaves, the lesions prevent normal development, resulting in malformation or complete drying or burning of the leaf.• Show reduced strength and produce of grape vines.• As the gall develops, the tissues that typically lead water from the roots to the shoots lose their capacity to work• Photosynthetic matters from the leaves to the roots turn out to be very disordered.	<ul style="list-style-type: none">• Crown gall is probably more prone in limed soil than in corrosive soils so sterilize the soil.• Use disease-free stock when establishing a new vineyard• Disease-ridden vines ought to be detached from the place former to cultivation• Evading machine-driven damage through traditional applies will decrease the occurrence of the disease.
Grapevine fan leaf[15]	<ul style="list-style-type: none">• Due to the congenital “<i>nepovirus GFLV</i> (Grapevine Fan Leaf Virus)” of the infected cuttings or rootings of the vines.	<ul style="list-style-type: none">• Preeminent in spring, around blossoming and berry set, while pruning	<ul style="list-style-type: none">• Leaves turn out to be slanted and uneven with hard saw-like margins, nearer primary veins, and an open petiolar sinus[16].• Red varieties: Green veins and reddening	<ul style="list-style-type: none">• Causes extensive yield losses, lessens fruit value and diminishes the durability of grapevines in the vineyard• Berries become uneven in	<ul style="list-style-type: none">• Planting certified disease-free grapevines that have nematode resistant rootstocks in new soil far away from the location of your infected grapes.

			<ul style="list-style-type: none"> • between veins • White varieties: mild yellowing • Downward rolling of leaves 	<ul style="list-style-type: none"> • size • Yield loss can go up to 80% 	<ul style="list-style-type: none"> • Keep weeds tightly controlled around any grape plantings to eliminate vector plants and replant grape areas thickly with nematicidal plants
Mealy Bug	<ul style="list-style-type: none"> • Warmer growing climates 	<ul style="list-style-type: none"> • During the winter months • From Spring to Summer 	<ul style="list-style-type: none"> • The male nymph forms a cottony cocoon in which the pupal stage is found mainly in the winter season • the pink mealybug results on leaves • Development of sooty mold fungi 	<ul style="list-style-type: none"> • Weakens the grownup vines • In case of severe mealybug infestation young vines often die. • Raisins cannot be prepared from such infested bunches 	<ul style="list-style-type: none"> • Do not over water or overfertilize — mealybugs are attracted to plants with high nitrogen levels and soft growth.

IV. CONCLUSION

Grape is one in every of the foremost vital fruit crops of the globe and it comprises several valuable parts necessary forever. The crop incorporates a wide ability, and grapes might cultivate at lower temperate, sub-tropical and tropical weather conditions and varied agro-ecological settings. The food, nutrition, healthy and pecuniary values of the crop can be of substantial importance for the population of the Region.

Similar to the alternative plant species, grapevine is vulnerable to ecological impacts, diseases and pests. There area many grape diseases and pests all over the world. These diseases include fungal, bacterial, viral and pest diseases.

Fungi are responsible for major plant diseases such as powdery mildew, grey moulds, downey mildew. Former studies exhibited that as a result of both low inoculum levels in the vineyards and low pruning-wound exposure, trimming grapes in late winter can considerably lessen the threat of infection by the canker-causing pathogen.

This paper intended to share an original methodology to address the association of the grape disease, pest occurrences and climate. The information herewith will certainly benefit agronomists to take several preventive measures in order to produce top-quality grapes through effective disease management.

V ACKNOWLEDGEMNT

The authors gratefully acknowledge the contributions of Prashant Pawar, Owner of Prashant Agro Farms and Mr. Shinde, Grape Agriculture consultant, for assistance about the occurrence of several diseases on Grapevine and the challenges faced by the farmers, and Dr. M.R. Sanghavi, Professor, SNJBCOE, Chandwad for comments that greatly improved the manuscript.

We thank the “anonymous” reviewers for their so-called insights.

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A Review on Grape Disease Detection and Classification using Image Processing

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Abstract - Plant disease has become one of the major concerns for farmers and has now evolved into a significant threat to the quality of food consumed by the people. Hence, it becomes necessary to identify these diseases at the early stages of their growth and find possible solutions to avoid them. This paper focuses on reviewing the different approaches of disease detection and classification for grape plants. This paper will provide a detailed review of the different approaches to detect and classify grape diseases. Significant steps involved in disease prediction using image processing are image acquisition, data pre-processing, image segmentation, feature extraction and image classification are discussed. Standard techniques used in each step of image processing are reviewed along with various detection and classification techniques such as Convolution Neural Network (CNN), Deep Learning, Support Vector Machine (SVM), Fuzzy, K-Nearest Neighbors (KNN), K-Means Clustering, Deep Learning and Backpropagation. By referring to various articles, we identified the differences brought about by classification techniques and the different processes followed to obtain various results, thus helping researchers understand which methods can be selected to improve grape leaf diseases' identification and classification efficiency.

Key Words: Grape Disease Detection and Classification, Image Processing, Convolution Neural Network, Support Vector Machine, K-Nearest Neighbours, K-Means Clustering, Deep Learning, Backpropagation.

1. INTRODUCTION

In India, Agriculture is considered an essential field of occupation as over 60% of the population relies on this field for employment. It also plays a vital role in contributing to the Indian economy, accounting for about 19.9% of its total GDP. The rise in population demands an equivalently increased growth and production in the agricultural field. Food is required to supply nutritional requirements for labour so that the workforce is fed with energy to work efficiently in industries and other

economic sectors. Modern agriculture's main objective is to produce paramount yield with reduced expenditure.

India is one of the world's leading grape producers. Grape is one of India's most commercially viable crops used to make wines and raisins. Grapes are considered very important from a business perspective as they can be exported to different countries or used for table purposes. It has a good amount of nutritional minerals like vitamin C, K, and B. Maharashtra, followed by Karnataka and Tamil Nadu, are the significant contributors to the production of grapes in India, which constitutes about 80% of the grape production. However, grape plant diseases affect their quality and bring an enormous difference in the production rate, which causes a significant loss to farmers and adversely affects the economy and health. To prevent this from happening, an efficient technique to detect diseases early is the need of the hour.

Old traditional methods of detecting diseases through naked-eye are not feasible as they will not always be accurate. Some prefer to use insecticides and pesticides to resist these diseases, but using them may harm human health as they may not be used in appropriate quantities. Recent technologies play a vital role in developing new effective methods to detect and classify grape diseases. Grapes are prone to Downy mildew, powdery mildew, black rot, anthracnose, brown spot, mites, leaf blight, etc.

Timely diagnosis of diseases in grape leaves and accurate suppression of the spread of certain diseases are crucial to ensure the healthy development of the grape. Researchers have come up with various image processing and machine learning-based methods with differing results and efficiencies to overcome the issues. This paper discusses various techniques to analyse and classify diseases in grapes. Various models used to analyse and predict the disease are Convolutional Neural Networks (CNN), Deep learning, and Support Vector Machines (SVM).

A convolutional neural network is a subset of deep learning, and it is seen to be used chiefly to analyse visual

imagery. It is composed of several layers of artificial neurons. When an image is given input to the convolutional networks, every layer produces several activation functions passed to the next layer. Initially, it starts from primary feature detections, and as it passes through layers, it identifies complex features such as faces, objects, etc. Some of the models presented are DICNN, Faster-R-CNN, ResNet 50, UnitedModel, DR-IACNN, VGG16 and Inception V3.

One type of classification technique is the Support vector machine, which has received considerable attention. SVM falls under supervised machine learning techniques. In this approach, each data item is plotted to be a point in an M-dimensional space. Then classification is performed by finding the plane that acts as the differentiation factor between the two classes.

Deep learning is considered a branch of machine learning and concentrates mainly on the algorithms stimulated by the working and structure of artificial neural networks. It gradually learns to classify images, and as the name suggests, it can have hundreds of layers, eventually resulting in a deeper network. The SegNet architecture can be used for this kind of approach. VGG-16, ResNet50, Inceptionv3 and EfficientNet are some models which are generally considered for image data processing. The most common approaches or steps used to detect and classify plant diseases are image acquisition, image pre-processing, segmentation, feature extraction and classification.

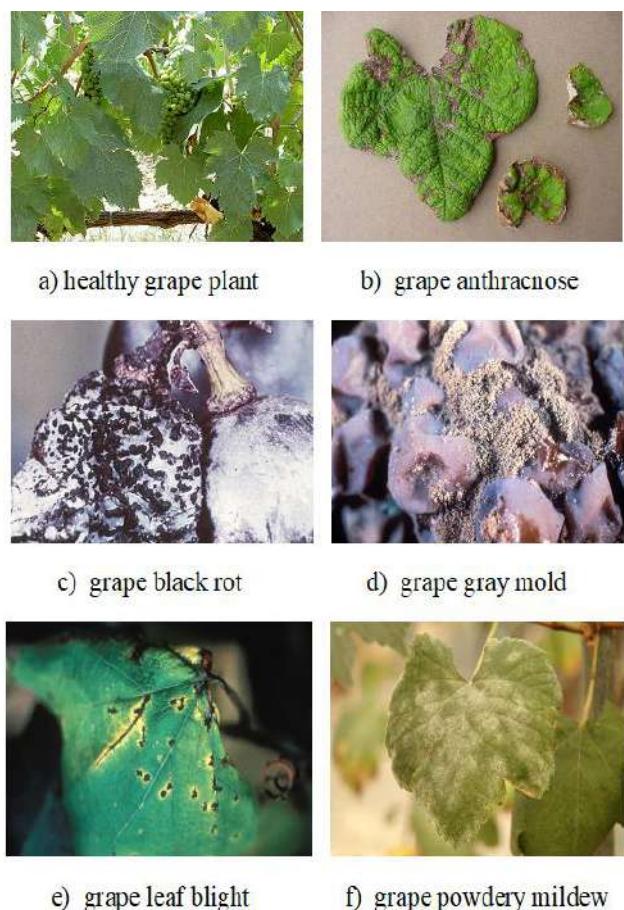


Fig-1: Different types of grape diseases

2. LITERATURE REVIEW

2.1 Convolutional Neural Network (CNN)

Liu B et al. [1] proposed an Improved convolution neural network-based approach to diagnose six general types of grape leaf diseases anthracnose, downy mildew, brown spot, black rot, mites, and leaf blight. Instead of the standard convolution, they applied a deep separable convolution to allay the amount of parameters and abate the Model over-compliance problem. Four thousand twenty-three images were collected from the field. Through public data sets, 3,646 images were collected, and a total data set of 107,366 grape leaf images is generated through enhancement techniques applied on images.

To strengthen the functioning of multi-dimensional extraction of features, an inception structure is applied. From scratch, a novel DICNN model was built and trained to construct the first two convolutional layers. In these two layers, the parameters of the two convolution layers were decreased, which reduced the intake of resources

and ameliorated the performance. 0.13% increase in accuracy was observed when compared to other traditional convolutional models. They achieved a precision of 97.22% on the test set and produced better accuracy when compared to ResNet and GoogLeNet.

S. Ghoury et al. [2] aimed at differentiating diseased grapes from healthy grape and grape leaves by performing tasks using a transfer learning approach that uses deep learning models like Faster R-CNN Inception v2 and Single SSD_MobileNet v1, which are pre-trained. Among the image dataset used, 124 were diseased images, and 136 were healthy images.

Faster R-CNN is a Regional Proposal Network (RPN)[2] to detect objects, which rely on region proposal algorithms to envision the locations of objects. For the Regional Proposal Network, a single network is used for generating region proposal operation, and Fast R-CNN classifies regions. "In Faster R-CNN, the RPN shares full-image convolutional features with fast R-CNN" [2]; this allows there to be an almost cost-free region proposal. An RPN is a completely convolutional network that determines object bounds and scores simultaneously, and this makes Faster R-CNN entirely CNN.

An Inception model is a pre-trained deep learning CNN which has a vast number of constraints that is trained on ImageNet dataset using "potent" and computers which are expensive. The training part for this model takes weeks to complete. The very first version of "Inception (inception-v1)" was launched as GoogleLeNet [2]. Later, the construct of inception was improved by [2] using the "batch normalisation technique and other ways", and the new version (Inception-v2) was introduced.

Classification accuracy of 78% to 99% was obtained through the Faster-R-CNN Inception v2 model; it could classify about 95.57% of the images in the testing part appropriately. Though it gives good accuracy, it has a drawback; it takes longer to process the images.

On the contrary, the SSD_MobileNet v1 model quickly processed the images, but it could only classify about 59.29% of the testing images correctly. This model has poor classification due to the noise and different background resolutions present in the images. If the images were organised, the classification accuracy was much higher (90-99)%. Hence [2] concluded that this model is unsuitable for tasks containing real-time classification, and the "Faster-R-CNN Inception v2 model"

could be chosen as a better option for real-time classification.

M. Ji et al. [3] came up with the United Model, a combination of multiple CNN; it helps extract distinct features and mainly aims at distinguishing diseased leaves from typical grape leaves. The basic architecture of the United Model is based on combining the width of InceptionV3 and the depth of ResNet50 so that the proposed model can improve representational abilities and learn more about representational features to provide the best performance in detecting grape disease. The Plant Village dataset is employed to gauge the proposed method. Compared to other basic single CNN models like DenseNet121, VGG16, InceptionV3, and ResNet50, the United Model performed better with a test accuracy of 98.57% and a mean validation precision of 99.17%. The trained model can't be applied for the diagnosis of grape leaf diseases in real-time scenarios within the intricate background as the training dataset utilised consists of samples in uninvolved background scenes.

X. Xie et al. [4] presented a feasible real-time grape disease detector contingent on an advanced deep convolutional network. They constructed a grape leaf disease dataset (GLDD) by applying a technology called digital image processing. To ensure sufficient GLDD 4449 images, both complex and straightforward backgrounds collected in actual vineyards and laboratories are collected. Faster R-CNN and deep-learning-based DR-IACNN model was introduced to obtain efficient feature extraction capabilities. "DR-IACNN model can also detect multi-scale diseased spots and small diseased spots by introducing the Inception-v1 module, Inception-Resnet-v2 module, SE-Blocks" [4]. It achieves 81.1% precision on a dataset of grape leaf diseases (GLDD) and detects at a pace of 15.01 FPS.

K. Thet et al. [5] aimed to overcome the inaccuracy of using the VGG16 Network as the classification of grape leaf diseases was not up to the mark. So, they presented a transfer learning method by improving the VGG16 network, one of the CNN architectures. This system differentiated the healthy leaves from the leaves affected by five common grape leaf diseases such as anthracnose, downy mildew, black measles, etc. Dataset was collected from Myanmar Grapevine Yard, which comprised 6000 images. To improve the correctness of fine-tuning VGG16 for grapes, the Global AveragePooling (GAP) layer is used in place of VGG16's two entirely associated layers before

the final classification SoftMax layer. In comparison to other systems like VGG16, SVM classifier and VGG16 fully connected layers, the proffered system outshined with 98.4% accuracy compared to others [5].

In the paper [6], G. Ghosh starts by using segmentation for finding the first diseased region and then extracts colour and texture features, then resizes them to the pixel intended. The steps implemented were: Data acquisition, Image Processing, and Image Segmentation [6]. Initially, the dataset is augmented, and distorted images in a suitable format are done and saved into the training set. Then these images undergo some preprocessing, such as resizing the image and smoothing the images. Following the data preprocessing, extraction methods such as RGB (colour-based features) are applied to extract features in leaf images. Then, converting the labels to categories for model compatibility depending on the images to their respective class is performed [6]. Modeling the classifier is done using 80% of the data for training with the assistance of neural network methods. The model is validated with the remaining 20% of the data. With this kind of technique, an accuracy of 98% was achieved. As a result, the CNN model was able to classify four types of grape leaves diseases [6].

P. Amudala et al. [7] proposed combining multiple CNNs in a United Model to extract additional discriminatory features. The data set to validate this model was the plant village dataset. They developed a mobile application that recognised and distinguished disease indications on plant leaves [7]. CNN architecture is based on Inception V3, which ResNet50 used to classify the diseases of a grape leaf into four different classes, namely esca, Arabidopsis leaf mark, black rot and safe images [7]. The proposed model had achieved a mean validation accuracy of 99.17% and test exactness of 98.57% [7].

2.2 Support Vector Machine:

P. B. Padol et al. [8] used the Support Vector Machine for grape disease classification. The process starts with finding the diseased region using segmentation by K-means clustering [8], followed by extracting colour and texture features. Finally, the SVM classification technique detects the type of disease on leaves [8]. This paper's image preprocessing step consists of resizing, thresholding, and Gaussian filtering [8]. The classification technique consists of two phases, namely, training and testing stages by applying the classifier. The classifier is equipped using feature values and their respective target

values [8]. Once the classifier is trained with the training set, it is then validated using the test dataset. The classifier classifies the images based on the training images and classification relative to them. Downy Mildew and Powdery Mildew are the two classes of grape leaves that were classified [8]. For this, a total of 137 grape leaf images were used. The given system accurately assessed 88.89% for Downy and Powdery grape leaf disease [8].

A. Adeel et al. [9] have presented an automated model for grape disease detection centered on notable features selection and saliency estimation. A contrast stretching approach is presented, approximating and extracts the unhealthy regions and extracts other features like colour features. The local contrast haze reduction (LCHR) technique is used in the first step. Extraction of colour, texture and geometric characters is then put together by canonical correlation analysis (CCA). Noise is reduced through Neighborhood Component Analysis (NCA) during the fusion. Classification of the extracted features is done by multiple class SVM. The proposed model is tested on the dataset of grape leaf diseases acquired by Plant Village. The accuracy attained through this M-class SVM is 94.1% which is superior compared to the other classifiers like Q-SVM, ESD, cubic SVM, and cosine SVM. The limitation to this model is that it gives lesser accuracy for complex images. For further enhancements, they plan on building a model using reinforcement learning (RL).

This paper by N. Agarwal [10] focuses on building a system using a multiclass Support Vector Machine (SVM) that will discern the disease of grape plants [10]. The process used is a general procedure involving image processing techniques applied to the data images to extract the essential components for further examination. Further, classification is done using multiclass SVM with the construction of a binary classifier 'k'. For this paper, the k is considered to be four. The data point is allocated to the class with the most prominent decision function value [10]. Three types of diseases have been detected and classified in this paper: Black rot, Leaf Blight, Esca, and a normal healthy leaf of a plant used for training and testing [10]. The results were very accurate for black rot and unaffected cases of the grape leaf disease detection. Still, they gave a considerably average performance, with Esca and L Blight contributing to an overall accuracy of 90% [10]. The paper suggests some future modifications to be made by automatically selecting a few of the features extracted from the K-Means clusters [10]. And also,

wavelength-dependent features can be added to the database, which might improve the accuracy [10].

H. Waghmare et al. [11] brought forward a technique for recognising grape plant disease using texture analysis and pattern recognition [11]. The process starts with performing segmentation on the images after the background removal. To spot the diseased parts of the leaf, segmented images are scrutinized through a high-pass filter. A unique fractal-based texture feature is used to retrieve the segmented leaf texture. As the fractal-based features are locally unchanging [11] and hence they provide a remarkable texture model. A multiclass Support Vector Machine method is then used to classify the extracted texture pattern. This paper detects and classifies two significant diseases, namely downy mildew and black rot [11]. "The approach used in this paper consists of four main steps: the acquisition of grape leaves, followed by the extraction of grape leaves background and statistical analysis and disease classification" [11]. The dataset consists of a total of 450 images which comprises healthy, diseased, and pest-infected images [11]. Image preprocessing, such as resizing the images to the required format, makes the image suitable for further processing. The background subtraction is done using the segmentation portion of interest from the image [11]. Feature extraction is performed from the infected region on the leaf according to properties like colour, correlation, congruity, and contrast[11]. The final step is to analyse the features and classify using a Support Vector Machine that categorizes the plant leaves into two classes. With this method accuracy of 89.3% was achieved. However, with a 100: 30 training-testing ratio, an accuracy of about 96.66% was obtained [11].

S. Barburiceanu et al. [12] "proposed new feature extractors for colour texture classification based on Local Binary Patterns (LBP) operators, which are invariant to rotation, illumination, and change of the observation scale, being also robust to Gaussian noise"[12]. The presented model operates in RGB colour space to classify grape leaves containing Gaussian noise and noise-free images by employing a state-of-the-art image de-noising algorithm embedded into a multiscale LBP feature extraction process [12]. The colour increases the ability to classify and discriminate power, increasing accuracy in noise and noise-free conditions. Using SVM, the proposed extractors greatly improve the accuracy of 97-98%in both noise and noise-free images compared to grayscale LBP-based approaches.

This paper by G. Li [13] produced a system to identify and diagnose grape downy and powdery mildew based on image recognition [13] and SVM techniques. The segmentation of disease images is executed using the K-Means clustering algorithm. The Support Vector Machine classification technique [13] was applied to the dataset after converting it to a suitable format. The process applied starts with image acquisition, followed by segmentation, and then the feature extraction is done on the images. Finally, an SVM classifier is applied to these images to achieve results. The dataset consists of fifty images, in a 3:2 ratio of grape downy mildew images to grape powdery mildew images [13] for training. For testing the model, thirty-five images, including twenty grape downy mildew images and fifteen grape powdery mildew, are used. For the thirty-five images, the recognition rate was 91.43% [13].

2.3 Fuzzy Neural Networks

In this paper by D. Kole et al., The proposed system identifies the downy mildew disease [14]. Downy mildew is a serial fungal disease [14]. The technique used is based on a significant fuzzy factor. The dataset used consists of thirty-one images of diseased and healthy images. The technique of image processing used consists of two major stages. The first stage is to lower features in which predominant features are obtained [14]. The next phase is to detect downy mildew disease there in grape leaves [14]. After the feature reduction phase, the values of features chosen for all test images are obtained. Then all the normalised feature value present in the normalised feature matrix generated in the first stage is replaced by a fuzzy value of the nearest cluster of the respective feature [14]. Then the calculation of the mean fuzzy value for each image is done. The images having an average fuzzy values more than or equal to the experimental threshold value are detected as downy mildew disease [14]. The success rate achieved was 87.09%.

2.4 K Nearest Neighbors:

This paper by N. Krithika et al. proposed identifying diseases in a grape plant by using the leaf skeleton of the grape as the focus of detection. The process starts with the identification of leaf skeletons [15]. A tangential direction-dependent segmentation algorithm is presented for the skeletons retrieval [15]. Once the classification of the grape leaf images is done, the colour channels and histograms of H are generated, and the pixel values are noticed to differentiate the healthy and diseased tissues

[15]. Then, the extraction of features and classification of them is done using the KNN classification algorithm [15] in order to detect disease in the grape leaf. In this paper, the image processing is performed by first acquiring the RGB grape leaf images [15] and then finding Hue Saturation Value(HSV) and L*a*b colour spaces helps in the further process [15]. The obtained images are preprocessed for further identification process [15]. Hence, the proposed method mainly detects a leaf skeleton's luminance and characteristic linear image [15]. GLCM features are extracted, and the classification of the diseases is carried out utilizing the images obtained [15]. Further, the classification of grape leaf diseases is done efficiently using the KNN approach.

This paper by A. Bharate et al. gave a system that applies techniques involved in image processing to perform the classification of grape leaves automatically into healthy and unhealthy [16]. The feature extraction is performed to obtain the colour and texture features from the leaf image [16], followed by applying the KNN classification algorithm to classify the leaf diseases. Step one of the given system involves the gathering of data and database creation for the data [16]. The database includes a total of 90 images in which 45 images are termed to be healthy and 45 images termed to be unhealthy [16]. GLCM is used to calculate the texture features. Testing is done using KNN on 30 images. An accuracy of 96.66% was achieved using the KNN classification technique. When the same dataset was classified using the SVM technique, an accuracy of 90% was achieved. Hence it has been concluded that the KNN classifier gives accurate and efficient results when compared to that of SVM classifier.

2.5 K Means Clustering

In this paper, M. S. Utsad et al. proposed a system that processes the grape leaf imagery by applying segmentation and K Means clustering algorithm to detect the image's diseased part [17]. Colour, shape and the other features were extracted from the image segmented based on the most matched features classification of diseases using an SVM classifier. The K Means clustering algorithm is a well-known approach generally applied to solve low-level image segmentation tasks [17]. The paper proposed K Means segmentation method to segment target arrears [17]. A major advantage of using the K Means clustering technique is it works on local and global information of images [17]. The other advantages of using this kind of clustering technique is that it is fast, powerful, flexible and

the implementation is simple. With this technique, the accuracy achieved was 91%.

2.6 Deep Learning:

M. Kerkech et al.[18] have presented an optimised detect Mildew disease in vine built on deep learning segmentation method and optimised image registration using multimodal Unmanned.

Aerial Vehicle (UAV) images with a deep learning segmentation procedure that has been used for the detection of vine disease using multimodal UAV images. The model includes three main steps, and the first step is alignment of image, the second step using SegNet architecture to perform segmentation of visible and infrared images in order to identify four classes namely the shadow class, the ground class, the healthy class and symptomatic vine, the last step involves of give raise to an disease map which is performed by fusion of the segmentation results which are obtained from the visible and infrared images [18]. In this case, the method is constructed by integrating infrared images and visible images derived from two different sensors. "The image registration method" was used to enable the combination of images from two different sensors. The proposed model achieved accuracy greater than 92% for disease detection in vineyards. The limitation of this study is the diminutive size of the sample used for training, due to which there was a visible decrease in the performance of segmentation done using deep learning.

The paper [19] proposed a new system for detecting vine diseases like esca in UAV and RGB sensor images. This method integrates the strengths of the deep learning approach (specifically CNNs) with various different "color spaces and vegetation indices" [19]. The obtained images were divided into square grids with varying sizes and pixels. Each block of the grid had to be classified as either healthy or diseased. The model was classified using a deep network and a combination of vegetation indices and colour spaces. Results concluded that "CNNs with YUV colour space combined with ExGR vegetation index and CNNs with ExG, ExR, ExGR vegetation indices" produce optimal results with the value being more than 95.8% accuracy. Some limitations of this system include a recurring problem and the number of labelled data. The Proposed system can be improved by increasing the UAV image database with new vine disease samples.

2.7 Back-propagation Network:

S. S. Sannakki et al. suggested a system in which the input is the images of grape leaves with a complex background. Thresholding is employed to mask green pixels, and anisotropic diffusion is used to remove noise from the images [20]. Then the segmentation of grape leaves is performed using K-Means clustering. Followed by the segmentation process, the diseased fragment is identified. When the feed-forward back propagation neural network is trained for classification [19], Better results were achieved.

[20] The author has considered two types of diseased grape leaves-downy mildew and powdery mildew. Feature extraction is carried out by color co-occurrence methodology that uses an image's texture to arrive at unique features representing the image. The training of neural networks for pattern recognition resulted in 100% accuracy when using hue features alone. Dataset has 33 images; 29 were used for training, the remaining were used for testing and validation [20]. Research can be improved by exploring the benefits of these techniques by including samples of healthy and other diseases of grapes.

J. Zhu et al.[21] have presented an approach to inspect grape leaf diseases automatically using image processing and back propagation neural network BPNN. Diseased images are de-noised using the Wiener Filtering method. The Otsu method is used to segment the grape leaf diseased regions, and to enhance the lesion shape, and morphological algorithms are applied. Further, to extract the entire edge of the lesion region, the Prewitt operator was applied. This system mainly extracted five effective grape leaf parameters: shape, area, perimeter, circularity and rectangularity. The last step was to analyse grape leaf diseases by implementing BPNN. The results showed an average accuracy of 91%, and this method can recognise the five primary grape leaf diseases with high classification accuracy.

2.8 Support Vector Machine and Random Forest Tree:

S. M. Jaisakthi et al. [22] put forward a system to detect grapevine diseases through image processing and machine learning techniques. At first, the region of interest (ROI) is segmented from the rest of the background image by utilizing the segmentation method called grab cut. Then the diseased part identified after segmentation is additionally segmented using global threshold and semi-

supervised technique. The extracted attributes from segmentation have been classified into main categories such as healthy, esca, rot and leaf blight using Support Vector Machine, Random Forest Tree and AdaBoost. Compared to other classifiers such as RF and AdaBoost(Decision tree), SVM obtained a superior testing accuracy of 93%.

3. GENERAL ARCHITECTURE

The block diagram of the general architecture is shown in the figure below. The block diagram represents various stages involved in identification and detection of grape leaf diseases. Each stage of the block diagram is described in detail in accordance with the block diagram.

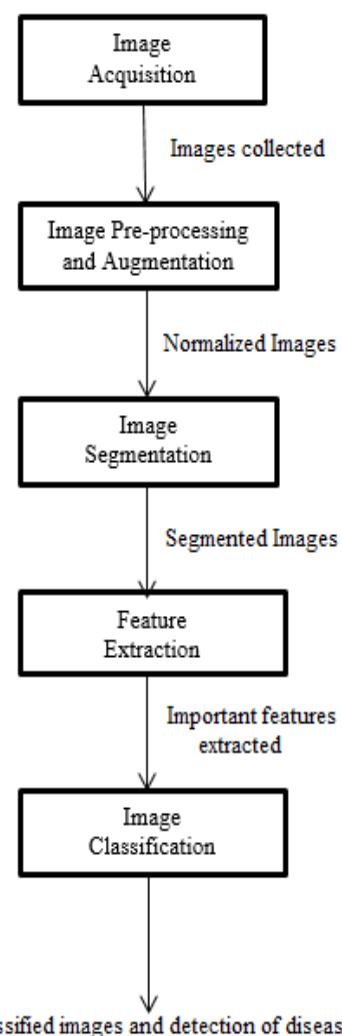


Fig-2: General Architecture for detection and classification of grape plant diseases

3.1 Image Acquisition

To identify and detect diseases in grape leaves, the first step is to collect the data necessary in images. V. Mishra et al. mentioned that the primary motive of image acquisition is to transform optical images (actual data) into an array of numerical data that can later be altered by a computer [23]. Before any processing is applied to the images, the images must be converted to a suitable format, making processing more efficient. In this process, the light energy from an object is converted into electrical signals by combining sensitive sensors to the particular type of energy. These minute subsystems work together to provide a machine vision algorithm with the most accurate representation of the object. The components include:

1. Triggers: For triggering the images at any point in time, the camera has to be configured. This mechanism signals the camera to capture images. Most applications in the modern world use triggered images. This trigger can be in PLCs (Programmable Logic Controllers), sensors and push buttons for manual usage. Triggers can be considered to be used based on the type of camera being used.
2. Camera: The purpose of using cameras is to take the incoming light from an object/scene and convert it into digital signals, i.e. pixels, using CMOS or CCD sensors.
3. Optics: The light from the source must be focused adequately by a lens on the sensor to capture the image with maximum clarity.
4. Illumination: Illumination is one of the most critical factors in a machine vision system. The lighting should be able to illuminate uniformly throughout all the visible surfaces.

In paper [1], paper [8], paper [11], paper [13], paper [16], paper [17] and paper [20], the image acquisition process is incorporated using a digital camera to capture a sum of 7,669 images of grape leaves. For papers [2] and [22], the source of acquisition of images is the internet. And for paper [2], 136 healthy images and 124 disease grape images were considered. In paper [3], paper [6], paper [7], paper [9], paper [10], paper [12] and some of the images from paper [2] were all acquired from the PlantVillage dataset. For the paper [4], the grape disease images from GLDD were collected under various climatic conditions

[4], and other leaf images were acquired in Yamethin township. For paper [18], Image acquisition is performed using an Unmanned Aerial Vehicles (UAV) drone, which consists of a high-resolution Survey2 sensor [18]. The drone was used to take continuous images of the vineyard plot. In paper [19], a UAV system with an RGB sensor [19] was utilized for image acquisition. In paper [21], the image acquisition stage is carried out by obtaining images from machine vision inspection system, a CCD, including a lighting system and a computer [21]. The lighting system consists of an LED which helps in noise reduction in the images.

3.2 Image Preprocessing and Augmentation:

Data preprocessing is done to make the data fit into a particular format to be uniform and suitable for further processing. Data preprocessing includes data manipulation and operations on images which aim to reduce undesired distortions and improve the quality of images. Image preprocessing includes resizing, colour corrections, the orientation of the images etc.

The main steps include:

Image Resizing:

The images are resized to achieve uniformity in terms of image and its size[17]. The original images are bigger, due to which it takes a long time to process. Hence images are resized into small sizes to avoid time consumption. In [6],[7], and [11], images were resized into 256 x 256. Similarly, images are resized to size 300 x 300 and then thresholding to obtain green colour parts [8]. [3] VGGNet, DenseNet and ResNet images were resized to 224 x 224 and 229 x 229 for GoogLeNet. Images were compressed to 800 x 600, retaining the proportion to make the resolution of images invariant by applying the Interpolation Method [13]. To enter VGG16 network resizing of images to 150 x 150 were carried out by Linear Interpolation method [5] is

$$y = ((y_2 - y_1)/(x_2 - x_1))(x - x_1) + y_1 \quad (1)$$

Image Colour Transformation:

The input “RGB images” are converted to “Hue Saturation Value (HSV) color space” and this conversion is what is called a color transformation. HSV is closer to human perception [11]. After transformation, the Hue component is generally considered for further process. As it is the dominant color [11] and does not consider the saturation and intensity component because it doesn’t provide any

helpful information [17]. The color spaces represented by grayscale images are enhanced by

$$N p, q = \frac{F p, q - \min(F)}{\max(F) - \min(F)} \quad (2)$$

F and N represent the original and new pixel values and indexes of pixels are represented by p and q.

Otsu's technique is employed to grayscale images. The images obtained have a region of interest called disease spots and hence RGB image is modified into different lab colour spaces and HSI model [10]. Multilevel Otsu thresholding segments the images into different regions by choosing threshold values based on the biggest inter-class variance between the background and foreground [11]. This technique improves accuracy when applied to transformed images.

Image Background Subtraction:

To remove undesired backgrounds from the images and to extract the required region of the image, "background subtraction" techniques are adopted [17]. Colour based background subtraction techniques are used for achieving more accuracy. In this technique, based on RGB intensity values, unwanted backgrounds are removed. As green coloured pixels consist of healthy parts, only these are kept as it is whereas the other pixels are colored black [11].

3.3 Image Augmentation:

The process of combining operations such as image shifting, rotation, shear and flips etc. in order to generate more training images is called image augmentation. It is an essential technique as it helps to overcome the overfitting problem and helps to generalise better [5]. This helps the model learn more variety of patterns during training, avoid overfitting problems and helps to attain greater performance during detection. In the view of the weather's impact during shooting, intensity factors like contrast, sharpness and brightness are considered [4]. The corresponding positions of the camera and diseased leaves are simulated using rotation (90, 180 and 270 degrees), horizontal and vertical symmetry operations [1]. Gaussian noise is utilized to mimic the effects of equipment factors. Furthermore, PCA jittering is applied to augment the input dataset and ameliorates the quantity and diversity of grape leaves.

[21] The Wiener filtering method drawn on wavelet transform (WT) was applied to de-noise the images. Since Grayscale images include a certain amount of noise. This is to be removed before segmentation can be performed on the images. In signal de-noising and image processing, WT has been broadly used because of its time-frequency, de-correlation, localization property, flexibility and multi-resolution [21]. WT also has simple computation, exhibits convenience and effective de-noising effect in de-noising images. The calculation formula of the dimensional Wiener filter is expressed as:

$$g(i, j) = E + \frac{\sigma^2 - v^2}{\sigma^2[f(i, j) - E]} \quad (3)$$

Where g(x, y) is the grey value of pixel (i, j); E is the local grey mean of pixel (i, j); the local. The region is the neighborhood of pixel (i, j), which is generally a 3x3 or 5x5 neighborhood; σ^2 is the local variance of pixel(i, j); v^2 is the noise variance; and g(x, y) is the de-noising gray estimate of pixel(i, j) [21].

The advantages of image preprocessing are stated as follows:

1. It helps to improve the images in human interpretation.
2. Images can be stored and retrieved easily.
3. The pixels of the image can be manipulated at the desired density and ratio.
4. The digital image can be made available in any desired format.

3.4 Image Segmentation

Image segmentation divides the images into smaller subgroups of images or pixels to reduce the complexity of images, and image analysis can be done easily. The splitting and grouping of pixels to form a sub-image can be done using various image segmentation algorithms. In paper [9], the segmentation technique used is colour segmentation which follows the colour features and a saliency method extracting only valuable objects from the image and discarding the rest. This method involves four steps:

1. LAB colour transformation.

2. Selection of appropriate channels based on weighted function is carried out.
3. Refinement using morphological operations.
4. Map and draw Region of Interest [9].

In the paper [8][13] [10] [20], K-Means clustering is the technique being applied for segmentation. The clustering technique can be defined as a procedure by which huge data sets are grouped to form clusters of homogeneous segments or sets of data. K-means clustering is used to segment the target area (diseased parts) from coloured parts of the leaf by optimising the partitions based on the user-defined initial set of clusters. It groups objects or pixels based on the number of attributes into K number of clusters.

The steps required to carry out the K-Means algorithm is:

1. First, partition the dataset into K number of groups or clusters and assign data points randomly.
2. For every data point, Euclidean distance from each data point has to be calculated by $\sqrt{((x_1 - x_2)^2 + (y_1 - y_2)^2)}$ (4) and (x_1, y_1) (x_2, y_2) are two data points.
3. If a data point is in close proximity to its cluster, then leave it unchanged.
4. If a data point is away from its cluster, shift it near its cluster.
5. Repeat all steps until all data points are catered.
6. Clustering will stop when all clusters are stable [8].

After enhancing the pixels in the skeletons, segmentation of skeletons was performed using color and smooth segmentation. Smoothness Segmentation is defined as:

$$\text{Smooth } (c) = 1/N \sum m \in D(|\psi(c) - \psi(m)|) \quad (5)$$

Here N constitutes the number of pixels and D is the side length. If the smooth degree of pixels is greater than the threshold, it will be termed as noise and eliminated from the image [15].

Another segmentation technique includes threshold segmentation, as described in the paper [21]. Otsu threshold segmentation is adopted to segment the diseased regions of grape leaf, and minimum intra-class and maximum inter-class variance are optimal criteria for the otsu method. This area was expanded to fill a small hole and connect the ends separated by standard morphological manipulation. The Prewitt operator is the first derivative operator used for edge detection in images

[21]. Grab cut segmentation algorithm has been used in paper [22]. This algorithm uses a Gaussian mixture model (GMM) to label pixels as foreground or background, having the first rectangle, which is the approximate segment between the background and the foreground. From the background or foreground, the diseased leaf parts are extracted with the help of the Global threshold method, which is used to convert grayscale image to binary image. For segmentation, the RGB image is converted to a BGR image so that the blue pixels of the affected area are excluded. Filtered image thresholding is applied, and finally the lesion is determined [22].

3.5 Feature Extraction

The creation of a collection of features from the raw data provided initially is known as feature extraction. The data that is being dealt with in the modern-day consists of data with enormous amounts of features. If the number of features available becomes as big as the data considered or even reaches numbers beyond the data considered, this may lead to a machine learning model suffering from model-overfitting. Feature extraction can generally be viewed as a method provided that can get around major problems yet describe the data efficiently. Most of the papers considered adopt techniques to extract various features such as shape, colour and texture features.

In paper [8], color and texture features are extracted to attain the best accuracy as color features are suitable for Downy Mildew, and texture features are needed for Powdery Mildew.

Steps to extract color features for an image [8]:

1. The RGB image is converted in HSV color space.
2. Uniform subdivision of the image into 3×3 blocks is done.
3. For every block of the nine blocks, mean colour is evaluated applying the formula
4. $x' = \left(\frac{1}{N}\right) x_i \quad (6)$

Where x_i is the pixel intensity and N is the total number of pixels.

5. Variance for every block is evaluated by the formula

$$\text{Variance} = \frac{1}{N} \sum_{i=1}^N (x_i - x')^2 \quad (7)$$

6. Skewness is used to find the surface of the image for each block.

Another important feature is extraction based on shape characteristics to describe the geometrical properties of the lesion irrespective of the grey values. Some of the major parameters in shape characteristics are target area, target regional circumference; Lesion circularity, rectangularity and shape complexity are computed by formulas:

$$\text{Lesion circularity } C = 4\pi A/L^2 \quad (8)$$

$$\text{Lesion rectangularity } R = A/Ar \quad (9)$$

$$\text{Lesion complexity } e = L^2/A \quad (10)$$

The image parameters of the lesion can be passed as a feature vector for classification. This extraction method is effective for separating lesion areas in leaf images.

Texture features are used as discriminators when images don't have well-defined colours or shapes. Local pattern formation describes the texture formed. Local Binary Pattern (LBP) is a capable feature as it is invariant to illumination conditions. LBP uses simple primitives to describe complex structures in images. Opposite colour LBP feature extraction is used to analyze the texture [11]. To address the noise sensitivity and obtain distinctive features MRELBP (Median Robust Extended Local Binary Patterns) was proposed, and BM3DELBP (Block Matching and 3Dfiltering Extended Local Binary Patterns) descriptors were employed to reduce Gaussian noise [12]. In the paper [12], the MRELBP and BM3DELBP operators are extended to colour using the relative color scheme. Here, the operator is individually applied to each color channel, collecting the colour pattern of the opponent.

In papers [16] and [22], features like texture and colour are extracted and used as input for sorters to improve results. Gray Level Co-occurrence Matrix (GLCM) is a good approach because Grape leaves have a repeating pattern. The GLCM approach was developed through spatial grey-level dependent matrices (SGDM's) [20]. Co-occurrence matrices

Measure the probability of a pixel at one grey level occurring at a different distance and orientation from another given pixel of the second grey level [20].

Texture Feature Extraction through GLCM:

1. Begin
2. Read colour images and find various intensity levels in the image.

3. Compute GLCM image by identifying the GLCM's size. Find intermediate matrix A by determining how often a pixel p appears in a particular spatial relationship with pixel q.
4. By dividing every element of the matrix by the sum total of elements in the matrix GCLM is calculated.
5. Calculate properties like contrast, correlation, energy and homogeneity for images using GLCM.
6. End

Color Feature Extraction [20]:

1. Begin
2. Read colour images.
3. Determine the percentage of red, green and blue colors in a data image which can be termed as extraction of the three components.
4. Conversion of colour image to HSV image is to be performed.
5. Extract hue, intensity and saturation of an image
6. Calculate the mean, variance, and range for each component extracted in steps 3 and 5.
7. End

So far, most studies have been extracting statistical features of RGB and converting them to LAB format. Therefore, the paper [10] added several properties of the HSI image format to increase the feature set and improve accuracy. It is known that the HSI image does not change even when the background illumination changes [10].

To extract skeleton information, luminance characters are essential as the light intensity of the skeleton should be more than other pixels. Hence Tangential Direction (TD) method is adopted to extract skeleton pixels.

The luminance difference is calculated by [15]:

$$d(e, An) = mLAn (|(c) - (m)|) \quad (11)$$

Where x is the pixel, c is the center, An is the angle, and the short line is LAN, and the function () is used to find the brightness value of the pixel. Then the angle with the smallest brightness difference is selected as TD of e. Then, de-noising is performed on the selected candidate pixels from the skeleton image [15].

3.6 Image Classification

Classification techniques are applied to classify data based on decisions. The theory describes that the classification

problem relies on the training data set containing the observation value and its category membership to identify which category set a new observation value belongs to.

CNN is part of a deep learning neural network that is primarily used for image identification and processing and specially designed for processing pixel data. CNN technique involves multilayer perceptrons which are designed to result in low processing requirements. Each neuron present in the CNN layers takes several inputs, and then it considers a weighted sum over the taken inputs, where it is made to go through an activation function which further responds back with the output achieved. The layers of CNN are composed of hidden layers, including input layers, output layers, and multi-convolutional layers, pooling layers, fully connected layers and normalization layers. CNN can be viewed to be prone to overfitting data as there is full connectivity between the layers. The reduced limitations and increased image identification and processing efficiency lead to a highly efficient system, simpler to train the model, yet limited to image processing and natural language processing.

Some of the models proposed by the researcher are DICNN which trains the first two layers separately so that the intake of parameters is reduced and the performance is better. Faster R-CNN is based on a Regional Proposal Network (RPN) [2]. It has a single and fully convolutional network. It is called Faster-R-CNN because RPN predicts object bounds and scores simultaneously as the combination of the width of InceptionV3 and the depth of ResNet50 United Model was introduced for better accuracy and representational abilities. To detect multi-scale diseased spots and small diseased spots, the DR-IACNN model was presented by including the Inception-v1 module, Inception-Resnet-v2 module, SE-Blocks. Shortcomings in VGG16 were overcome; the Global AveragePooling (GAP) layer is used instead of VGG16's two completely connected layers before the ending classification SoftMax layer, which increased its efficiency compared to VGG16 fully connected layers, SVM classifier and VGG16. CNN architecture is based on Inception V3, which ResNet50 used to classify the diseases of a grape.

Support Vector Machine has gained considerable attention as a classification technique. Support Vector Machine could be preferred as it tends to work with high dimensional data and avoid the curse of dimensionality. This classification technique's approach is considered unique as it uses a subset of training examples to

represent the decision boundary. This classification method aims to find a hyperplane in the M-direction space (M - number of features) where data points can be clearly classified. SVM technique helps in global optimum solutions, whereas the artificial neural networks (ANN) and rule-based classifiers tend to find only locally optimum solutions. Capacity control can be performed by SVM by maximising the margin of the decision boundary. SVM works with high efficiency on small sample sets as training time incorporated in this type of classifier is high.

The fuzzy set theory concept was invented by Zadeh. The concept of fuzzy set theory is a research approach that can handle subjective, ambiguous and inaccurate judgments and quantify the linguistic aspects and assessments of data that can be used for individual or group decision making. It has proven itself to be considered as a powerful tool for helping in the decision making process. For a fuzzy classification technique, a certain set of fuzzy rules are applied to the linguistic values of its features. An object can be classified. All rules considered have a number weight between 0 and 1, which applies to the number given by the former. There are two distinct parts involved in this. The first part includes the background evaluation, and Input should be fuzzified, and the necessary fuzzy operators are applied. The second part involves applying the result achieved in the first part to the consequent, generally known as inference. The fuzzy output can be achieved when the inference applies the fuzzy reasoning mechanism.

KNN is based on the supervised learning method and is a machine learning algorithm. In KNN, when a test sample is given, first, the computation of proximity with the rest of the data points in an N-dimensional space is performed where N is the number of attributes.

The algorithm for 'k' number of nearest neighbors and D set of training examples works as follows:

1. For each test sample $e = (x', y')$ do
2. Compute $d(x', x)$, the distance between and every example $(x, y) \in D$
3. Select $D_e \subseteq D$, the set of k closest training examples to e.
4. $y' = \text{argmax}_v \sum_i I(v = y_i) \subseteq D_e$ [12]
5. End For.

The algorithm specifies to start by computing the distance (or similarity) between each test sample and all the

examples used in training to determine the nearest neighbor list. This kind of computation may be costly if a large number of training examples are considered. But the number of computations needed for finding the nearest neighbor can be reduced using certain efficient indexing techniques. Once the closest neighbor is determined, the next step is to classify the test samples based on the number of classes to which the closest neighbor belongs. KNN can be considered advantageous over the other classification technique as no model building is required to be done based on the fed data. But as it is an instance-based classifier, i.e. it uses specific training samples to make decisions without any model building, classifying a test sample may be costly as the computation of proximity should be performed between the test example and all the training examples. The nearest Neighbors classification technique can produce wrong predictions unless the appropriate data preprocessing and proximity values are considered.

K Means is an algorithm based on unsupervised classification that is also called clusterization. Unsupervised classification specifies that the data set either does not have any labels or the labels are not used. Here, the classification of data is done using the properties and characteristics of the data. The K- Means algorithm involves three steps. K Means classification technique involves grouping objects into ' k ' different groups, which is done based on their characteristics. This grouping minimises the final sum of the distances between the cluster and each data object. Euclidean distance is generally considered and used for this distance.

The algorithm involves three steps:

1. Initialisation.
2. Assignment of the data objects to the centroids.
3. Updation of centroids.

In this algorithm, the first step involves choosing the number of clusters (k) and creating k centroids in the data space, which can be chosen randomly. The second step in the algorithm suggests that a centroid should be assigned for each centroid. The centroid position is updated considering the new centroid, the average of the positions of objects which belong to the particular cluster. The second and third steps are repeated until there is no more movement in the centroid or it moves below the specified threshold value of distance in each step.

Deep learning can be viewed as a subset of machine learning. Deep learning uses an ordered level of artificial

neural networks (ANN) to carry out machine learning processes. Deep learning systems allow machines to process the data in a non-linear approach. Deep learning models consist of multilayers of neural networks for processing data and performing certain computations on a huge amount of data. As in the modern-day, most machine learning algorithms work on data with thousands to millions of features. The efficiency of certain algorithms may be degraded due to a large number of features for a single data object. In the case of deep learning techniques, the algorithm progressively learns more about the data object as it goes through every layer in the neural network. Hence deep learning algorithms become important to process or classify data objects with a large number of features. Deep learning acts as a powerful tool for unstructured data. But deep learning can easily fall into the "over fitting" problem resulting in a failure to generalise the data objects well, and applying deep learning to less complex data might result in overkill. Hence, deep learning needs access to extensive data and is considered to be less effective when compared to linear models or boosted decision trees for less complex data. But deep learning can also act as the most effective tool when a complex data set is considered.

An artificial neural network is a set of connections composed of I/O units, each associated weight. Back propagation neural network is a standard method for training artificial neural networks.

The main functionality of BPN is to calibrate or make minor adjustments to the weights of a particular neural network depending on the error rates obtained in the previous iteration. Accurate adjustments of the weights lead to the depreciation of error rates and results in a dependable model as it increases the generalisation.

For a single weight in the neural network, the backpropagation algorithm evaluates the gradient (change in the weight concerning change in error) of loss function for that weight by the chain rule.

Backpropagation algorithm:

1. Inputs X shows up through the pre connected path.
2. Input is geared using actual weights W. Usually, the weights are selected randomly.
3. Outputs are calculated for every neuron, starting with the input layer, the hidden layers, and finally, the output layer.

4. Evaluation of errors in the outputs is done.
$$\text{Error} = \text{Actual Output} - \text{Expected output} \quad (13)$$
5. From the output layer, move back to the hidden layer to tune the weights to reduce the error.

4. CONCLUSIONS

Detection and classification of grape leaf disease can be done using various techniques. In this paper, we have studied the various approaches used by researchers to find an optimal and effective solution for identifying and detecting grape leaf diseases. Each approach has a distinctive quality. With each paper, there are differences in the dataset, the kind of disease to be identified by the particular approach and then the approach itself. This article outlines recent research methods, and it helps in future research work. The five main steps in image processing are image acquisition, image pre-processing, image segmentation, feature extraction and image classification. Some image acquisition sources were digital or mobile cameras, internet, Plant Village, Grape leaf Disease dataset (GLDD) and Unmanned Aerial Vehicles (UAV) like drones. Some of the main steps in data pre-processing are Image Resizing, Image Colour Transformation, Image Background Subtraction and Image Augmentation. Some commonly used image segmentation techniques are K-Means clustering and the Otsu threshold segmentation method. Feature extraction is based on color, texture and shape. Local Binary Pattern (LBP), Gray Level Co-occurrence Matrix (GLCM) and Tangential Direction (TD) are a few texture-based feature extraction methods. The classification techniques reviewed in this paper are Convolutional Neural Networks (CNN), Support Vector Machine (SVM), the fuzzy set theory, K Nearest Neighbor (KNN), Deep Learning and Backpropagation neural networks. This paper presents an overview of different techniques used in grape leaf disease detection and classification, which can be helpful in further research.

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BIOGRAPHIES



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Grapes disease detection using transfer learning

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ABSTRACT

Early and precise diagnosis of diseases in plants can help to develop an early treatment technique. Plant diseases degrade both the quantity and quality of crops, thus posing a threat to food security and resulting in huge economic losses. Traditionally identification is performed manually, which is inaccurate, time-consuming, and expensive. This paper presents a simple and efficient model to detect grapes leaf diseases using transfer learning. A pre-trained deep convolutional neural network is used as a feature extractor and random forest as a classifier. The performance of the model is interpreted in terms of accuracy, precision, recall, and f1 score. Total 1003 images of four different classes are used and 91.66% accuracy is obtained.

KEYWORDS

Deep Learning, CNN, Transfer Learning, Image Classification, Random Forest

1. INTRODUCTION

Disease identification and classification in plants, in the early stage, is one of the most important agricultural practices. Every year a large number of crops get infected by diseases, resulting in huge economic losses and shortage or increased demand for food in the market. Therefore a quick and robust method has to be made to identify and classify diseases in plants. A lot of advancements have been made in machinery, pesticides used, and other chemicals, but early identification of diseases is the most important aspect. Manually identification is inaccurate, time-consuming, and expensive. In this paper, we have suggested a CNN based model for the early identification and classification of diseases in grapes plants. CNN is the basic Deep Learning tool used in this paper. Deep Learning refers to the use of artificial neural network architectures (ANN), that contain a large number of processing units. The most

successful type of models for image analysis to date is convolutional neural networks. CNNs contain many layers that transform their input with convolution filters of a small extent. We have used Transfer learning to make a robust and accurate model. We have proposed a CNN based VGG-16 model as a feature extractor and random forest as a classifier. Based on that, we find a confusion matrix and calculated features like precision, recall, and F1 score to evaluate the accuracy of model. These factors can be calculated by using parameters like true positives, true negatives, false positives and false negatives, where true positives and negatives are correctly predicted and false positives and false negatives are wrongly predicted. Precision is the ratio of correctly predicted positive observations to total predicted positive observations. Recall is the ratio of correctly predicted positive observations to all observations in class. F1 score is the weighted average of Precision and

Recall, so it takes both false positives and false negatives into account.

2. LITERATURE REVIEW

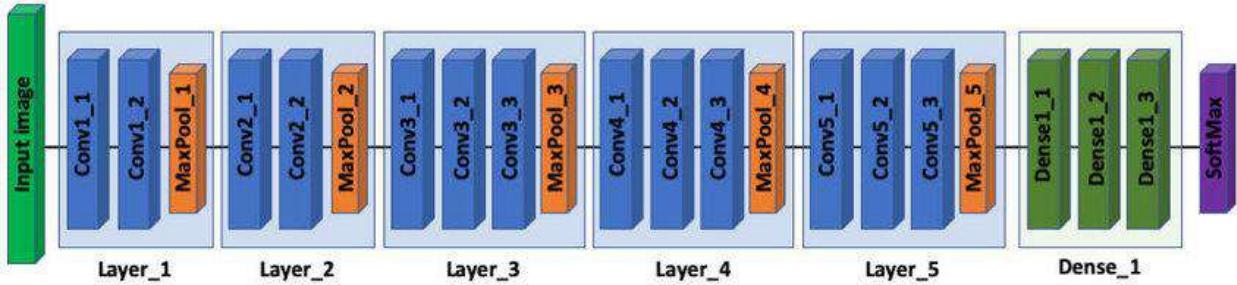
In [1] authors have used image processing techniques and a Support vector machine classifier to classify diseases in grapes plant. They used 90 images and obtained 89.9% accuracy. In [2] authors proposed an IOT based model using temperature, relative humidity, leaf wetness, and moisture as parameters and predicted grapes diseases using the Hidden Markov model. In [3] authors used transfer learning to classify grape leaf diseases using SSD Mobile Net architecture and R-CNN Inception V2 model. In [4] authors used image processing techniques and an artificial neural network to detect cotton leaf diseases. They used data in four classes and obtained 84% accuracy. In [5] authors used k-means for image segmentation, gray level co-occurrence matrix as feature extractor, and random forest as a classifier. In [6] authors used transfer learning to detect rice plant diseases. They have used AlexNet architecture as feature extractor and support vector machine as image classifier and obtained 91.37% accuracy. In [7] proposed a model based on principal component analysis and backpropagation network. They achieved 94.29% accuracy for two classes grape downy mildew and grape powdery mildew. In [8] diagnosed two grapes diseases using thresholding and anisotropic diffusion to preprocess images and K-means clustering for image segmentation. In [9] authors trained AlexNet and GoogLeNet deep learning models to identify 26 diseases in 14 crop species. They obtained 99.35% accuracy. In [10] authors evaluated CNN performance on two different computer-aided diagnosis applications, namely thoraco-abdominal lymph node detection and interstitial lung disease classification. They also evaluated different under-studied factors of employing deep convolution neural networks to computer-aided detection problems. In [11] color, shape and texture features were extracted from

samples of two grape diseases and two wheat diseases. Backpropagation networks, radial basis function, generalized regression networks and probabilistic neural networks were used as the classifiers to identify diseases.

3. METHODOLOGY

Deep learning techniques have shown very accurate and precise results in image recognition [12], image segmentation[13], emotion recognition[14], etc. Deep learning technique is an end to end learning, it learns features at different levels of abstraction as layer increases. In transfer learning initialization of CNN weights occur from a pre-trained network. After analysis, it has been found that transfer learning has better performance as compared to training the model from scratch.

In this model, we have used VGG16 and Random Forest. VGG is an acronym for visual geometric group and it is a pre-trained deep convolutional neural network model. It is trained on over 10 million images, learned how to detect generic features from images. VGG16 has 16 layers among them 13 are convolution layers and 3 fully connected layers. The architecture is very simple it has 2 contiguous blocks of 2 convolution layers, followed by max pooling, then it has 3 contiguous blocks of 3 convolution layers, followed by max pooling, and in the last 3 dense layers. Fig[1] shows the architecture of VGG16. But in our model we have used VGG16 as a feature extractor only, the last three dense layers are removed and a Random forest classifier is used. Fig[2] shows our proposed model where VGG16 is used as a feature extractor and Random forest as a classifier. Random forest is a robust and accurate classification technique. It creates a set of decision trees from randomly selected subset of training set. It then aggregates the votes from different decision trees to decide the final class of the test object.



Fig[1] Architecture of VGG16

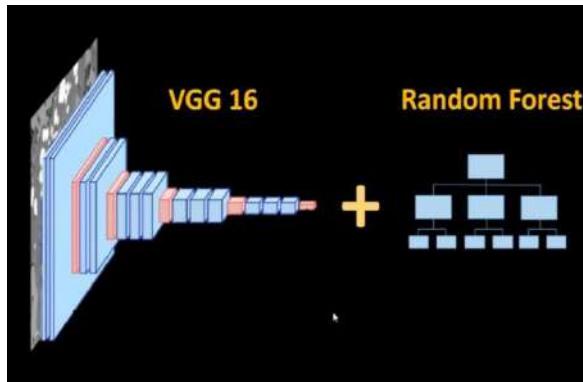


Fig [2] Model Architecture

4. RESULT AND DISCUSSION

4.1 DATA DESCRIPTION

Total 1003 images from different classes: i) Black Rot; ii) Black Measles; iii) Leaf Blight; iv) Healthy leaves are used. Table 1 shows the description of used data with sample images of each class.

A) Black Rot: It is caused by the fungus *Guignardia bidwellii*. Black rot occurs in hot and humid weather. It attacks all the green parts – leaves, shoots, and fruit.

B) Black Measles: It causes superficial spots and on the fruit and leaf. Black Measles or Spanish Measles has long plagued grape growers and its cryptic expression of symptoms. During the season, the spots may coalesce over the skin surface, making the fruit black in appearance.

C) Leaf Blight: It is caused by the fungus

Helminthosporium turcicum pass. Leaf blight generally occurs in humid climates by producing reddish-purple or tan spots on the leaves. It attacks seedlings and older plants.

Class Name	Number of Images	Image Sample
Black Rot	297	
Black Measles	312	
Leaf Blight	303	
Healthy Leaves	300	

Table 1. Details of four classes with sample images of each class

4.2 EXPERIMENTAL SETUP

The proposed model is implemented in the spyder python environment, using VGG16 as a feature extractor and random forest as a classifier. Total 1003 images of grapes plants are used. The dataset is divided into four classes Black Rot, Black Measles, Leaf Blight, and Healthy leaves. In the image acquisition phase images are resized and converted into RGB format. Then the list is converted into an array and normalized pixel values between 0

to1. Then VGG16 is used for extracting the features, without changing the weights and the random forest is used for image classification.

The performance of the system is interpreted in terms of accuracy, precision, recall, and f1 score. The accuracy for the 80% - 20% training – testing dataset is 91.66%. In Fig [3] Confusion matrix is shown.

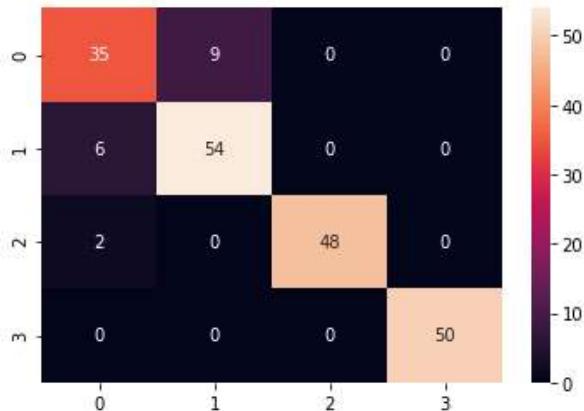


Fig [3] Confusion Matrix

Table 2. shows precision, recall, f1 score of all four classes in 80% - 20% training – testing dataset for all four classes.

Class	Precision	recall	f1 score
Black Rot	0.81	0.80	0.80
Black Measles	0.86	0.90	0.88
Leaf Blight	1.00	0.96	0.98
Healthy Leaves	1.00	1.00	1.00

Table 2. Precision, Recall and f1 scores of four classes for 80%-20% dataset

Accuracy of the model is also calculated for different training - testing divisions and shown in Table 3.

Training-Testing Division (%)	Classification Accuracy (%)
60-40	89.21
70-30	90.68
80-20	91.66

Table 3. Classification accuracy for different training-testing ratios.

5. CONCLUSION AND FUTURE SCOPE

Limited work have been done in quick and automatic disease identification and classification in plants. In this paper transfer learning based model has been proposed to classify diseases in grapes plants. The model has obtained 91.66% accuracy in 80% - 20% training – testing dataset. Moreover, a confusion matrix is produced to evaluate the model. The performance of the model can be further improved using large datasets.

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Automatic Detection of Grape, Potato and Strawberry Leaf diseases using CNN and Image Processing

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Abstract. Day by day the cultivation of plants and albumen are increased speedily in order to fulfill the demand of human being and all the animals in this universe. Recently the production rate of crop is abated due to different crop diseases. Agricultural scientists tried hard to finding the medication for the plant disorder. But the manual identification takes huge amount of time and less efficient. For the quick detection of plant disease different types of new technologies involvement with the cultivation sector bring as blessing. In this research work, Deep learning process is used to diagnose the affliction and finding its cure through the images of transited leaf of “grape” and “strawberry”. In modern world researchers can develop more accurate and efficient system for object detection and recognition using Deep-learning-based process. Here we used Convolutional-Neural-Network (CNN) algorithm to train the dataset where the accuracy rate is 93.63%. The farmer all over the world especially in Bangladesh can get the facilities form this work to the increment of production rate of grape and strawberry fruits through the reduction of disease and attack of insects.

Keywords: Machine learning; Deep Learning; CNN; Computer Vision; Plant Disease.

1 Introduction

In Bangladesh most of the people are engaged with the agricultural industry and about 80% people's life are directly or indirectly dependent with the agronomical work. The agricultural department plays an important role in the economic sector in Bangladesh. The cultivation of most of the crop and fruits remain whole year long which helps our economic condition moving forward. Rice and wheat is the most popular crop in Bangladesh. The cultivation of 'Grape' and 'strawberry' are rose day by day and the popularity of this fruit is skyrocketed. As a result the farmer shows great interest to cultivate these shorts of fruits than any previous decay. At the end of winter the cultivation of 'Grape' is started. The grape plant started to grow from spring to summer season and it started to ripe at the end of summer and early of fall. The season of strawberry production are varied with the variation of location. In our country the season of strawberry production started from April and lasted in July.

The major problems of the production of these fruit are the infection of the leaf of these fruits plant. To cope with the demand of our countries growing people the increment of fruits is must. As a result different types of pesticides are used which causes a huge damage in our environmental ecosystem. By using artificial intelligence and image processing technique, the disease identification from the disorder plant leafs is possible. In this research work, the grape and strawberry leap disease is detected and the possible cure is provided with the attachment of Deep Learning technology. Mainly CNN is used for the development of the system to train and testing the system. The desire of this paper is to determine the grape and strawberry leaps disorder and provide possible cure. The disease for 'Grape' is: Black measles, Black rot, Leaf blight and for 'Strawberry': Leaf scorch. This system is also capable to detect the healthy leaf.

Black measles is also called Spanish measles or Grapevine measles or Esca. When the spot is superficial it is known as measles. There are seven types grapevine diseases names "pierce's disease, phylloxera, downy mildew, powdery mildew, grey mold, Black rot, vine trunk diseases". The main responsible for most of the grapevine diseases are Bacteria and fungi. Insects and environmental condition is also responsible for spreading these types of disease. This disease is infected the plant's all airy part and the warm and humid weather helps to grow fungus. The temperature range 60 and 90 degree fahrenheit and rainy climate allow to increases the infection. At first the leaves and shoots show round brown spots and then die. The fungus attacks the berries part of fruits. The moisture is loss after obtain gray spots from brown reddish than black blue and black dots obtained.

The fungus is responsible for leaf blight disease. The sorghum leaves are mainly produced by this disease. It is mainly occurred under the condition of humid. During this disease the leaves shows reddish purple or tan spots. This disease mainly attack on the seeding and older plants. Strawberry leaves have different types of disease for instance leaf spot, leaf scorch, leaf blight and so on. The fungus 'Diplocarpon earliana' is responsible for leaf scorch disease. When leaf scorch disease is appear the leaves upper surface shows many small, irregular, purplish spots or blotches and the blotches middle point become brownish. Fungus mainly attacked the leaves during whole winter season and in spring the spore forming structure appears in dead leaves. In midsummer the structure produces spores. These spores infected the plant within 24 hours with the

presence of free water. The infection rate of older leaves is larger than the middle aged leaves.

The system which we design is capable to detect the above disease perfectly and efficiently provide the steps for farmer to get read those diseases. The education level of farmers in our country is not good enough for detecting the disease using scientific technologies, as a result our countries farmer are not used CNN anywhere. Most of the farmer use hand-made and measurement tools and for harvesting and detecting methods is non-scientific. They made their decision using eye view and blind guesses. Around the world there have lots of developed countries for instance USA, Denmark, China, Germany are using image processing, AI(*artificial Intelligence*), CNN (*Convolutional Neural Network*) for detecting diseases on harvesting field.

2 Literature Review

In our research work, some source paper reviewing is done and their summary is added in this section as literature review. For plant disease detection, classification and surveying properly lots of innovative techniques are established by researcher. In this section these researcher works have been describe below.

In 2018 an international conference paper is published by Umar Ayub through which he tried to find out crop diseases in the Pakistan using DATA MINING model [1]. In this conference paper they denoted the Pakistan farmer losses in their agricultural industry due to different types of diseases occurring because of the insect attract. They mainly introduced different types of procedure such as neural network, supporting vector machine, decision tree and so on and all these model are involve in data mining process. In 2006 an international conference paper is published by Esker in order to detect disease named ‘*Pantoea Stewartii subps*’ and this disease is found in corn plant [2]. In this paper they introduced three models which are working with prediction, “*Stevens*”, “*Stevens-boewe*” and “*Iowa state*” are these three model name. In the agricultural sector a huge amount of pesticides are used in the department of corn and its estimation was given using Economical Threshold Concept of some USA personal named Craig Osteen, A. W. Johnson and Clyde C. Dowler [3] and this research work provides massive benefit to the farmer of the corn department.

The main target of our work is to fulfill the demand of detecting and providing appropriate cure of different types of diseases for Grape, Potato and Strawberry plant using their leafs picture in order to making the difficult task for the farmer to detect disease of plant into easy task and increase the accuracy of detection rate. We mainly used image processing techniques for manipulate the data and used CNN model for identification of the diseases and improves its accuracy. This technique is capable to provide real-time result and suitable cure.

3 Proposed Methodology

Image processing is a very powerful technique for analysis a picture pixel wise. The system is constructed through image processing for detecting disease from affected leafs where the disorder is not found with eye. With the proper knowledge of grape and strawberry diseases of a person, the use of technologies is still very useful and easy. The healthy and affected leaf image is applied as input of the system, than the system provides output after processing the input picture. The system is detected disease and healthy picture successfully.

3.1 Flowchart of the Methodology

The flowchart shown below in Fig.1

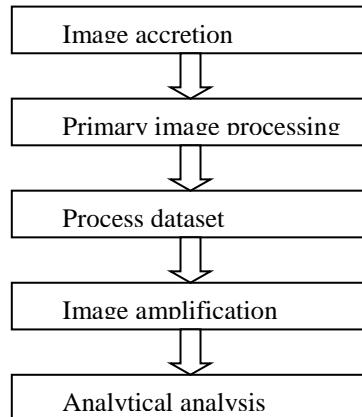


Fig.1. Flowchart

Image Accretion: Though dataset is the most essential issue to complete any research work, the researcher needs to arrange as many data as possible at the beginning of the work. The accuracy of the research result becomes more expectable when the collected data is sufficient. At the beginning of our work we successfully collected more than 5000 images (Grape, Strawberry). Most of the source of aggregated data is from grape and strawberry field which is harvested currently and rested data collected by our self. For making the system more convenient any type of image formats for instance .gif, .bmp, .jpg can be applicable as input for the system.

Primary Image Processing: The dataset which is collected before starting the work is subdivided into some small folders. We Select 5400 valid usable data for this model. The dataset is designed with eighty (80) percent training data and twenty (20) percent testing data. We fixed Alternaria (67 images), Anthracnose (80 images), Downy Mildew (94 images), Healthy (80 images), powdery mildew (80 images) as well as Black Rot (233 images) during the testing performance. Apart from this we fixed Alternaria

(850 images), Anthracnose (670 images), Downy Mildew (1120 images), Healthy (720 images), powdery mildew (920 images) as well as Black Rot (877 images) at the time of training operation. We reshape every single image in a unique pixel value and the selected pixel value is 265×256 . After reshaping the image, it is essential to increase the image quality and de-noising the image and for doing these activities different types of image processing method is applied. The elected dataset which is gather together for doing our work perfectly is illustrated in the down of this section and denoted as Fig.2.



Fig.2. Assembled Dataset

System Architecture: Using single level or multilevel CNN model the system can be designed. Since the multilevel model gives better performance, we preferred multilevel model and the model step-by-step description is introduced in this section. At the initial layer known as first layer we used ReLu activation function, Input_Shape, Filter_size, Kernel_size “1”, (256, 256, 3), “64”, (8×8) respectively and the padding and Strides are “SAME” and (1×1) respectively. There have no any considerable difference between first and second layer with the exception of Max_Pool and strides (2×2) and (2×2) respectively.

$$ReLU(X) = MAX(0, X) \quad (1)$$

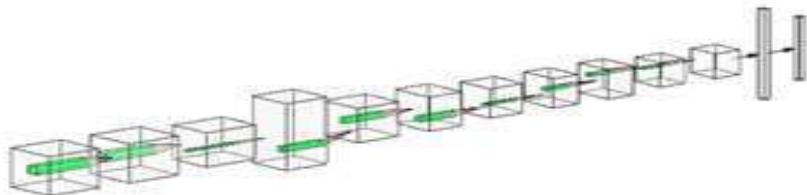


Fig.3. Proposed Convolutional Neural Network

In third layer we used ReLu activation function, Input_Shape, Filter_size, Kernel_size “1”, (128,128, 3), “32”, (5×5) respectively and the padding and Strides are “SAME” and (1×1) respectively. There have no any considerable difference between third and forth layer. In fifth layer we used ReLu activation function, Input_Shape, Filter_size, Kernel_size “1”, (64, 64, 3), “16”, (5×5) respectively and the padding and Strides are “SAME” and (1×1) respectively. There have no any considerable difference between fifth and sixth layer. In seventh layer we used ReLu activation function, Input_Shape, Filter_size, Kernel_size “1”, (32, 32, 3), “8”, (3×3) respectively and the padding and Strides are “SAME” and (1×1) respectively. There have no any considerable differ-

ence between seventh and eighth layer. The ReLU activation function has been reduced into fifty percent of 512 units in the flatten layer [4]. The final result of the model is determined using SoftMAX activation function.

$$\sigma(Z) = \frac{e^{z_i}}{\sum_{j=1}^K e^{z_j}} \text{ for } i = 1, \dots, k \quad (2)$$

The learning rate is 0.001 which is used in this proposed model as ADAM optimization.

Optimizer and Learning Rate: The result of the Deep Learning and Computer Vision shows sufficient change by selecting optimization method. Esoteric Adam paper, “Different subsamples data is evaluated by summing sub function and the subsample is produced by composing lots of objective functions; the optimization algorithm shows it’s efficiency in increment manner on the assumption of taking gradient steps” [5]. At present the Adam optimization model shows well adaption with most of the application of natural language processing. This algorithm is capable to compute adaptive learning rates individually using various parameters from gradients first and second moment estimation. In our proposed model used learning rate = 0.001 using ADAM optimizer amidst.

$$V_t = (1 - \beta_2) \sum_{i=1}^t \beta_2^{t-1} \cdot g_i^2 \quad (3)$$

Recently the classification and prediction work is done by the neural network and cross-entropy provides better performance than classification and MSE. In General, the training does not stalls out because of the unable to get enough minor by Cross-entropy error and the weight changes. The categorical cross entropy has been used as loss function in our proposed method “(4)”.

$$L_i = \sum_j t_{i,j} \log(p_{i,j}) \quad (4)$$

Image Augmentation: Through augmentation process an image can partition into abundant augment. The main purpose of the augmentation of images is:

- To find the simplified and changing model of image representation.
- To changes the shape and angles of images for more data production.
- The image is rotated using maximum range is forty and the width and height shifting range and rescaling value is 1/5 and 1/155 respectively, 1/5 uses as the zooming range also. The horizontal flip consider as True during augmentation and for best accuracy finding the fill nearest mode is shown in Fig.4
- The sheer range controls the angle in the direction of counterclockwise which allow our images to be sheared.
- At the beginning of processing the image data is multiplied with numeric value which known as ‘Rescale’. The collected input images are RGB images and the range of each image coefficient is 0-255, but for our model these range of values is too high for processing. That’s why zero and one are our target value range and this value is obtained by scaling the images with 1/255.

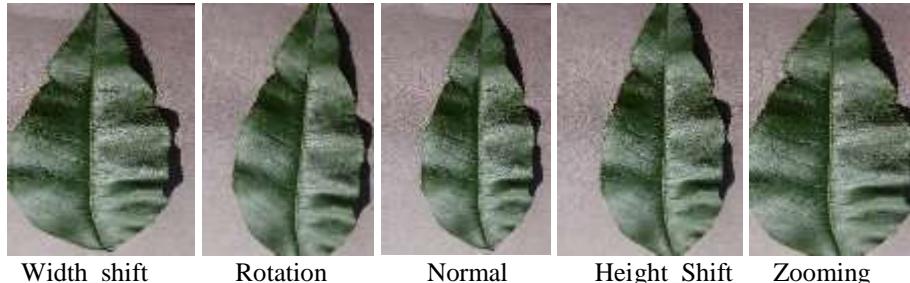


Fig.4. Example of Image Augmentation

3.2 Training The Model

Around 30-batch size is used for training the model among different validation dataset. During processing time, the accuracy of validation and reduction rate is supervised by the method of learning rate reduction. After completing 35 epochs the supervision between reduced learning rate and validation accuracy is worked manually. After that 10-25 epochs processed and the casual learning rate is set in certain time.

Layer Visualization: The layer visualization of softly changed image symbolizes and present visually. The multilayer image visualization is denoted into below figure:

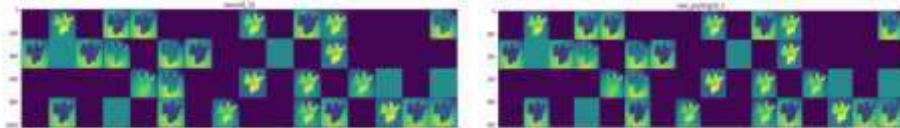


Fig.5. 3×3 Matrix Format Layer Visualization

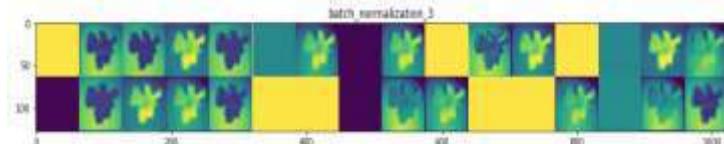


Fig.6. 2×2 Matrix Format Layer Visualization

4 Result and Discussion

The model which is introduced here has been worked with different data sets and obtained expected result after training, testing as well as validation and the detail description is introduced at the lower section of this part.

4.1 Analytical Analysis

This model provides 78.01 percent as training accuracy and 35.11 percent as validation accuracy. When one by one run is completed successfully, the result of the train-

ing model faced more accurate improved value. The training accuracy becomes 88.99 percent and the validation accuracy is 60.98 percent when the 10th run is completed. In this time the learning rate shows decreasing pattern and reached at 0.0005. The model observed 92.8 percent training accuracy and 94.89 percent validation accuracy and 3.124e-07 is the learning rate after thirty successful runs. While the final run is completed, the model provides us the final result as the training accuracy is **93.63** percent and validation accuracy is 97.01 percent.

4.2 Accuracy Graph

The accuracy graph is designed by managing for factor such as training loss and accuracy and validation loss and accuracy. The huge amount of data used for this model is not noise free hence some distortion is taking place and for fitting and describing the loss and accuracy curve fitting is perfect choice. The accuracy graph is divided into two sections over and under part. The over fitting part gives description and reference for the loss of data and denoted as loss. On the other hand, the under fitting portion provides us the accuracy of the model. The training line is noted as blue color and the pink color is denoted the validation line and the graphical presentation is displayed below in Fig.7.

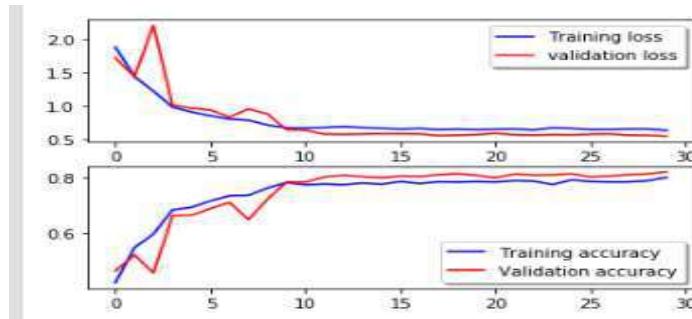


Fig.7. Accuracy and loss graph for Training and Validation

4.3 Confusion Matrix

The confusion matrix is known as the error matrix table or error table through which the performance of the model is displayed. For design this error matrix it is essential to find out the number of true and false images among all the images for individual diseases and these true and false images are represented into a table which is introduced below in TABLE I.

Table 1. Accuracy and Error Data

Disease	True	False	Total
Altemaria blight	67	0	67

Anthracnose	41	45	86
Downy mildew	91	3	94
Powdery Mildew	44	36	80
Healthy	59	11	70
Black Rot	58	22	80

From the confusion matrix it is clear that the diagonal position value is greater than the any other position where the shape of the diagonal position is (4x4). The color of the diagonal position is deeper (Blue) than the any other position value which clearly indicate that this position maximize the data and provide best performance. The confusion matrix and the classification table is given in Fig.8 and TABLE II respectively.

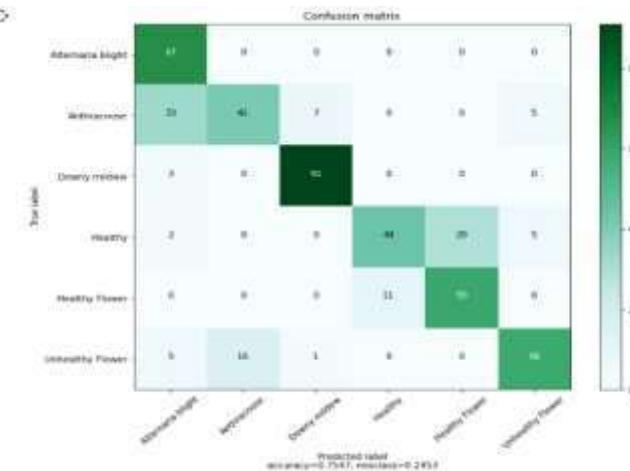


Fig.8. Confusion Matrix

Table 2. Classification Report

Disease	precision	recall	F1-score	support
Alternaria blight	0.61	1.00	0.76	67
Anthracnose	0.72	0.48	0.57	86
Downy mildew	0.92	0.97	0.94	94
Healthy leaf	0.80	0.55	0.65	80
Healthy flower	0.67	0.84	0.75	70
Unhealthy flower	0.85	0.72	0.78	80
accuracy			0.75	477
Macro avg	0.76	0.76	0.74	477
Weighted avg	0.77	0.75	0.75	477

4.4 Result Analysis of Different Model

Our initial task to read and analysis some previous work which is directly or indirectly related to the work doing in this paper. In order to easily understand our model performance here some other researcher work model is compered in this section. From this comparison it is clear that our model provide more accurate result which is denoted below in TABLE III.

Table 3. Accuracy Comparison Among Different Models

Work	Accuracy (%)	work	Accuracy (%)
Sharada et al. [6]	85.53	s.phadikar et al. [8]	79.50
Prem et al. [7]	89.93	Jyoti and tanuja [9]	93.00
Proposed model	93.63		

5 Conclusion

The farmer who is directly related to our agricultural industry specially in Grape, Potato and Strawberry department are always faced lots of unwanted damage of their fruits due to numerous diseases. The work which has been done here is capable to detect these diseases automatically and provides accurate cure so that the farmer can increment their production in a massive way. The model which we introduced here are capable to quick disease detection and for doing this work Image Processing techniques and CNN model is used. The affected portion of leafs or fruits are segmented and then analysis using very powerful CNN model which provides very accurate result within very short time. Therefore the ancient analog method which consumed a huge amount of time and less efficient for detecting plant disease is omitted and the farmer detect their plant disease using this automatic process. The model which we introduced is not associated with multimedia. That why, our main target is to associate this model with multimedia.

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Grape Leaf Disease Detection and classification Using Multi-class Support Vector Machine

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ABSTRACT—In the era of technology burst and usage of software as an alternative for the manual involvement for decision making, every field is trying to find its own comfort and cost cutting solutions in replacing software methods for best possible expert opinion. SVM, is initially proposed for binary classification technique, with simple manipulation can be used for a multiple class case. This project tries to attempt for improvement in classifying the leaf diseases. Most of the work until now involves extracting statistical features of RGB signal converted into LAB form[1]. HSI image has a reputation that the hue does not change even when the background light over the image changes. Hence few of the properties of HSI image are added to the database[2]. SVM is applied for classification for a larger space points. (properties)

Keywords

Texture, Color, Grey level Cooccurrence matrix, Feature Extraction, K Means Clustering.

I INTRODUCTION

In India productivity of grape is highest in the whole world and there is still possibility to increase it. Grape export from India is about 54,000 tones valued at 48,000 (1000US\$) that makes a share of nearly 1.45 % of total export of grapes in world. Nearly 70% of population is depending on agriculture. Grapes are an important fruit in India. Due to disease on grape plant there is loss of about 10-20 % of grapes.

Therefore, we should identify the diseases at the beginning phase and suggest solutions to the farmers so that harms can be avoided so that productivity can be increased. Therefore, we came up with the idea of helping the farmers to identify the diseases at the initial stage and we will also help to provide

them with necessary control measures. We have build a system that

will detect the diseases of grape plants through image processing where Farmers will take snapshots of the disease affected leaves, where the image will go pass the various steps to detect and identify the disease.

The two main things which needs to be focused, are: accuracy and speed. In this research work, an automatic detection of grape leaf diseases is presented, this method is based on K-means as a clustering procedure and SVM as a classifier tool using some texture feature set. The proposed methodology is an improvement of the approach proposed in [1].

As a test, we use a set of leaves which are taken from the website <https://www.plantvillage.org/> from their database of grape plants. Our code has been tested on three diseased leaf they are: Black rot, Esca, LBlight and healthy leaves [3]

II THE PROPOSED APPROACH STEP BY STEP DETAILS

The general idea is that, the system for any vision related algorithm of image classification is practically the same. At first, the computerized pictures are procured from nature utilizing a camera. Then image-processing techniques are applied to the obtained pictures to extricate helpful components that are vital for further examination. From that point onward, a few explanatory segregating systems are utilized to classify the pictures as indicated by the particular issue within reach. Figure 1.1 delineates the fundamental technique of the proposed vision-based recognition algorithm in this examination

1. Image Preprocessing

Before actually moving towards image analysis, the image should be preprocessed to obtain the better results. The main motto of image processing is to enhance, to smoothen and to remove noise that are caused during capturing the image [14]-[15].

- The extent of the input image must match the span of the images that were put away in the database during training phase.
 - To reduce the storage capacity
 - To reduce the processing time
- b) Enhancing the image

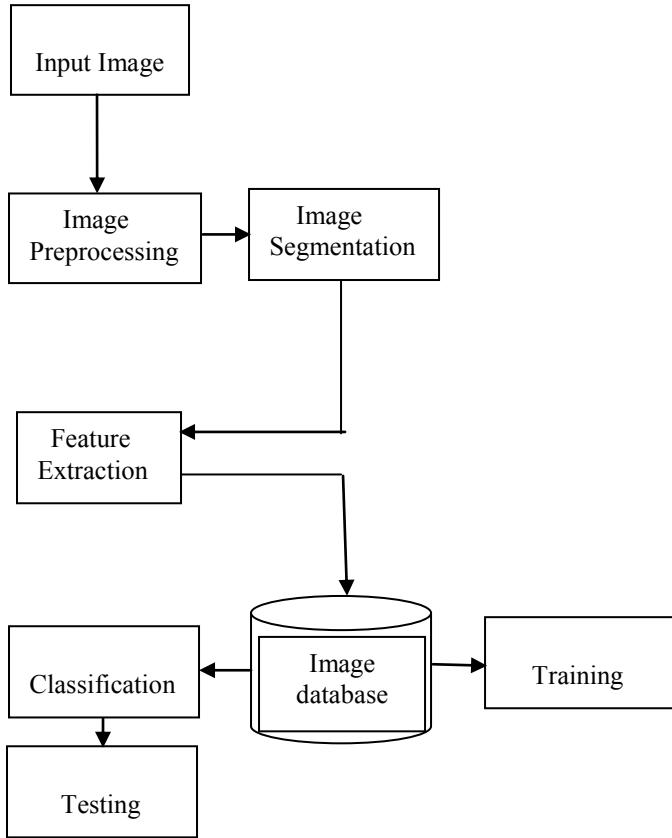


Figure 2.1 Flowchart of proposed method

Flowchart of proposed method

system are as follows.

- Resizing the image
- Enhancing the image
- Smoothening of image.

a) Resizing the image

Image resizing is done mainly due of three reasons [14]-[15]

Image enhancement is the way toward modifying advanced images so that the outcomes are more appropriate for further image examination. For instance, you can expel noise, sharpen, or light up a image, making it simpler to distinguish key elements [14]-[15].

c) Smoothening of image

Noise might interfere while capturing the image because of camera flash. Thus, it is very important to remove the noises from the image. Here we have made use of median filter for reduction of noise. The median filter smoothes the image where the intensity value of every pixel in an input image gets substituted by a mean of the intensity values from neighboring pixels [4].

2. Image Color Transform

In plants the intensity of leaf veins is distinctive and color is different for disease spot in this manner if Otsu's thresholding technique is applied to grayscale image then the resultant binary image will contain not only disease spot but also vein., but as region of interest is only disease spot therefore RGB image is first transformed into some different color space, here we have transformed the image into LAB color space and also HSI color model. After that Otsu threshold technique will be applied on color component of the transformed image to get the infected part of the leaf accurately [6].

a) HSI Color Model

HSI is a devise independent color model that is based on the perception of human. Here 'H' denotes HUE, which indicates pure color and is related to the wavelength of light. 'S' denotes saturation which indicates colorfulness and I denote the intensity which means the amplitude of light. Here we have taken Hue component only [1] for segmentation since we are only interested in the color of disease spot.

b) LAB color space

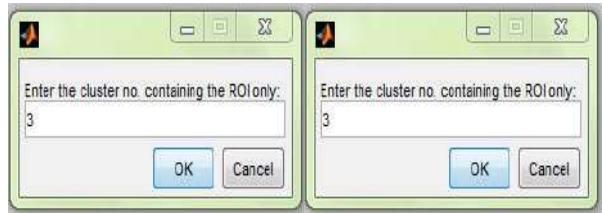
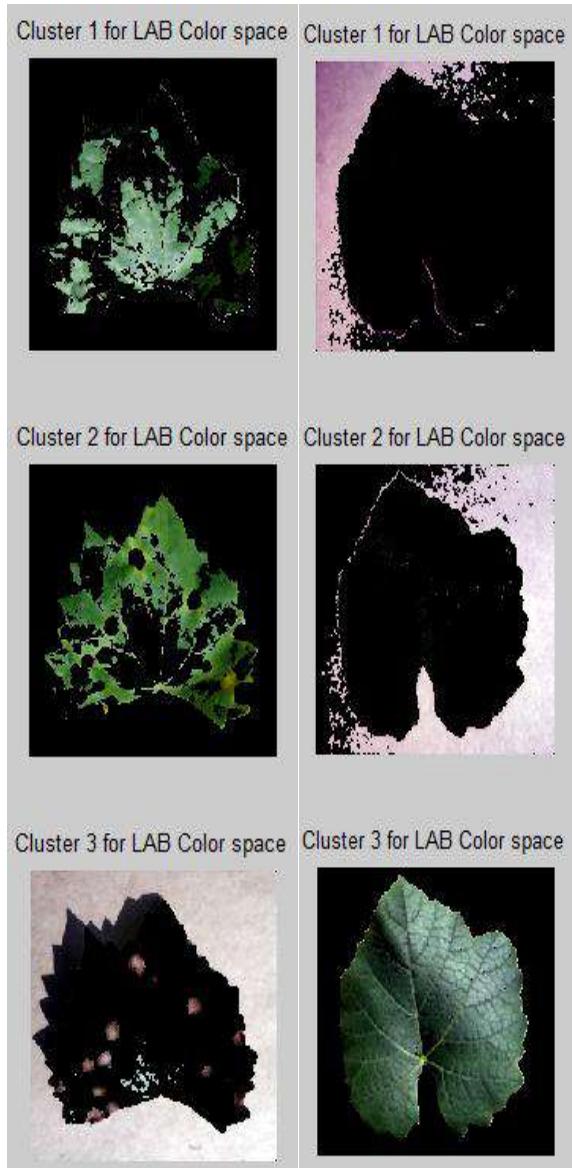
Intensity and color information of LAB color model is independent of each other. In CIELAB color model, 'L' describes color Luminosity; 'A' describes the color varying from green to red; 'B' describes the color varying from blue to yellow. Here we have taken two components from LAB i.e. A and B since it only contains useful color information [2].

3. Image Segmentation

For Segmentation, we have used K-means as a clustering procedure [8]. The K-means clustering method is used to classify objects (pixels in our case) based on no: of attributes into K number of Groups or clusters. The classification is performed so as to minimize the sum of square of distances in between the objects and the corresponding class centroid. However, we have utilized K-means clustering to divide or partition the leaf image into three groups in which one or

Fig. 3.1 Diseased and healthy segmented leaf

leaf is various ed. Best results are observed when the number of clusters is 3 From the three clusters obtained, we have to manually select the cluster in which disease is clearly visible.



Feature Extraction:

This step is the most important phase of our overall designed system. Most of the work until now involves extracting statistical features of RGB signal converted into LAB form. HSI image has a reputation that the hue does not change even when the background light over the image changes. Hence some of the properties of HSI image are added to the database. So, we increased the feature set by adding some of the features exhibited by the HSI format. Increased set will add to better average accuracy, as we have a larger set to compare and decide from. The features set to be used are as follows:

From Grayscale image 4 features that were extracted are Contrast, Correlation, Energy and Homogeneity. From Lab colour space 9 features that were extracted are Mean, Entropy, Standard Deviation, Variance, RMS, Skewness, IDM, Kurtosis, and Smoothness and lastly From HSI colour space 9 features that were extracted are Mean, Standard Deviation, Entropy, RMS, Variance, Smoothness, Kurtosis and Skewness [10].

The features Contrast, Energy, Correlation and Homogeneity are obtained from Grey-level cooccurrence method. The features Mean, Entropy, Standard Deviation, Variance, RMS, Skewness, IDM, Kurtosis, and Smoothness are calculated from color transformed image i.e. LAB colored segmented image and HSI colored segmented image using the standard MATLAB function.

4. Classification

For classification, we have used one vs all multiclass SVM classifier [9]. In this approach, there will be construction of 'k' binary classifier, in our case k = 4 and the label of +1 is assigned to every class in its turn and label of -1 to the remaining (k-1) class. During classification, the data point is assigned to the class having largest value of decision function. We have written the function for multiclass SVM and called it as shown below to classify the test sample

```
result = multisvm1(TrainFeat, TrainLabel, test)
```

where TrainFeat is the training database having 22 columns one for each feature and 120 rows for each 120 leaves. TrainLabel is the label associated with each image i.e. whether it belongs to class1 or class2 or class3 or class4. Result is the value returned by the multisvm1 function, it can take the value

as either 0 or 1 or 2 or 3 for Brot disease, Esca disease, Lblight disease or healthy leaf respectively.



III. DATABASE CREATION

Database contains the images of 3 type of diseases i.e. Black rot, Esca, Lblight and a healthy leaf of plant that will be used for training as well as testing. For each of diseased and infected leaf features were extracted and database is created. There are 22 columns corresponding to 22 features that comprises of 4 features From Greyscale, 9 features From Lab colour model and 9 features From HSI colour model.

we were unable to find standard database for grape leaf disease. Therefore, we prepared our own database by gathering raw images of grape from the website <https://www.plantvillage.org/> from their database of grape plants. The advantage of using images from the above-mentioned website is that they didn't required much more preprocessing as it is captured by using high quality camera. In this work total 160 grape leaf images (containing both initial stage as well as final stage images) are used containing 40 of each disease and healthy leaves.

IV. RESULT ANALYSIS

Simulation experiments in this research work are done on a laptop with Intel(R) Pentium® Dual CPU T3400 @ 2.16 GHZ with 2 GB memory.

In this work total 160 grape leaf images (containing both initial stage as well as final stage images) are used containing

Dataset	Total test sample	Correctly classified	% Accuracy
Black Rot	10	9	90 %
Esca (Black Measles)	10	8	80 %
Leaf Blight	10	7	70 %
Healthy	10	9	90 %
Combined	40	33	82.5 %

40 of each disease and healthy leaves. For training phase 30 Black rot, 30 Esca, 30 Lblight and 30 healthy leaves were taken and 10 Black rot, 10 Esca, 10 Lblight and 10 healthy leaves are used for testing.

The overall performance of SVM classifier is summarized into Table II. It can be seen from the Table II that SVM perform extremely good with Black rot and healthy class of grape leaves but gives considerably average performance with Lblight and esca class of grape leaves. On an average, we are getting an accuracy of 90%. Table I shows the results of the previous work, which shows an average accuracy of around 82.5 % i.e. by extracting only LAB colored features. Table III shows comparison of this system with previous system.

Table I: Classification Result of SVM in Case of LAB colored Model Classifier Output

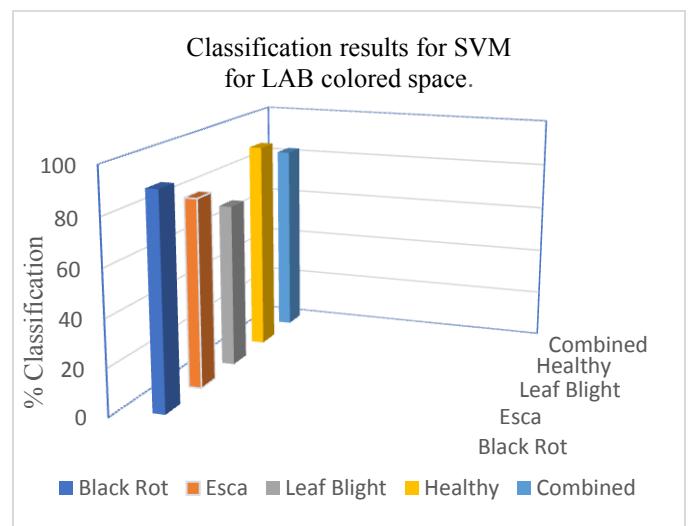
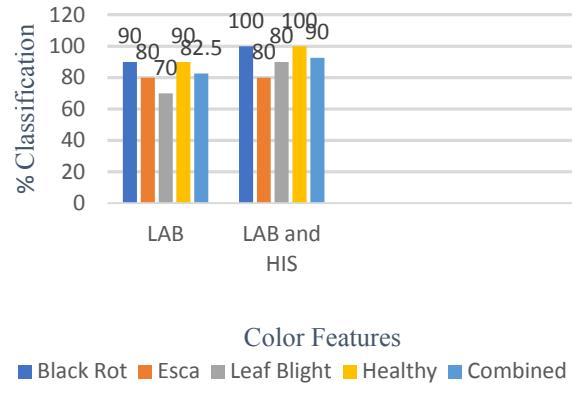


Table II: Classification Result of SVM in Case of LAB Colored Model and HSI Colored Model

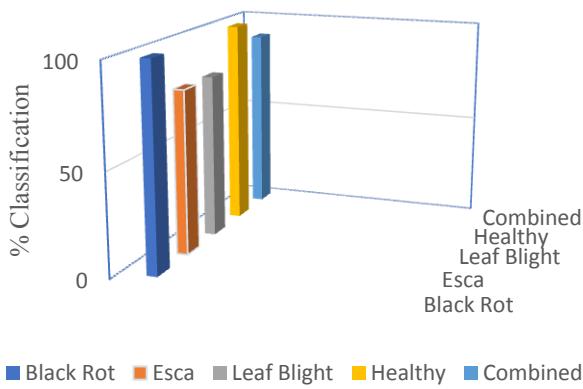
Dataset	Total test sample	Correctly classified	% Accuracy
Black Rot	10	10	100 %
Esca (Black Measles)	10	8	80 %
Leaf Blight	10	8	80 %
Healthy	10	10	100 %
Combined	40	36	90 %

Percentage classification of various diseases comparative analysis



% Accuracy	Linear	RBF	Quadratic	Polynomial
LAB	67.545	74.454	80.8059	76.7454
LAB and HSV	70.887	85.0298	88.8363	89.774

Classification results for SVM for LAB and HSI colored space.



The Bar chart below shows comparative study of the proposed method with the previous method

We have also evaluated the performance of our classification system using 10-fold cross-validation, a common method to deal with small training sets in machine learning. Firstly, dataset is divided into equally (or nearly equally) K -subsets. Then, the cross-validation process is performed using (K-1) subsets for training, and 1 subset for testing. This is repeated k times to use all possible combinations of training and validation sets. Hence, we take the average of performance of N runs. The algorithm performance measure can be calculated as the average of the performances of 10 runs. SVMs algorithm was employed with different kernel functions including Linear, Quadratic, Polynomial and RBF

It can be seen from the Table III that SVM perform extremely good with quadratic and polynomial kernel function, giving an accuracy in between 88% to 90% for the proposed method but gives average performance with Linear and rbf kernel function, giving an accuracy in between 70% to 85%.

The below curves are the plot of Accuracy, Error comparing the four kernel functions that are Linear, Quadratic, polynomial and rbf.

Table III: Comparison of % Accuracy using 10-fold cross validation for different kernel function

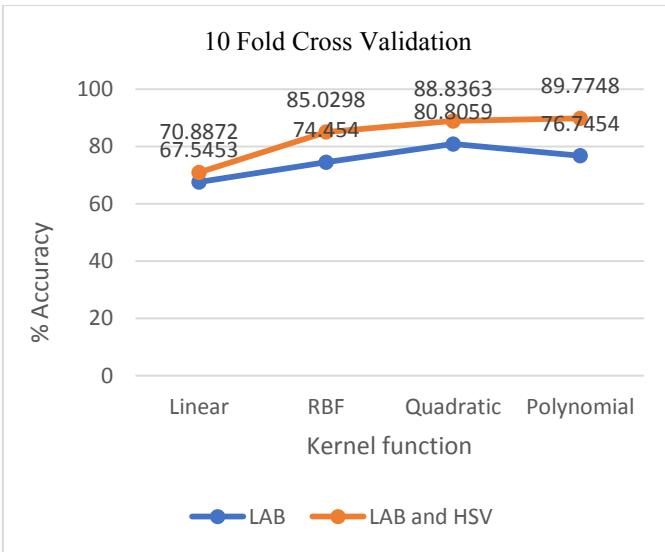
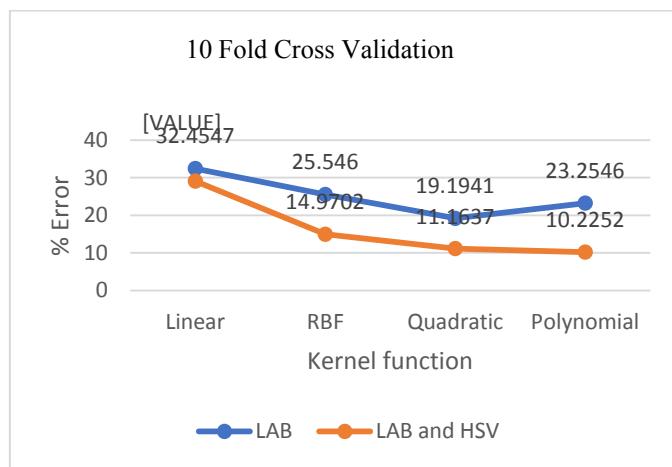


Table IV: Comparison of % Error using 10-fold cross validation for different kernel function



V. CONCLUSION

In this paper, applications of Multiclass SVM are formulated for classification of grape leaf diseases which are observed in Grapes plants. The given system uses resizing, enhancement and smoothing for image preprocessing. Then we have transformed the image into LAB color model and also HSI color model. To segment the diseased area, the K-means clustering technique is used for segmenting the image into

three clusters and manually selecting the cluster containing the diseased spot. Then both texture as well as color features are extracted from the selected cluster using GLCM and standard MATLAB functions respectively. The extracted texture and color features is then used to train Multiclass SVM classifiers into healthy or diseased classes.

In this paper, major disease commonly observed in Grapes plant such as Brot, Esca and LBlight are taken into consideration to carry out the experiment. The given system using features from both LAB and HSI color model gives **90%** average accuracy for all three-diseased leaf and healthy leaf compared to **82.5%** in case of taking only LAB color model for feature extraction

VI. FUTURE WORK

we will dedicate our future works on automatically selecting the cluster in k-means clustering using some of the features extracted from all the k clusters. Along with LAB and HSI, features can be extracted from YCbCr color space and also wavelet based features can be added to the database which might increase the accuracy.

% Error	Linear	RBF	Quadratic	Polynomial
LAB	32.4547	25.546	19.1941	23.2546
LAB and HSV	29.1128	14.9702	11.1637	10.2252

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Grape Leaves Diseases Classification using Ensemble Learning and Transfer Learning

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Abstract—Agriculture remains an important sector of the economy. Plant diseases and pests have a big impact on plant yield and quality. So, prevention and early detection of crop disease are some of the measures that must be implemented in farming to save the plants at an early stage and thereby reduce the overall food loss. Grapes are the most profitable fruit, but they are also vulnerable to a variety of diseases. Black Measles, Black Rot, and Leaf Blight are diseases that affect grape plants. Manual disease diagnosis can result in improper identification and use of pesticides, and it takes a long time. A variety of deep learning approaches have been used to address this issue of the identification and classification of grape leaf diseases. However, there are also limits to such approaches. Therefore, this paper uses deep learning with the concept of ensemble learning based on three famous Convolutional Neural Network (CNN) architectures (Visual Geometry Group (VGG16), VGG19, and Extreme Inception (Xception)). These three models are pre-trained with ImageNet. The performance of the proposed approach is analyzed using the Plant Village (PV) dataset of common grape leaf diseases. The Proposed model gives higher performance than the results achieved by using each Deep Learning architecture separately and compared with the recent approaches in this study. The proposed system outperformed the others with 99.82% accuracy.

Keywords—Ensemble learning; grape leaf diseases; convolutional neural network (CNN); transfer learning

I. INTRODUCTION

Agriculture is one of the most important sectors in the world, providing humans with food, raw materials, and other essentials. According to the United Nations (FAO) Food and Agriculture Organization, the world's population will reach 9.1 billion by 2050. As a result, to meet the nutrient needs of such a large population, the food growth rate needs to be boosted to 70% by 2050 [1]. Plant disease is one of the leading causes of crop loss. A plant disease is an abnormal condition that modifies the appearance or function of a plant. The visible effects of the disease on plants are described as symptoms. A symptom is any detectable change in the plant's color, form, and/or functions in response to a pathogen or disease-causing agent. The leaf is the most essential portion of the plant to inspect for illness. Plant leaf diseases are divided into three categories: fungal, viral, and bacterial [12, 13].

A. Fungal Diseases

Parasitic organisms have a system of branching threads that make up their bodies. Fungi can enter the host via stomata, but

many can pierce a solid surface. Once within, they can either expand through the live cells or stay primarily in the gaps between them. Black Rot, Black Measles, Leaf Blight, and Leaf Rust are signs of these diseases.

B. Viral Diseases

Viruses are not dispersed by water or wind, unlike bacteria and fungi. But insects and worms are the primary vectors of viral pathogens to plants.

C. Bacterial Diseases

Bacteria are small. There are two hundred kinds of bacteria that cause diseases in plants. Their form determines their classification. Spherical, rod-shaped microorganisms and twisted rods are the three primary kinds that may be known. There are many symptoms of a bacterial infection. Leaf Spot is considered the most prevalent of them.

Plant diseases, and how to quickly diagnose and address them to improve the health of crops, are among the most important problems that face agriculture and have an impact on its trade. Identifying the disease before it spreads over the farm to other plants and treating it is a massive challenge in and of itself. It takes a lot of time and effort to determine what kind of disease it has. Furthermore, not all disease types can be accurately identified by the farmer's naked eye.

Initially, plant infections can be detected with the help of an agricultural professional who is familiar with plant diseases. However, manual plant disease identification and determination is a strenuous task and takes a long time. A person's knowledge and experience determine the accuracy of a manual prediction [2].

To overcome the above problems, many studies on machine learning (ML)-based technologies, such as support vector machines (SVM) [3], K-nearest neighbors (KNN) [4], have recently been applied to improve decision-making to classify plant diseases [5]. However, all these proposed approaches face several challenges, including identifying regions of concern for processing and analysis (feature representation). Now, Deep Learning (DL) is considered the next evolution of machine learning, such as convolutional neural networks (CNN) [6]. This work proposes an approach for classifying grape plant diseases based on Ensemble Learning that aggregates three customized CNN architectures with trained weights (VGG16, VGG19, and Xception). The following are the study's major contributions:

- Enhance classification performance.
- Reduce overfitting.

The rest of this paper is structured as follows: In Section II, related works present the most common plant disease terminologies and techniques. The proposed model and materials are illustrated in Section III. Section IV discusses the results of the proposed model and compares them with other related models. Section V, the conclusion. Section VI, the future work.

II. RELATED WORK

Many methods for disease classification from the plant leaf have been presented, especially on the Plant village dataset. The Plant village Dataset [7] is a well-known, publicly available crop leaf collection that contains thousands of images. It has been used in various research and achieved good results. Some of these are as follows:

Akshai KP et al. [8] proposed a method to classify images of grape plant diseases from the Plantvillage dataset using the trained model. The CNN, VGG19, ResNet-152v2, and DenseNet models are all trained. The DenseNet model was the most accurate, with a score of 98.27%. For the convolution layer, a rectified linear activation function, or ReLU activation function, is utilized, and for the output layer, a Softmax activation function is used. The images were reduced to 224x224 pixels using Kera's image data generator, then augmentations like rotation, zoom, and shift were added. At a ratio of 80:20, the dataset is split into training and validation sets. This work had the problem of splitting the dataset into training and validation only and testing the model with the same data, which led to overfitting.

Y. Nagaraju et al. [9] proposed a fine-tuned VGG-16 network to categorize eight different apple and grape leaf types together. The Kera's library is used to load the pre-trained VGG-16 network. In a typical model, the SoftMax (classifier) layer is removed, and a new output layer (classifier) with a SoftMax activation function is added. The disease dataset for apples and grape leaves is split 80:20 with an accuracy of 97.87%. This work had the problem that although using 30 epochs, the accuracy was 97.87%.

E. Hirani et al. [10] proposed deep learning methods for identifying plant diseases. A Plantvillage dataset is used at a ratio of 80:20, with 70295 images for training and 17572 images for validation. This work used three methods: a customized convolutional neural network, INCEPTIONv3, Small Transformer Network (STN), and Large Transformer Network (LTN), with an accuracy of 95.566%, 97.14%, 97.66%, and 97.98%. This work had a problem with the resolution of images at 256*256 that needed more computation and time in the training and testing phases.

K. Z. Thet et al. [11] proposed a fine-tuning VGG16 with the GAP layer instead of VGG16's two fully connected layers before the SoftMax layer to classify the diseases on grape leaves. This work has achieved 98.4% more accuracy than others. It mostly focused on five diseases that are prevalent in Myanmar Grapevine Yard. This work had a problem with the

overall performance where the number of epochs and batch size were not determined.

III. PROPOSED METHODOLOGY

A. Dataset Description

The Plant Village dataset [7] is used to examine the proposed model performance in the classification of grape leaves diseases. It is a large and freely accessible database. It contains over 55,000 RGB images divided into 38 classes representing 14 different plant species. There are 12 healthy leaf classes as in Fig. 3 and 26 unhealthy leaf classes as in Fig. 1, 2, 4 out of 38 total. The grape leaves images are used in this study, which includes 4,062 images divided into four classes shown in Table I. The following is a summary of each selected disease [13, 14]:

1) *Grape: black rot*: Black rot fungus attacks on leaves grown in warm, wet seasons, the black rot fungus attacks the upper surface of the leaves, turning them reddish-brown and causing round to angular dots to emerge. As the spots merge, irregular reddish-brown blotches appear as shown in Fig.1.

2) *Grape: leaf blight*: It is also a fungal disease on leaves grown in high humidity conditions, caused by Exserohilum turcicum. At first, small yellow dots emerge along the leaf margins, then grow to become brown patches as shown in Fig. 4.

3) *Grape: esca (black measles)*: The esca fungus can affect leaves at any time during the growing season, but it is most common in July and August. The symptom is an interveinal "striping". In red varieties, the "stripes" are dark red, while in white cultivars, they are yellow. Fig. 2.

B. Proposed System

In this work, a powerful approach for classification grape leaves diseases based on Ensemble Learning has been presented as shown in Fig. 5.



Fig. 1. Grape_Black_Rot.



Fig. 2. Grape_Esca (Black Measles).



Fig. 3. Grape_Healthy.



Fig. 4. Grape_Leaf_Blight.

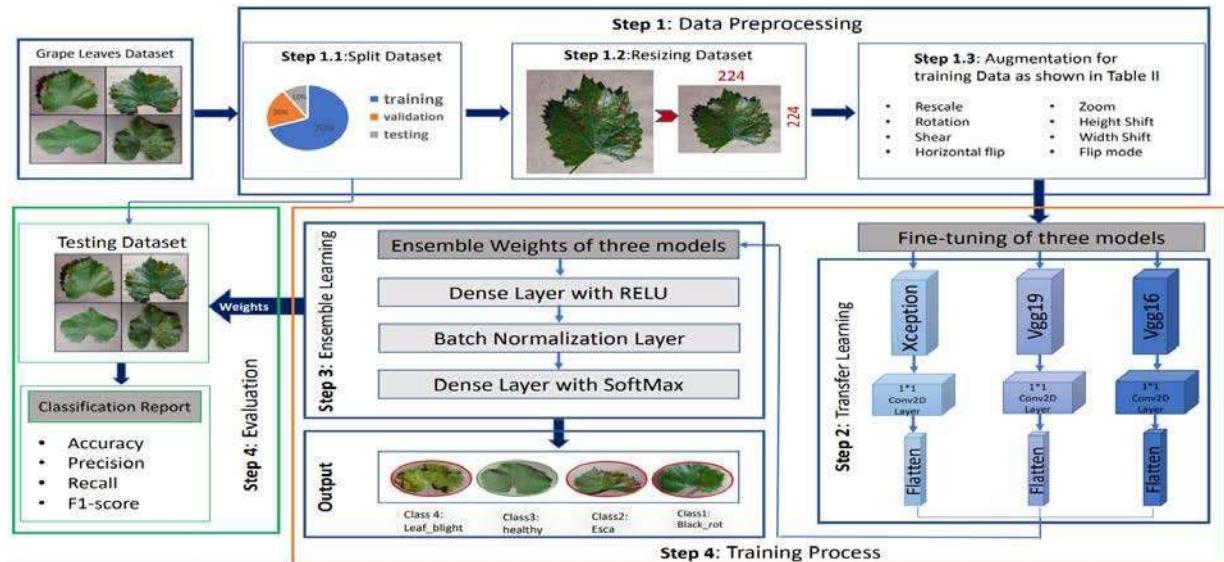


Fig. 5. The Framework of the Proposed Model.

1) *Data preprocessing*: Preprocessing of the dataset is one of the major roles in training a model. First, divided dataset into three categories: training 70%, validation 20%, and 10% for testing, as shown in Table I. Second, grape images are resized to 224*224*3 pixels. Third, applied data augmentation techniques to generate more training data and avoid overfitting. These techniques include rescale, rotation, shear, horizontal flip, zoom, height shift, width shift, and flip mode on the training set. The data augmentation is applied only to the training data shown in Table II.

TABLE I. DESCRIPTION OF PLANT VILLAGE DATASET

Grape Dataset						
Fig	Class Name	Cause of disease	Total samples	Training Samples (70%)	Validation Samples (20%)	Test Samples (10%)
1	Black Rot	Fungus	1180	826	236	118
2	Esca		1383	969	276	138
3	Leaf blight		1076	754	215	107
4	Healthy	-----	423	296	85	42

TABLE II. AUGMENTATION TECHNIQUES SUMMARY

Techniques	Values
Rescale	1.255
Rotation	30
Shear	0.1
Horizontal flip	True
Zoom	0.3
Height shift	0.2
Width shift	0.2
Flip mode	Nearest

2) *Model building*: Transfer learning is a great approach because it allows to use a pre-trained CNN model with multiple datasets to train a specific dataset.

VGG-16 and VGG-19 [15] refer to the "Visual Geometry Group". They're two different versions of the same structure. The differences between them are as follows, respectively: The VGG-16 consists of 16 layers of the deep neural network, whereas the VGG-19 consists of 19 layers. Both networks contain blocks, where each block is composed of 2D convolution and pooling layers. The Conv2D layer [16] extracts a feature of the image using filters or kernels. The filter is passed throughout the width and height of the input and the dot products function between the input and filter is calculated at every position. Convolution Layer Formula (1).

$$n_{out} = \lceil \frac{n_{in} + 2p - k}{s} \rceil + 1 \quad (1)$$

It also contains ReLU (Rectified Linear Activation Function) [17, 18] that returns all negative values set to zero (2). The function and gradient in ReLU (2) and (3).

$$\text{ReLU}(x) = \max(0, x) \quad (2)$$

$$\frac{d}{dx} \text{ReLU}(x) = 1 \text{ if } x > 0; \text{ otherwise } \quad (3)$$

The Conv2D layer is followed by a pooling layer to reduce the computation and the number of parameters. Max pooling (4) is one of the most used pooling operations. Then the matrix is flattened into a vector. The flattened vector is passed into the FC (Fully Connected) layer. FC is used to connect each node in one layer to each node in another layer. The last layer is SoftMax. It is located at the end of the FC layer, which predicts a multi-class.

$$S(x) = \max_i x_i \quad i = 1 \quad (4)$$

Xception [19] refers to Extreme Inception. First, the data passes through the entering flow, then eight times through the

middle flow, and finally through the exit flow. Batch normalization is applied to all convolution and separable convolution layers. Separable convolutions are time-saving and more efficient than classical convolutions.

The proposed model depends on a customized CNN with trained weights from the VGG16, VGG19, and Xception models. The learning scenario starts with receiving grape leaves images from the input layer. The input layer is shared with three pre-trained networks. Three models are reshaped by freezing all their layers. But we removed the top layer (output layer) from each model to add the proposed output layers.

Added two layers, a Conv 1x1 layer with 1024 filters with padding-zero and stride-one, to collect the most important features and allow for reduced dimensionality followed by a flattening layer to convert the matrix to the tensor of one dimension (vector). As illustrated in Fig. 6-8.

3) *Ensemble learning*: After applying the flattening layer to each model, added the merged layer to aggregate the flattening layer from each network and use it as an input (new input) for the ensemble learning model. Then, added a dense

layer that allowed every neuron in this layer to connect to the next layer by weight followed by a batch normalization layer, which allows each layer to make learning more independent. Finally, added the output layer with the SoftMax activation function to predict the final output.

4) *Training phase*: The proposed model compiled with the Adam optimizer [20] is a stochastic gradient descent method with a learning rate equal 2e-5. The loss function is a categorical cross-entropy [21] that is used in the multi-class classification task equation (5) to calculate the loss. The proposed model is fitted at epochs where value equals 10, train batch size equals 16, and validate batch size equals 8.

$$\text{Loss} = -\sum_{i=1}^{\text{output size}} y_i \cdot \log \hat{y}_i \quad (5)$$

5) *Testing phase*: The best-saved weights were loaded after those testing images were loaded. Finally, images were resized to 224*224 and fed the testing images to the model to classify four classes of the grape leaves' diseases.

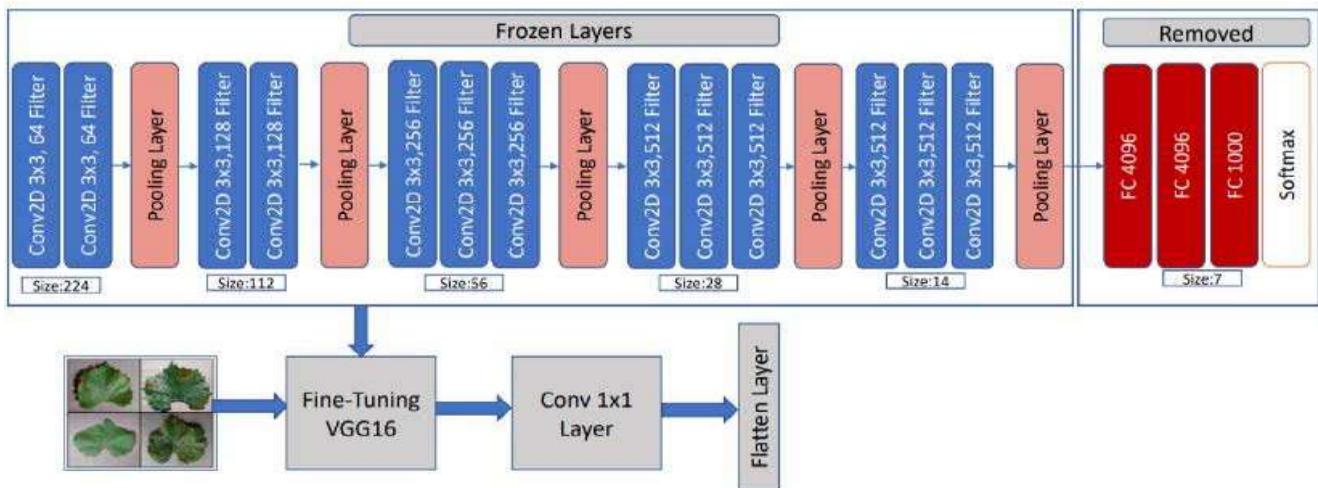


Fig. 6. Fined Tuned for VGG16.

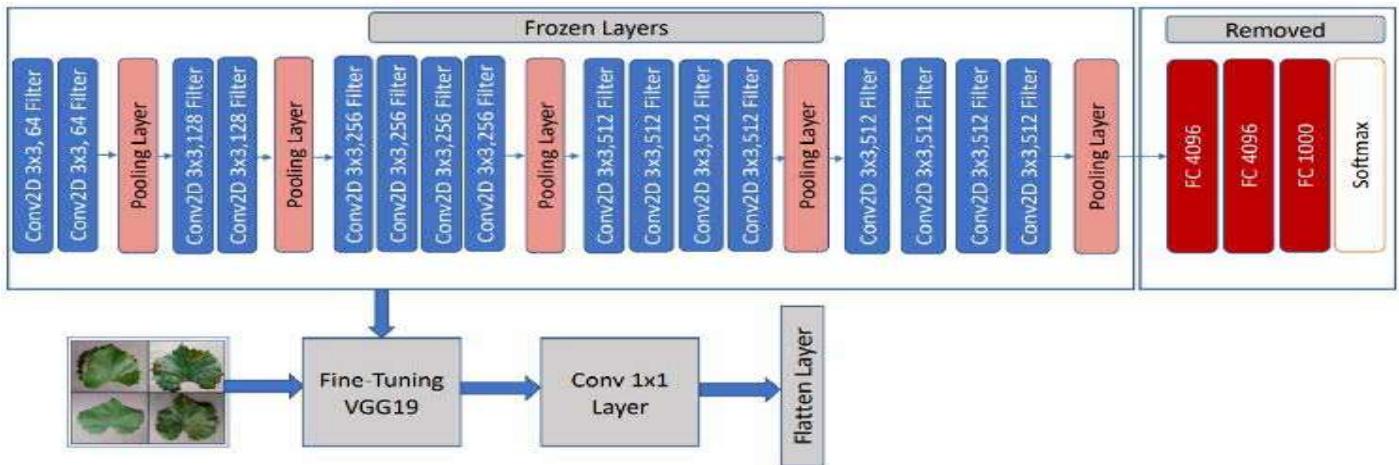


Fig. 7. Fined Tuned for VGG19.

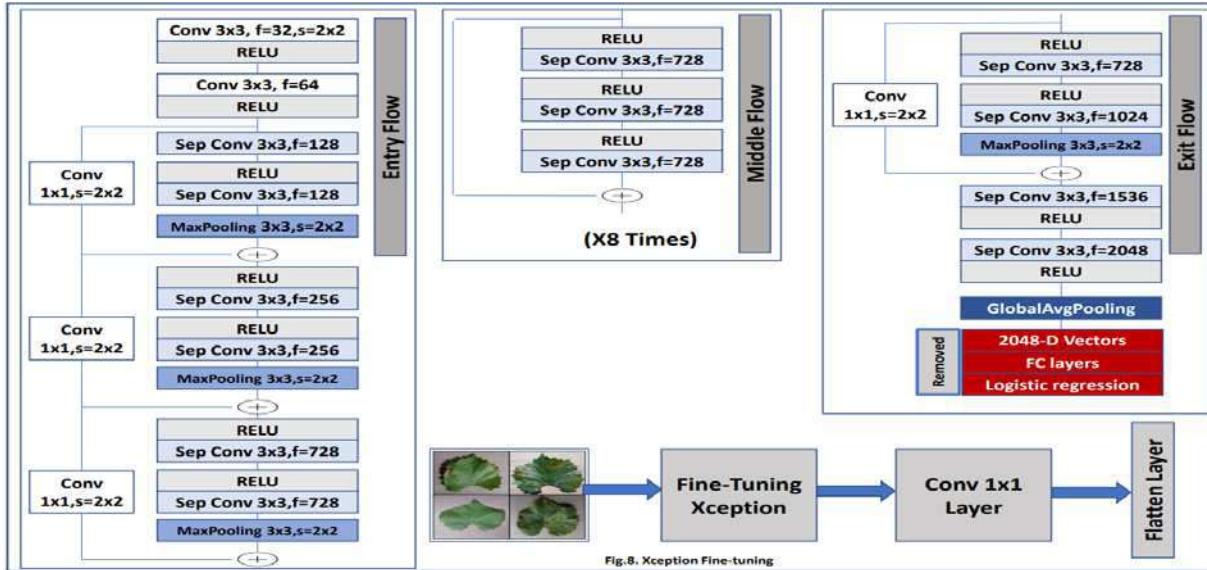


Fig. 8. Fined Tuned for Xception.

IV. EXPERIMENTAL WORK & RESULTS

A. Experimental Settings

This work demonstrates that the highest accuracy is achieved with a relatively small dataset of grape leaves in the plant village dataset using ensemble learning (e.g., VGG16 Model, VGG19, and Xception). The dataset is divided into a ratio of 7:2:1 as shown in Table I. All experiments are implemented using Colab [22] provided by Google, the Keras framework [23] that can run on top of TensorFlow, and the Python programming language. All experiments were conducted on a 12 GB NVIDIA Tesla K80 GPU (Graphical Processing Unit) and 12 GB of RAM.

B. Experimental Evaluation

The performance of the proposed model is evaluated using accuracy (9), precision (6), recall (7), F1-score (8), and confusion matrix in the testing phase equations shown in Table III. Moreover, loss, accuracy, validation loss, and validation accuracy are calculated during different epochs in the training phase, as shown in Fig. 10-17. Also, we compared our proposed model performance as shown in Table V with other models (e.g. [8]) that work on the same dataset as shown in Table IV and with each architecture used in the proposed model separately. Summary of the training model in the Fig. 9 to understand the underlying parameters.

TABLE III. PERFORMANCE EQUATIONS SUMMARY

Assessments	Equation	Equ.No
Precision (P)	$\frac{TP}{TP + FP}$	(6)
Recall (R)	$\frac{TP}{TP + FN}$	(7)
F1-Score (F)	$2 * \frac{P * R}{P + R}$	(8)
Accuracy (Acc)	$\frac{TP + TN}{TP + TN + FP + FN}$	(9)

Where:

True Positive (TP) the model predicts the positive class correctly. True Negative (TN) model correctly classifies the negative class. In a false positive (FP), the model predicts the positive class incorrectly. In false negative (FN), the model predicts the negative class incorrectly.

The total training time for the proposed model is about 24 min 28 sec \pm 2 min with 10 epochs, and the test time is about 5 seconds. Other models in [8] use 20 epochs in training. However, our proposed method achieved the highest accuracy, showing the feasibility of our proposed method. Compared with existing methodologies, we can see that our proposed model has some degree of competition in terms of accuracy and precision, as shown in Tables IV and V. The robustness of our suggested approach is confirmed by these results.

TABLE IV. RESULT OF EXISTING MODELS

Model	Precision	Recall	F1-score	Accuracy	epochs
CNN [8]	94.60	94.58	94.56	94.58	20
VGG [8]	95.54	95.32	95.32	95.32	20
RESNET [8]	97.11	97.04	97.05	97.04	20
DENSENET [8]	98.31	28.27	98.28	98.27	20

TABLE V. CLASSIFICATION REPORT FOR PROPOSED MODELS

Model	Classes	Precision	Recall	F1-score	Support	Accuracy
Fined Tuned VGG16	Black Rot	1.00	0.92	0.96	118	0.96
	Esca	1.00	0.94	0.97	138	
	Healthy	0.98	1.00	0.99	107	
	Leaf blight	0.74	1.00	0.85	42	
Fined Tuned VGG19	Black Rot	1.00	0.97	0.98	118	0.99
	Esca	0.97	1.00	0.99	138	
	Healthy	1.00	1.00	1.00	107	
	Leaf blight	1.00	1.00	1.00	42	
Fined Tuned Xception	Black Rot	0.98	0.99	0.99	118	0.99
	Esca	0.99	0.99	0.99	138	
	Healthy	1.00	0.99	1.00	107	
	Leaf blight	0.98	1.00	0.99	42	
Ensemble Model (Proposed)	Black Rot	1.00	1.00	1.00	118	1.00
	Esca	1.00	1.00	1.00	138	
	Healthy	1.00	1.00	1.00	107	
	Leaf blight	1.00	1.00	1.00	42	

```

Layer (type)          Output Shape         Param #     Connected to
===== ====== =====
input_1 (InputLayer) [(None, 224, 224, 3 0   []
])
vgg16 (Functional)  (None, None, None, 14714688  ['input_1[0][0]']
)
vgg19 (Functional)  (None, None, None, 20024384  ['input_1[0][0]']
)
xception (Functional) (None, None, None, 20861480  ['input_1[0][0]']
)
conv2d (Conv2D)      (None, 7, 7, 1024) 525312    ['vgg16[0][0]']
conv2d_1 (Conv2D)   (None, 7, 7, 1024) 525312    ['vgg19[0][0]']
conv2d_6 (Conv2D)   (None, 7, 7, 1024) 2098176   ['xception[0][0]']
flatten (Flatten)   (None, 50176)       0          ['conv2d[0][0]']
flatten_1 (Flatten) (None, 50176)       0          ['conv2d_1[0][0]']
flatten_2 (Flatten) (None, 50176)       0          ['conv2d_6[0][0]']
concatenate (Concatenate) (None, 150528) 0          ['flatten[0][0]', 'flatten_1[0][0]', 'flatten_2[0][0]']
dense (Dense)        (None, 100)        15052900   ['concatenate[0][0]']
batch_normalization_4 (BatchNo (None, 100) 400       ['dense[0][0]']
rmalization)
dense_1 (Dense)      (None, 4)         404       ['batch_normalization_4[0][0]']
=====
Total params: 73,803,056
Trainable params: 73,748,328
Non-trainable params: 54,728

```

Fig. 9. Summary for the Proposed Model.

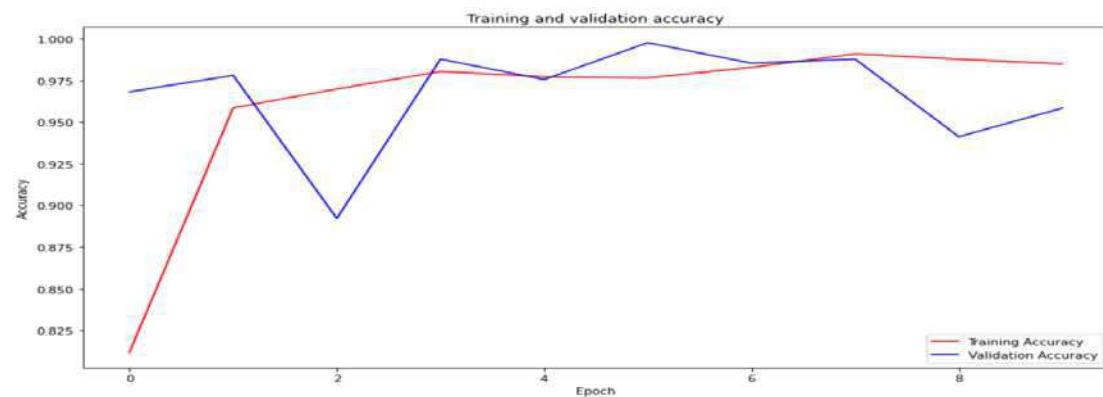


Fig. 10. Training and Validation Accuracy for VVG16.

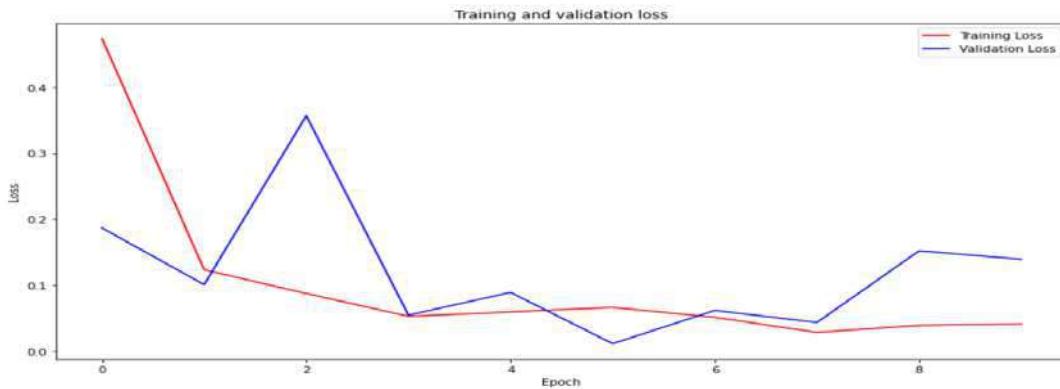


Fig. 11. Training and Validation Loss for VVG16.

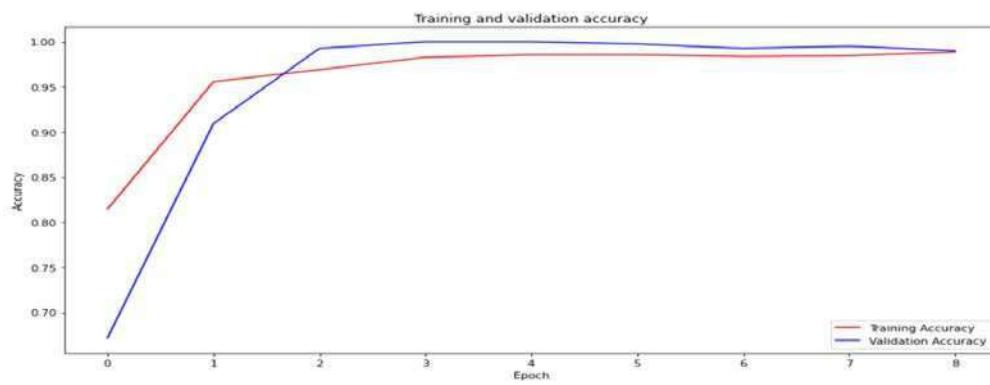


Fig. 12. Training and Validation Accuracy for VVG19.

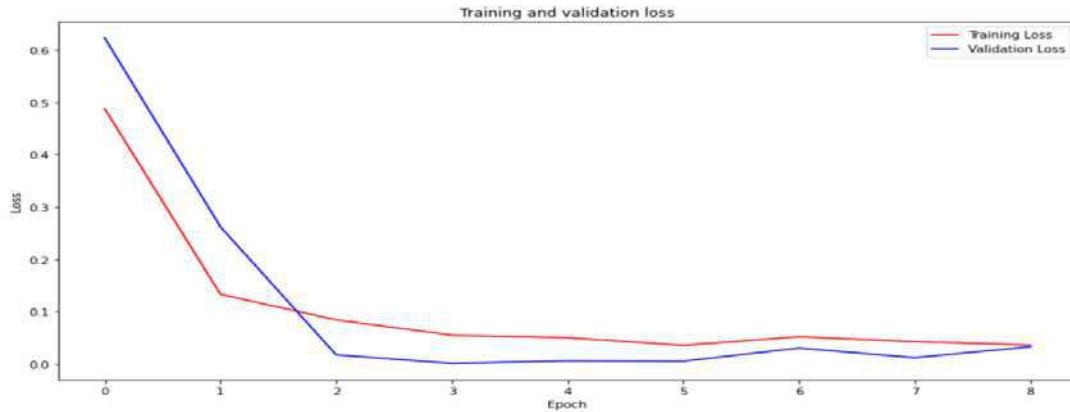


Fig. 13. Training and Validation Loss for VVG19.

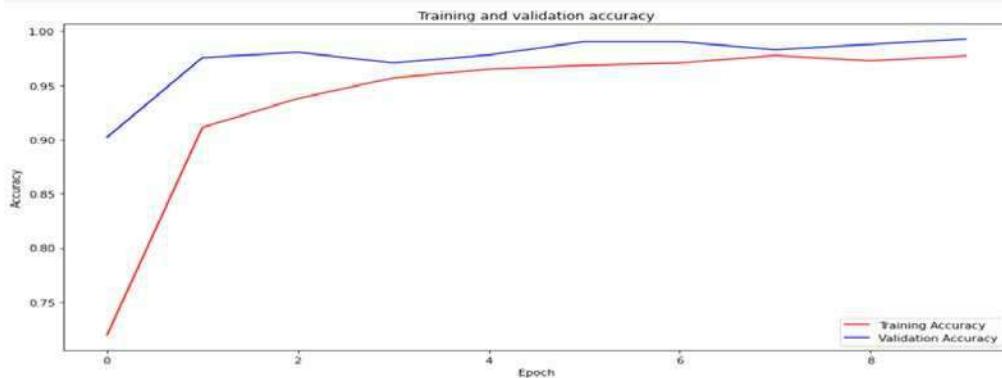


Fig. 14. Training and Validation Accuracy for Xception.

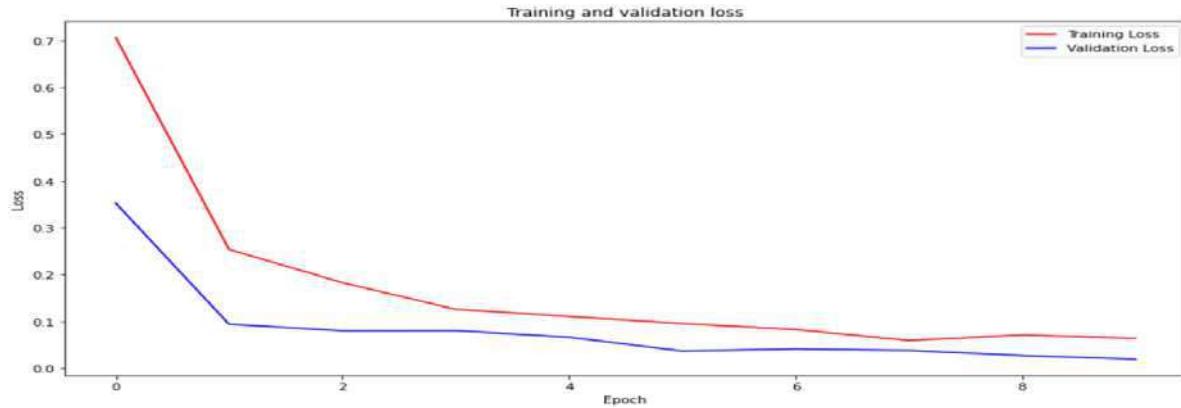


Fig. 15. Training and Validation Loss for Xception.

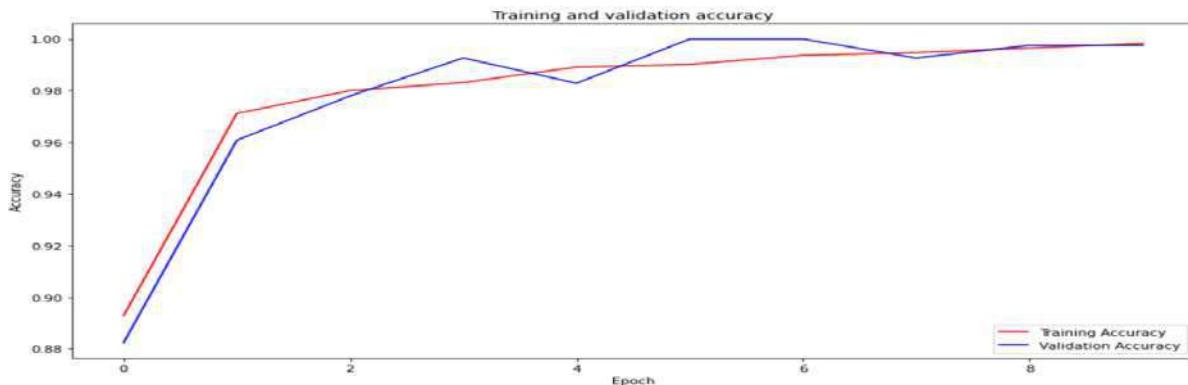


Fig. 16. Training and Validation Accuracy for Proposed Model.

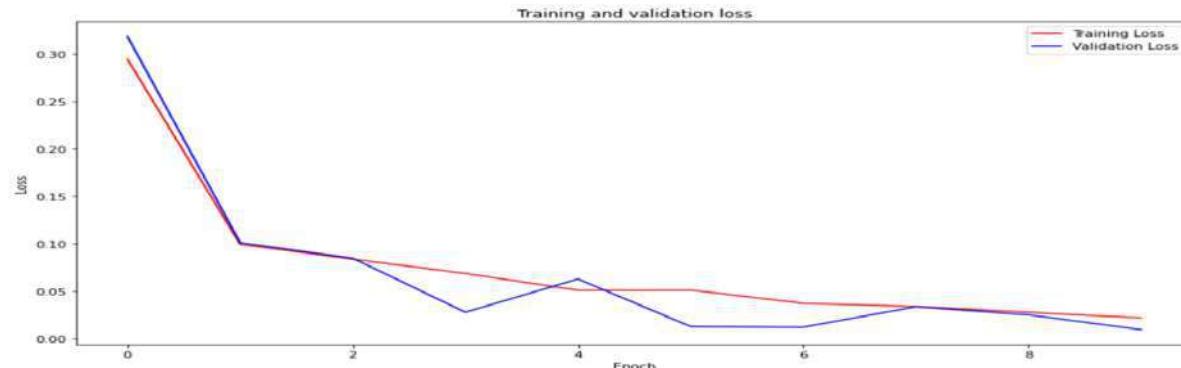


Fig. 17. Training and Validation Loss for Proposed Model.

V. CONCLUSION

Visual observation for classifying grape leaf diseases can be misleading because of a lack of prior knowledge and similarities among diseases. This paper introduces an automated mechanism for classifying grape leaves as healthy or diseased (e.g., black measles, black rot, and leaf blight) using transfer learning (e.g., VGG16, VGG19, and Xception). This classification has been done by extracting the features from the grape images using different pre-trained networks and then using the ensemble learning method for these networks to enhance the diagnosis accuracy. The novelty of the work lies in the fact that, instead of training each network alone and then concatenating the final results to get better results, all the networks are trained together, allowing the fully connected

layer to discover the best ensemble method to concatenate the results of previous networks. The proposed model achieved an accuracy of 99.82% compared to recent models that used grape leaf disease in the training process across the existing online Plant Village dataset. This work demonstrated the value and benefits of using ensemble learning and transfer learning. This study has achieved its objectives to improve the performance of classifying plant diseases and reducing overfitting.

VI. FUTURE WORK

Looking ahead, we hope to test the power of our model on more complex datasets and increase the number of categories of agricultural diseases.

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Grape Leaf Black Rot Detection Based on Super-Resolution Image Enhancement and Deep Learning

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Edited by:

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Specialty section:

This article was submitted to
Technical Advances in Plant Science,
a section of the journal
Frontiers in Plant Science

Received: 15 April 2021

Accepted: 07 June 2021

Published: 29 June 2021

Citation:

Zhu J, Cheng M, Wang Q, Yuan H and
Cai Z (2021) Grape Leaf Black Rot
Detection Based on Super-Resolution
Image Enhancement and Deep
Learning. *Front. Plant Sci.* 12:695749.
doi: 10.3389/fpls.2021.695749

The disease spots on the grape leaves can be detected by using the image processing and deep learning methods. However, the accuracy and efficiency of the detection are still the challenges. The convolutional substrate information is fuzzy, and the detection results are not satisfactory if the disease spot is relatively small. In particular, the detection will be difficult if the number of pixels of the spot is $<32 \times 32$ in the image. In order to effectively address this problem, we present a super-resolution image enhancement and convolutional neural network-based algorithm for the detection of black rot on grape leaves. First, the original image is up-sampled and enhanced with local details using the bilinear interpolation. As a result, the number of pixels in the image increase. Then, the enhanced images are fed into the proposed YOLOv3-SPP network for detection. In the proposed network, the IOU (Intersection Over Union, IOU) in the original YOLOv3 network is replaced with GIOU (Generalized Intersection Over Union, GIOU). In addition, we also add the SPP (Spatial Pyramid Pooling, SPP) module to improve the detection performance of the network. Finally, the official pre-trained weights of YOLOv3 are used for fast convergence. The test set test_pv from the Plant Village and the test set test_orchard from the orchard field were used to evaluate the network performance. The results of test_pv show that the grape leaf black rot is detected by the YOLOv3-SPP with 95.79% detection accuracy and 94.52% detector recall, which is a 5.94% greater in terms of accuracy and 10.67% greater in terms of recall as compared to the original YOLOv3. The results of test_orchard show that the method proposed in this paper can be applied in field environment with 86.69% detection precision and 82.27% detector recall, and the accuracy and recall were improved to 94.05 and 93.26% if the images with the simple background. Therefore, the detection method proposed in this work effectively solves the detection task of small targets and improves the detection effectiveness of the grape leaf black rot.

Keywords: small targets, grape black rot, super-resolution, convolutional neural network, deep-learning

INTRODUCTION

Grapes are one of the most commonly grown economic fruits in the world, which are often used in the production of wine, fermented beverages, and raisins (Kole et al., 2014). The larger the area used for the cultivation of grapes, the larger is the scale of the disease affecting the grapes and consequently, the probability of economic loss is higher as well. Generally, the early stages of

grape diseases are evident on the leaves. Therefore, the leaves can be used for the identification and diagnosis of diseases during the early stage. Black rot is one of the most common grape diseases in the world (Molitor and Berkemann-Loehnertz, 2011). Black rot is a fungal disease that exhibits a black spot on the grape leaves. This spot is relatively smaller as compared to the size of the leaves. This disease usually appears during the moist spring season and early summer. The black spot affects a wide area of the leaves (Pearson and Goheen, 1989). Currently, a manual method is mainly used for the identification of this disease. In this method, the farmers use their extensive experience to make a rough identification of the disease. However, it is notable that this approach not only requires a lot of manual labor but is also susceptible to the subjective factors (Chen et al., 2020). In order to ensure the grape production and economic well-being of the farmers, rapid and effective detection of black rot on grape leaves is important for the farming industry.

Currently, the machine vision technologies are widely used in various fields for detection and classification tasks. In the early stages of research on grape leaf diseases using machine learning, Agrawal et al. (2017) used SVM for the classification of grape diseases using leaves. The proposed method included image resizing, image enhancement, and image smoothing to save the memory and reduce the processing time. Waghmare et al. (2016) proposed the local binary patterns and machine learning for the detection and classification of grape diseases. The authors uniformly resize the images to 226 × 226 before further processing. In addition, the images are transformed from the RGB to HSV color space and the background subtraction is used to remove the unwanted background in the images. Es-Saady et al. (2016) proposed the automatic identification of plant diseases using leaves based on a serial combination of two SVM classifiers. The authors used different colors as the classification criterion in the first classifier. Then, in the second classifier, the shape and texture features of colored leaves were used for classification. Although the traditional machine learning algorithms have made some achievements in grape leaf disease detection, these methods require manual feature extraction. In addition, the accuracy of disease detection needs to be improved as well.

Recently, deep learning has been extensively used for the purpose of detection and classification in various applications. Felzenszwalb et al. (2008) proposed a region-based convolutional neural network (CNN) for target detection. There are few region-based detection algorithms presented in literature, such as RCNN (Girshick et al., 2014), Fast-RCNN (Girshick, 2015), and Faster-RCNN (Ren et al., 2017). Similarly, the well-known end-to-end detection algorithms include SSD (Liu et al., 2016) and YOLO (Redmon et al., 2016; Redmon and Farhadi, 2017, 2018). The CNNs have been used for the detection of grape diseases. Wagh et al. (2019) proposed an automatic grape disease identification system based on the AlexNet. This method has the ability to detect the bacterial spots and powdery mildew with an accuracy of 98.23%. Ji et al. (2020) proposed a unified model based on multiple CNNs for automatic identification of grape leaf diseases. This method was used for the classification of black rot, esca, isariopsis leaf spot, and healthy images. The average validation accuracy of this method is 99.17% and the test accuracy

is 98.57%. Liu et al. (2020) proposed an improved CNN for the identification of grape leaf diseases. The authors use this technique to identify anthracnose, brown spot, mites, black rot, downy mildew, and leaf blight. This method utilizes the depth-separable convolution instead of standard convolutional layers. As a result, this method achieves higher convergence speed and accuracy. Xie et al. (2020) proposed a rapid detector for grape leaf diseases based on deep learning. This technique automatically extracts the disease spot features and has the ability to detect four common grape leaf diseases with high accuracy and fast detection speed. Alessandrini et al. (2021) proposed a grapevine leaves dataset for early detection and classification of Esca disease in vineyards through machine learning.

However, it is noteworthy that the existing networks, such as AlexNet, RCNN, and Fast-RCNN, suffer from non-negligible miss-detections and low recall for the small spots. For instance, if the spot pixels are $<32 \times 32$ (Bosquet et al., 2018), or when the image resolution is not high. According to the definition of the international organization SPIE, a small target is a target area <80 pixels in a 256×256 image, that is, the target whose pixel proportion is $<0.12\%$ of the total image pixels. The small target recognition is still a challenge.

The super-resolution is an image processing method which is commonly used in the field of remote sensing (Xie et al., 2017; Arun et al., 2019), feature extraction, non-linear mapping, and image reconstruction. This technique has the ability to make small targets on the original image clear, even after the application of convolution. Bai et al. (2018a,b) applied the super-resolution for small target detection. The results show that this method effectively enhances the information of small targets, while improving the detection accuracy. Noh et al. (2019) proposed an accurate monitoring of feature super-resolution for small target detection. This method demonstrates the importance of using the appropriate high-resolution target features that share the same relative field of perception as the low-resolution input features to provide direct monitoring. Rabbi (2020) proposed remote sensing image small target detection based on an end-to-end edge-enhanced neural network and target detector network. The authors present the stochastic resonant network which has a faster response and yields the best results for small targets on satellite images.

In order to improve the detection accuracy of low-resolution small targets in the grape black rot spot detection, in this work, we propose a super-resolution image enhancement and deep learning-based detection of black rot in grape leaves. The proposed method used an improved loss function for performing detections. In addition, we also propose the spatial pyramid pooling (SPP) module in the detection network, which effectively increases the reception range of the backbone features and significantly separates the most important contextual features. Moreover, the proposed method improves the target recall and accuracy as compared with the max pooling technique.

The major contributions of this work are as follows.

- (1) We perform enhancement of grape leaves by using the bilinear interpolation.

- (2) We improve the YOLOv3 network. The IOU in the original yolo YOLOv3 network is replaced with GIOU. In addition, we also add the SPP module to improve the detection performance of the network.
- (3) We perform experiments and analysis to evaluate the effectiveness of the super-resolution image enhancement and improved YOLOv3 network for grape black rot detection.

MATERIALS AND METHODS

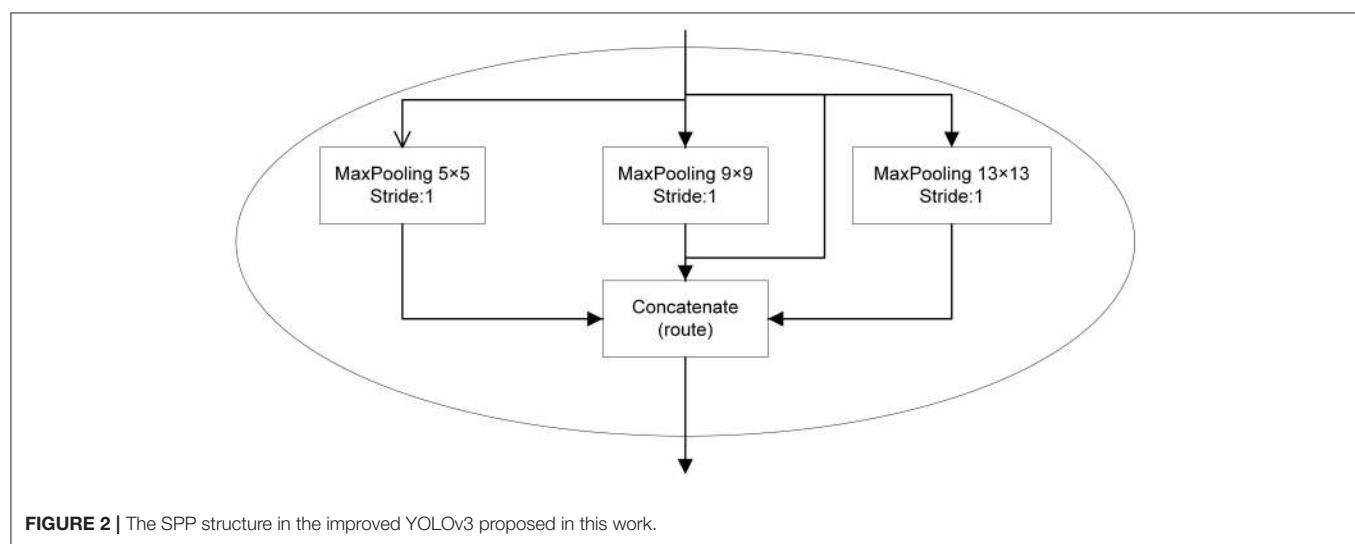
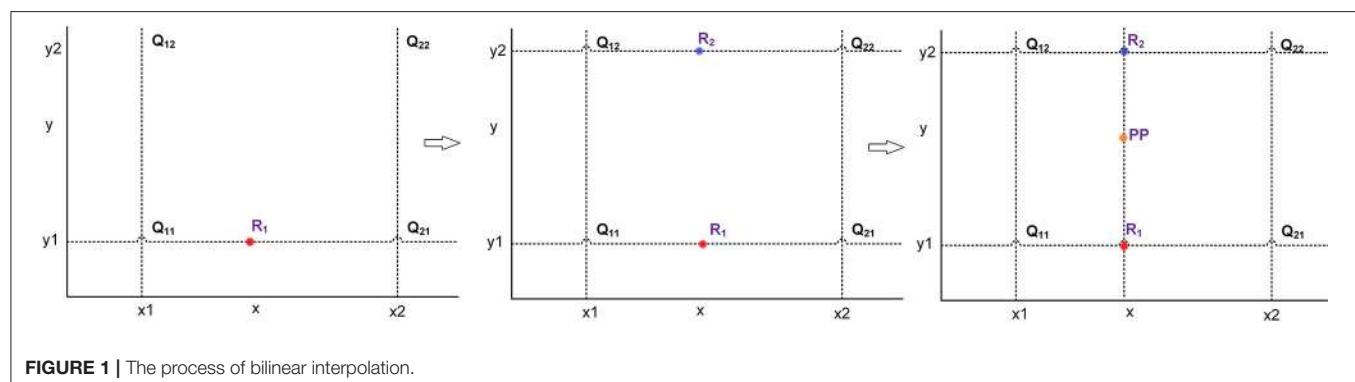
Data Set and Test Environment Setup

The data used to perform experiments in this work is the open dataset Plant Village. We select 1,180 images of grapevine leaf black rot for disease detection. We use LabelImg for annotating the diseased parts of the leaves. The average number of diseases present in an image is around 15, with more than 17,000 detection targets present in total. Before starting the training process, we divide 1,180 images into training and test sets. We select 1,072 images for training the network and 108 images as the test set for evaluating the network, which was named test_pv. In addition, 108 images of grape leaves with black rot spots in the orchard environment were collected as an extra test set, which was named test_orchard. We further divide the training

set into two parts during the process of network training, namely training set and validation set. The division ratio of training and validation sets is 9:1. In the convolutional neural network, the training set is used for model fitting, and the validation set is a separate sample set in the process of model training, which can be used to adjust the super parameters of the model and to preliminarily evaluate the ability of the model. The test set is used to evaluate the generalization ability of the final model. In this work, the number of epochs is 200, the input batch is 8, the learning rate is 0.001, and the size of the input image is 256×256 . The coco dataset format is used for the dataset used in this work. We use the pre-trained model weights to accelerate the convergence. We conduct the simulations on Windows 10 based on the pytorch deep learning framework. The computer on which the tests are conducted contains 8GB GPU GeForce GTX 1070Ti and an AMD Ryzen 5 1600X Six-Core Processor. The Python language is used for programming.

Super-Resolution Enhancement of Grape Leaf Images

In order to improve the resolution of the original image, we use a software method to produce a single high-quality and high-resolution image from a set of low-quality, low-resolution



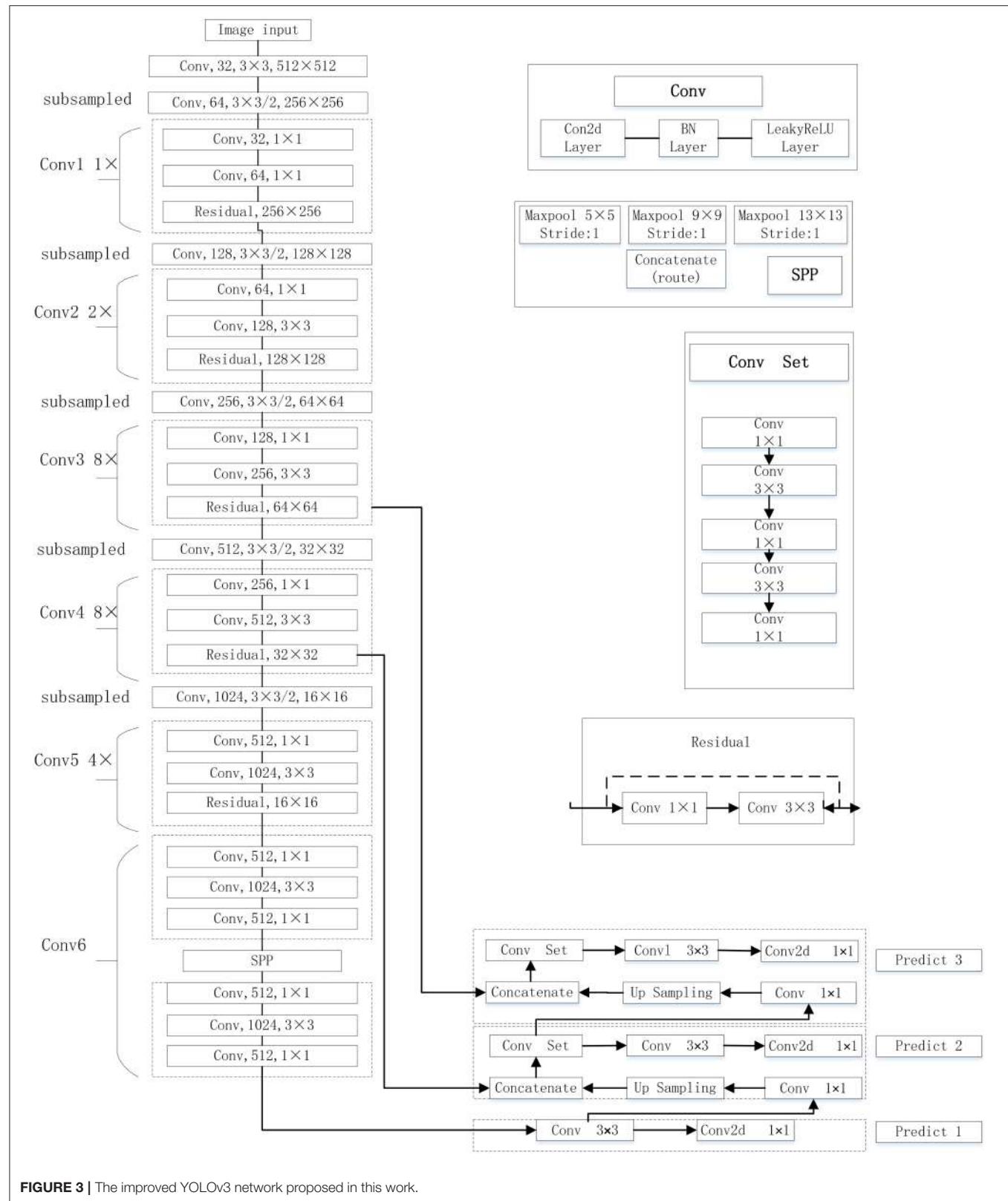
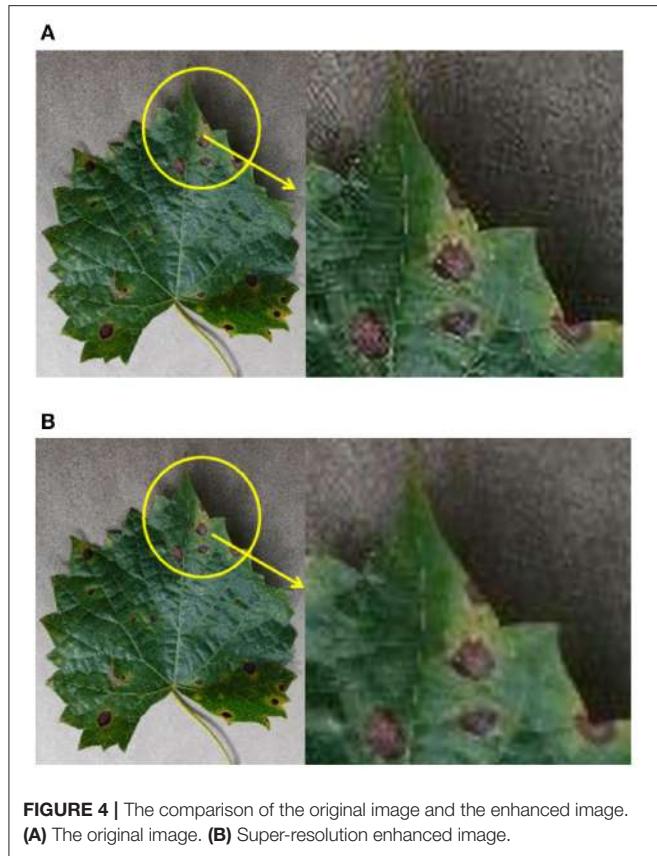


FIGURE 3 | The improved YOLOv3 network proposed in this work.



images. This method of transforming images is known as the super-resolution reconstruction (Shen et al., 2009). There are two types of image super-resolution reconstruction techniques. In the first technique, we synthesize a high-resolution image from multiple low-resolution images. In second technique, we acquire a high-resolution image from a single low-resolution image. The super-resolution techniques are divided into three categories, namely interpolation-based super-resolution, reconstruction-based super-resolution, and learning-based super-resolution. The interpolation-based super-resolution is relatively simple, and it is also widely used in various techniques. In reconstruction-based super-resolution, the main idea is to map the low-resolution images to high-resolution images. However, this technique is computationally expensive and requires a lot of computational resources. The learning-based super-resolution is implemented on the basis of convolutional neural networks (CNNs). In this work, we use the widely used interpolation method for image super-resolution. This technique is able to achieve results similar to the learning-based super-resolution images without requiring extensive computational resources. The bilinear interpolation (BL) is used for image super-resolution, which means that the original image is up-sampled for scaling operation. This is a technique for image scaling, which is mainly divided into two linear interpolation steps. First, we interpolate in the x-direction to find R_1 and R_2 . The R_1 is obtained according to the values of Q_{11} and Q_{21} , and the R_2 is obtained according to the values of

Q_{12} and Q_{22} . Then, the result of x-direction interpolation R_1 and R_2 are used to find the output of y-direction interpolation PP . The process of bilinear interpolation is shown in **Figure 1**.

In **Figure 1**, $Q_{11}(x_1, y_1)$, $Q_{12}(x_1, y_2)$, $Q_{21}(x_2, y_1)$, and $Q_{22}(x_2, y_2)$ represent the original pixel points. The first interpolation R_1 along x-axis is calculated by using Q_{11} and Q_{21} . The second interpolation R_2 along x-axis is calculated by using Q_{12} and Q_{22} . The interpolation result $PP(x, y)$ along y-axis is calculated by using R_1 and R_2 . The interpolation calculation process is shown in (1). The pixel points in the image are added in such a way that the image is transformed from low resolution to high resolution and super-resolution image is obtained.

$$\begin{cases} f(R_1) = \frac{x_2 - x}{x_2 - x_1} f(Q_{11}) + \frac{x - x_1}{x_2 - x_1} f(Q_{21}) \\ f(R_2) = \frac{x_2 - x}{x_2 - x_1} f(Q_{12}) + \frac{x - x_1}{x_2 - x_1} f(Q_{22}) \\ f(PP) = \frac{y_2 - y}{y_2 - y_1} f(R_1) + \frac{y - y_1}{y_2 - y_1} f(R_2) \end{cases} \quad (1)$$

Where, $f(Q_{11})$, $f(Q_{21})$, $f(R_1)$, $f(R_2)$, and $f(PP)$ represent the value of corresponding points, respectively.

Deep Learning Method for Grape Leaf Spot Detection

In order to improve the accuracy of grapevine leaf black rot spot detection, we design an improved YOLOv3 network. The YOLO (Redmon et al., 2016) is a typical CNN model used in target recognition, and YOLO v3 (Redmon and Farhadi, 2018) is the third version of the YOLO, which has advantages over v1 and v2 for the detection of small targets. In the improved network, we replace the loss function IOU (Intersection Over Union, IOU) with GIOU (Generalized Intersection Over Union, GIOU), and GIOU provides better regression boxes during the training process. In addition, we introduce SPP (Spatial Pyramid Pooling, SPP) before the output of feature layer, which is conducive to the detection of large differences in the target size in the image. We enhance the images by applying the linear interpolation before using the image as an input to the CNN, which is super-resolution of the image and can improve the effect of target detection.

Loss Function GIOU

In the original YOLOv3 target detection network, the engagement ratio IOU of the bounding box and the ground truth is used as the loss function. In the improved network proposed in this work, the IOU is replaced by GIOU in the deep learning network. The GIOU is calculated as shown in (2).

$$GIOU = IOU - \frac{|A_c - U|}{|A_c|} \quad (2)$$

where, A_c denotes the area of the minimum closure region of the two boxes, i.e., the ground truth and the predicted bounding box, and U denotes the intersection area of the two boxes. By using the GIOU as a loss function, we avoid the problem caused when the two target boxes have no overlap. So, the gradient is continuously updated and better regression boxes are available during the training process.

SPP Module

The SPP works on the idea of the spatial pyramid (He et al., 2014). On the basis of SPP module, we achieve the fusion of local and global features. This feature fusion enhances the expressiveness of the feature map which is conducive in the detection of large differences in the target size in the image. In the YOLOv3-SPP network proposed in this work, the SPP module consists of four parallel branches with kernel sizes of 5×5 , 9×9 , 13×13 , and 16×16 . In this work, the input of SPP model is the 16×16 size image after subsampling, and the output is the fusion of four parallel branches. The SPP module is placed after the 16×16 convolutional layer and before the output. This structure is shown in Figure 2.

Improved YOLOv3-SPP Network Architecture

The YOLOv3-SPP network proposed in this work is implemented by improving the original YOLOv3. The original YOLOv3 network uses Darknet-53 as the backbone network. The Darknet-53 mainly consists of 5 residual blocks. This structure uses the idea of residual neural network, and the idea of FPN (Feature Pyramid Networks, FPN). The up-sampling fusion is adopted to detect the target independently by fusing multiple feature maps at three different scales, including 16×16 , 32×32 , and 64×64 . The size of the minimum prediction frame is 8×8 (image size divided by grid size 512/64), which effectively obtains the feature information at low and high levels. This end-to-end network is not only more accurate but is computationally

efficient as well. In this work, the SPP module is introduced in the Conv6 layer of the YOLOv3. The YOLOv3-SPP network structure is shown in Figure 3.

Evaluation Indicators

We use the precision (P) and recall (R) as evaluation metrics. The precision of any algorithm is computed as

$$P = \frac{TP}{TP + FP} \times 100\% \quad (3)$$

where, TP represents the true positives, which is expressed as the number of manually labeled grape disease pixels that overlap with pixels in the region automatically detected by the model as grape disease. FP represents the false positives, which is expressed as the number of pixels in the region manually considered as background, but automatically detected by the model as grape leaf region pixels. We calculate recall by using the following expression.

$$R = \frac{TP}{TP + FN} \times 100\% \quad (4)$$

where, FN denotes the false negatives, which indicates the number of pixels that are manually labeled as the grape leaf area pixels, but are detected by the model as background area pixels.

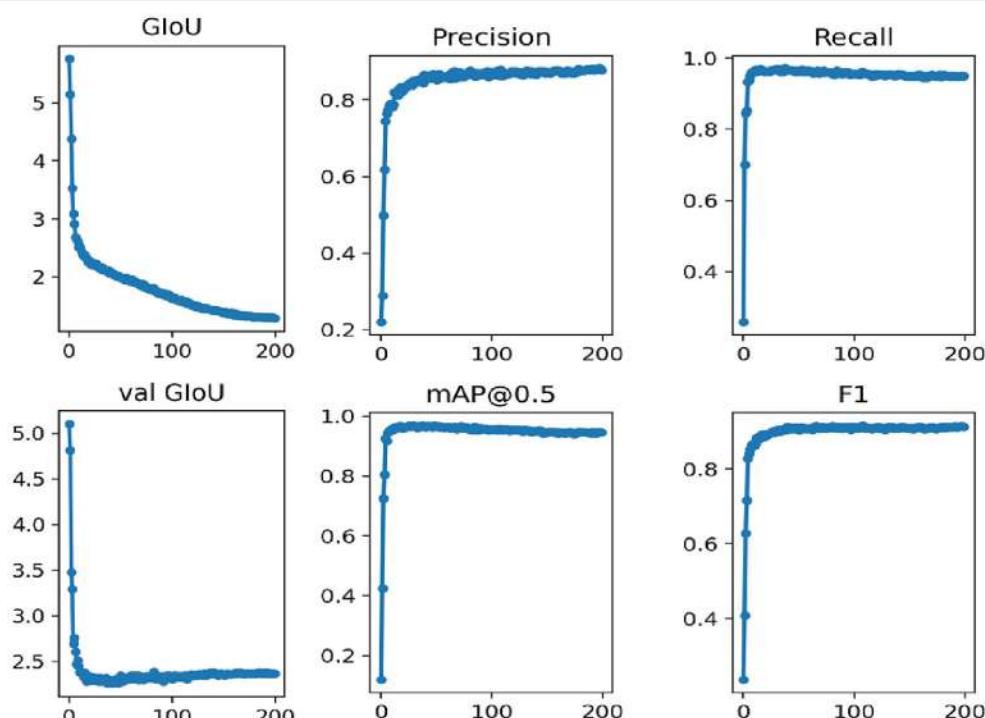


FIGURE 5 | The training performance of the original dataset YOLOv3-SPP network.

RESULTS

Super-Resolution-Based Image Enhancement Results

The size of an image in the original dataset is 256×256 , and the average image size is around 20 kb. After the application of super-resolution technique, we enhance the input image to a size of 512×512 . Now, the average image size is 100 kb. **Figure 4** shows the comparison between the original image and the resulting enhanced image. It is evident from **Figure 4** that the local parts of the image are equally magnified 4 times. The clarity of the image after the super-resolution is significantly higher than that of the original image.

Original Image YOLOv3-SPP Detection Results

In this work, we use the annotated images to train the network. The network is trained for 200 epochs which takes around 6 h. The training results are presented in **Figure 5**.

In **Figure 5**, the GIoU denotes the loss function used in this work, the val GIoU denotes the validated loss function, map@0.5 denotes the average accuracy, and F1 represents an evaluation metric which combines the effect of precision and recall. It is evident from **Figure 5** that the network converges rapidly for the first 100 iterations. In

addition, the loss function GIoU decreases rapidly until it gets flat around the 100th iteration. The evaluation metrics, i.e., precision, recall, map@0.5, and F1 also become flat at this stage.

Enhanced Image YOLOv3-SPP Detection Results

The enhanced image dataset with annotation information is fed into the YOLOv3-SPP network for training. Please note that the network parameters are the same as used in the case of training the network on original images. This training process consumes around 7 h. The training results are presented in **Figure 6**. It is evident from **Figure 6** that the model is continuously optimized during the epochs, and the loss function decreases rapidly in the initial iteration until it gets flat. This is consistent with training the network using original images which indicates that the improved YOLOv3-SPP network converges rapidly regardless of whether it uses the original images or the enhanced images as the input data. The trend of precision is similar to the case of training the network on original images. However, other evaluation metrics, i.e., recall, map@0.5, and F1 rise rapidly and reach a smooth state at the beginning of the training and show a small decrease after 100 iterations.

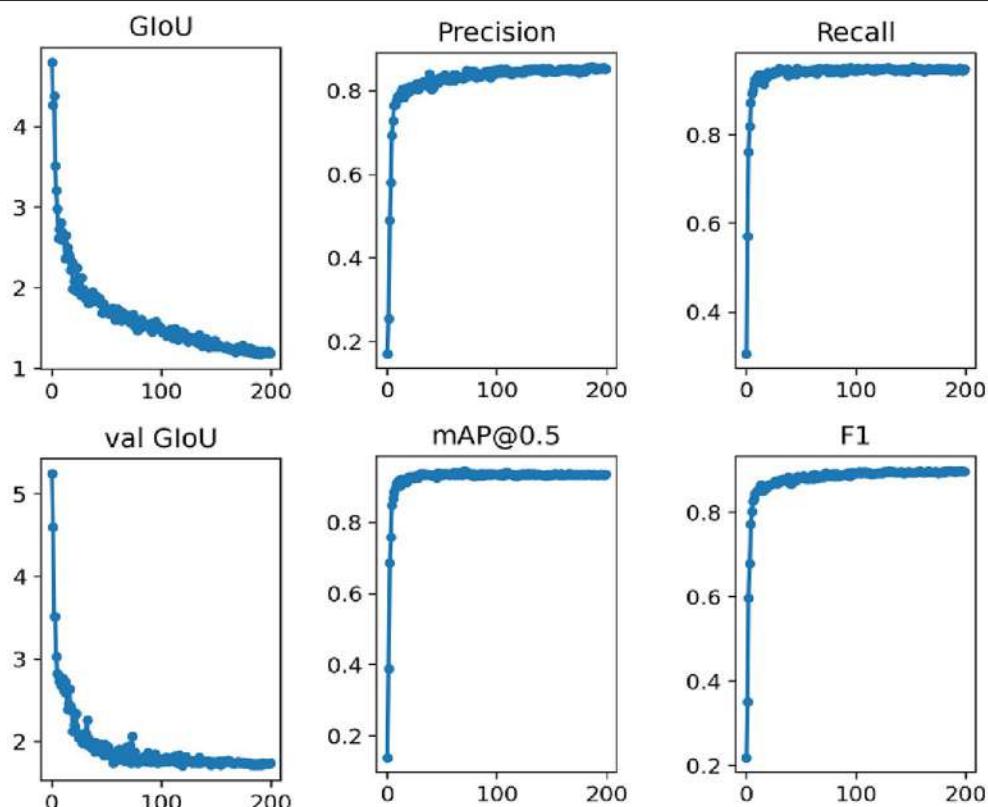


FIGURE 6 | The training performance of YOLOv3-SPP network by using the enhanced dataset.

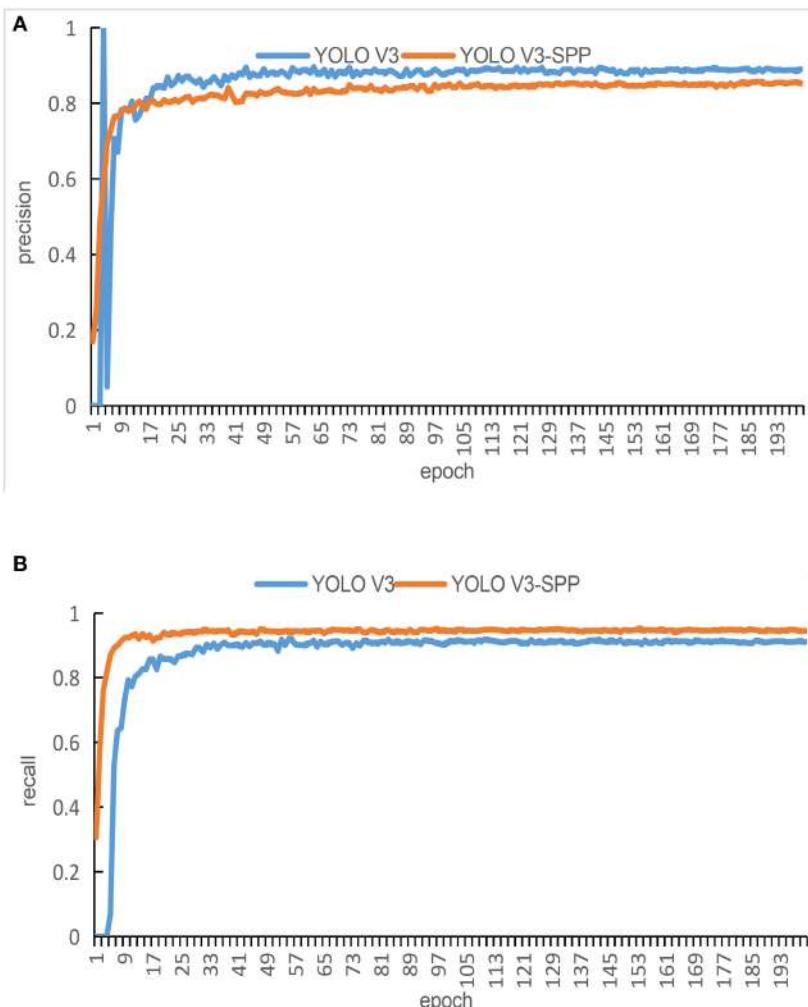


FIGURE 7 | The training results of the detection algorithm by using the original images. **(A)** A comparison of the original and improved YOLOv3 in terms of precision for detection. **(B)** A comparison of the original and improved YOLOv3 in terms of recall for detection.

DISCUSSION

Comparison of the Effect of YOLOv3 Network Improvement Before and After

In order to evaluate the performance of the proposed network in terms of detection accuracy, we train the original YOLOv3 network and the YOLOv3-SPP network by using the original images. The precision and recall of both techniques are compared in Figure 7. Figure 7A presents the comparison of precision and Figure 7B presents the comparison of recall of both algorithms.

It is evident from Figure 7A that the red curve converges faster than the blue curve. In addition, the blue curve shows huge fluctuations at the beginning epochs. These fluctuations continue for around 100 epochs. After 100 epochs in the training process, both curves reach a relatively stable state. The curve at the final epochs shows that the blue curve maintains an interval of about 2% from the red curve, i.e., the blue curve is more precise than the red curve. Therefore, in terms of the

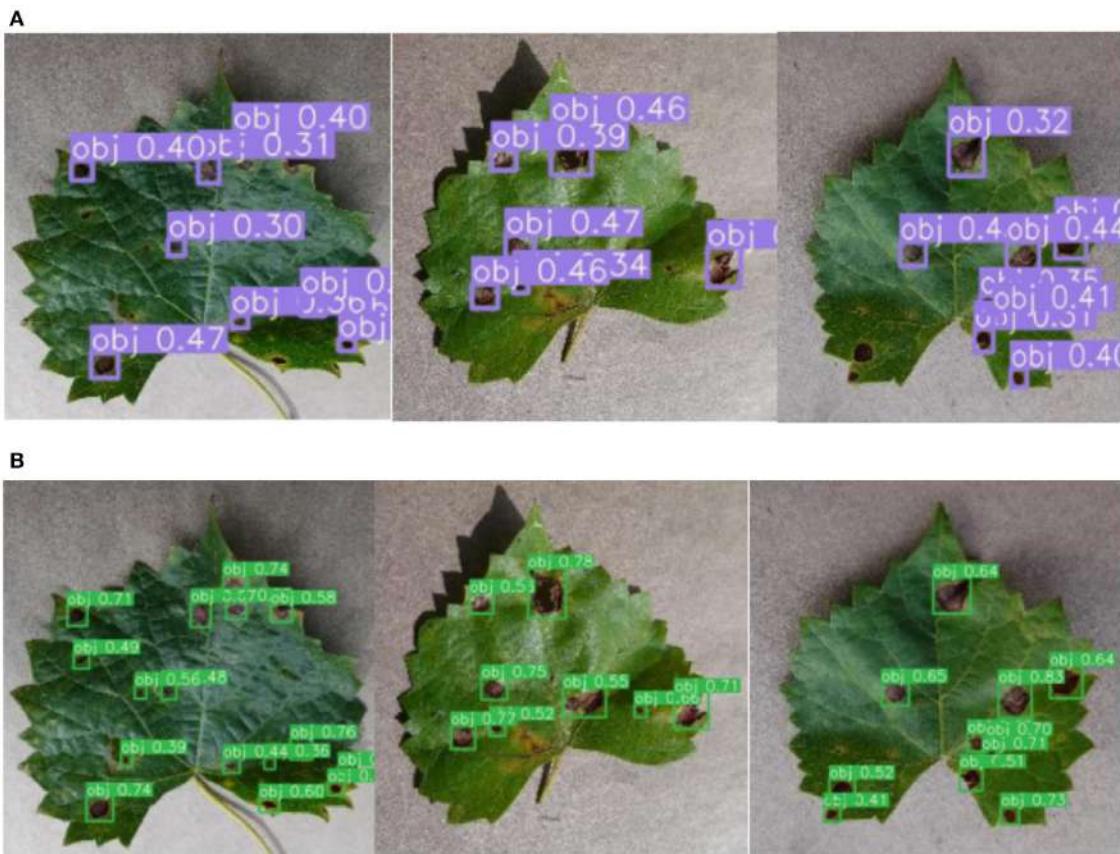
detection, the original YOLOv3 performs slightly better than the proposed YOLOv3-SPP.

It is evident from Figure 7B that the red curve converges faster as compared with the blue curve. There is an interval of about 3% between the two curves after reaching a steady state. During the entire training process of 200 epochs, the precision of the red curve is always greater than the blue curve. In terms of the detection, the proposed YOLOv3-SPP performs better than the original YOLOv3.

In order to further verify the detection accuracy of the original and the proposed YOLOv3, we present the recognition results of the test_pv in Table 1. There are 108 images with 1,532 spots of grape leaf black rot in the test_pv set. The results show that the proposed YOLOv3-SPP successfully identifies 1,427 spots. Contrary, the original YOLOv3 only identifies a total of 1,283 spots. It is also noteworthy that the proposed YOLOv3-SPP misidentified 87 spots, which is 58 less than the misdetections of original YOLOv3. The number of FN of YOLOv3-SPP was

TABLE 1 | The detection results of the test_pv before and after the improvement of YOLOv3 network.

Original image of the test_pv with 1,532 objectives	TP	FP	FN	Precision	Recall
YOLOv3	1,283	145	259	89.85%	83.75%
YOLOv3-SPP	1,427	87	105	94.25%	93.15%

**FIGURE 8 |** The comparison of detection results before and after the improvement of YOLOv3 network. **(A)** The detection results of the original YOLOv3 for original images. **(B)** The detection results of the improved YOLOv3-SPP for original images.

105, which was 154 less than that of YOLOv3. The proposed YOLOv3-SPP achieves the detection accuracy of 94.25% and a recall of 93.15%. These results are 4 and 9% higher than the original YOLOv3, respectively.

Figure 8 shows the detection results of the original and the improved algorithm. **Figure 8A** presents the recognition results of the original YOLOv3 and **Figure 8B** presents the recognition results of the improved YOLO V3-SPP. It is evident from **Figure 8** that the recognition results of the improved algorithm are significantly better than the original algorithm. It is noteworthy that the targets missed by the original network are also recognized by the improved network. This shows that the addition of SPP module and the replacement of the loss function in the improved algorithm improve the recall of the detected targets effectively. Although the accuracy of the improved network is slightly lower than the original network.

This indicates that the overall performance of the proposed YOLOv3-SPP algorithm is higher than that of the original YOLO V3, and the results of the improved method for grapevine leaf black rot detection are satisfactory.

Comparison of Different Super-Resolution Algorithms for Image Enhancement

In this work, the BL is used to enhance the images. The enhanced images are then used for target detection. In this work, before we select the BL as a choice for this work, we compare the two other different super-resolution methods, i.e., the nearest interpolation and the enhanced deep residual networks (EDSR) (Lim et al., 2017) with BL. The nearest interpolation is a traditional and simplest interpolation method which is used to enhance the image by directly copying the values of neighboring pixels. On the other hand, EDSR has the ability to handle multiple

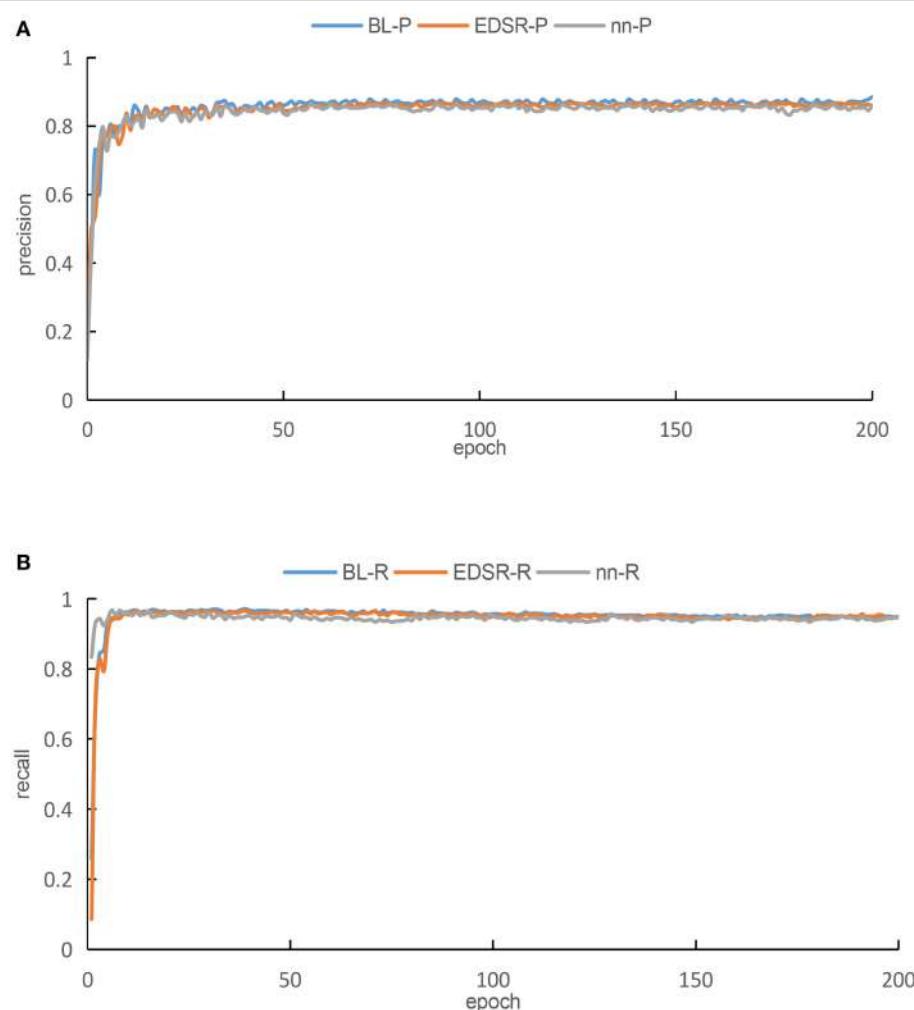


FIGURE 9 | The training results of YOLOv3-SPP network after image enhancement by using different super-resolution algorithms. **(A)** A comparison of accuracies for different super resolutions. **(B)** A comparison of recall for different super resolutions.

scaling factors (scales) of super-resolution simultaneously in a single network. The training process of EDSR models using multiple scales significantly improve the performance. However, EDSR-type architectures require bicubic interpolation. This interpolation technique is computationally expensive and needs more storage space as well.

In this work, we enhance the original images in the training dataset comprising 1,072 images by using all the three aforementioned super-resolution methods. These images are input into the proposed YOLOv3-SPP network for training. The training results are shown in **Figure 9**. Please note that **Figure 9A** presents a graph comparing the accuracies of different super-resolutions. As presented in **Figure 9**, the blue curve represents the result of BL, the red curve represents the result of EDSR, and the green curve represents the results of nearest interpolation.

As presented in **Figure 9A**, it is evident that when the images of the three different interpolation methods are fed into the proposed YOLOv3-SPP network separately, after 50 iterations,

TABLE 2 | The evaluation of test_pv by using different super-resolution methods.

Evaluation indicators	BL	Nearest interpolation	EDSR
TP	1,448	1,430	1,450
FP	65	78	70
FN	84	102	82
Precision	95.79%	94.83%	95.39%
Recall	94.52%	93.34%	94.65%

the precisions of all the networks tend to be stable. After 50 iterations, the precision of all three training methods fluctuates minutely, but the overall trend is stable. The comparison shows that the blue curve is better than the other two curves after achieving steady state. On the other hand, the green curve has a lower precision than the other two algorithms after becoming steady state. Therefore, we conclude that the BL technique

has the highest accuracy rate P as compared with the other two super-resolution enhancement methods under the same parameters. As presented in **Figure 9B**, when the images of the three different interpolation methods are fed into the YOLOv3-SPP network separately, the resulting recalls approach 1 after 20 iterations approximately.

Please note that the red and blue curves are almost equal, however, the green curve is slightly below the other two curves. After processing the original image by using the three super-resolution image enhancement methods, the recalls approach 1, which are all higher than directly training the network using

the original images. This indicates that the super-resolution enhancement of the images before using it as an input of the CNN for detection is better than using the original images directly. The evaluation metrics, i.e., precision and recall, make it evident that the network performs best when the image is enhanced using the BL technique as compared to the nearest interpolation. As compared to the EDSR method, the result of image enhancement performed using BL method has higher precision. and almost equal recall. However, the BL method has no complex residual convolution and is relatively less computationally intensive. We enhance 108 images in `tese_pv` according to the three

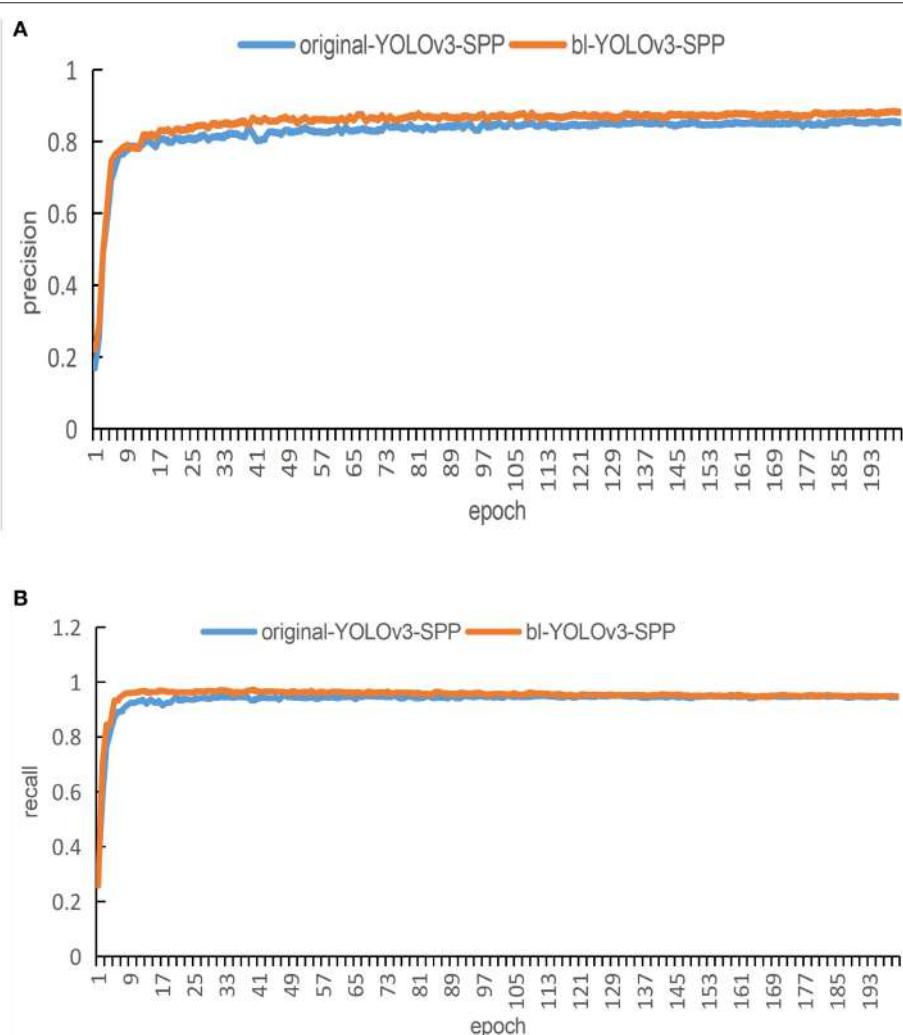


FIGURE 10 | The training results of the network before and after image enhancement. **(A)** A comparison of the detection accuracy under super-resolution image and original image. **(B)** A comparison of the detection recalls under the super-resolution image and the original image.

TABLE 3 | The detection results on test_pv set.

YOLOv3-SPP	Objectives	TP	FP	FN	Precision	Recall
Original image of test_pv	1,532	1,427	87	105	94.25%	93.15%
Super Resolution of test_pv	1,532	1,448	65	84	95.79%	94.52%

aforementioned methods and then use the resultant images to perform detections using the proposed YOLOv3-SPP network. The corresponding results are shown in **Table 2**. Please note that the BL method has the highest recognition precision for the spots and the recall rate is only 0.13% lower than the EDSR method. The results of simulations performed using test_pv show that all the image enhancement methods perform well, however, considering the overall performance using the evaluation metrics shows that the BL method is superior.

Comparison of the Detection Effect of Super-Resolution Image and Original Image Under the Improved Network

The training results of the proposed YOLO V3-SPP network by using the original and the enhanced images are presented in **Figure 10**. The blue and red curves in **Figure 10** represent the training results for original and improved images, respectively.

Figure 10A shows the comparison of detection accuracy under the super-resolution image and the original image. The results show that the red curve and the blue curve almost converge simultaneously, however, the red curve after smoothing is close to 0.9. The blue curve lags behind the red by about 1.2%. Both curves have occasional fluctuations during the process of convergence. After reaching 140 epochs, both curves smooth out. After enhancing the images using super-resolution, the accuracy

of the network is higher than the accuracy obtained by using the unenhanced images.

Figure 10B shows the comparison of detection accuracy under the super-resolution images and the original images. The results show that the two curves rapidly stabilize at the beginning of the training process. Please note that the blue curve is lower than the red curve for first 100 epochs, but after 100 iterations both curves are relatively stable. The figure shows that both curves exhibit good recall. This indicates that after enhancing the images using super-resolution, the performance of the network reflects that its recall is not lower than that of the unenhanced images.

The test result of the proposed YOLOv3-SPP trained with the original and the enhanced images in test_pv are shown in **Table 3**. The YOLOv3-SPP trained using the enhanced images correctly identifies a total of 1,448 spots, that is 21 more spots than the YOLOv3-SPP trained using the original images. In addition, the number of false identifications is reduced by 22, and the number of miss identifications decreased by 21. In terms of precision and recognition rate, the proposed YOLOv3-SPP network trained on the enhanced images improved the performance by 1.54 and 1.37%, respectively.

Figure 11 shows the recognition results before and after the images are enhanced. **Figure 11A** shows the detection results of YOLOv3-SPP trained using the unenhanced images. **Figure 11B** presents the detection results of YOLOv3-SPP trained using the enhanced images. As presented in **Figure 11**, the proposed

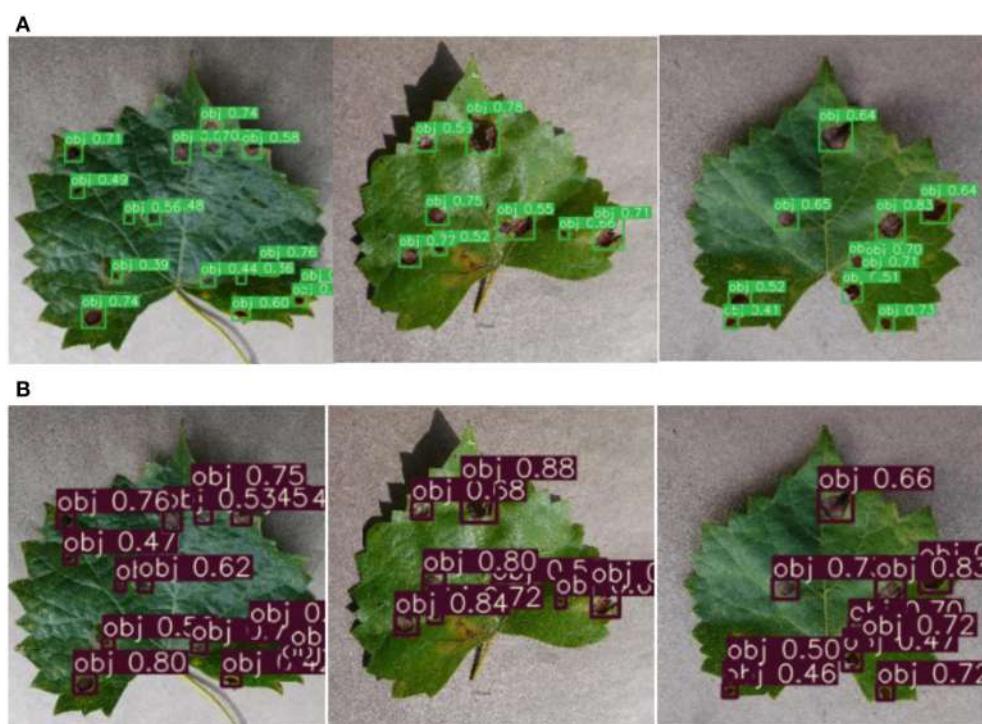


FIGURE 11 | The detection results before and after the data is enhanced for test_pv. **(A)** The detection results of YOLOv3-SPP trained on the unenhanced images. **(B)** The detection results of YOLOv3-SPP trained on the enhanced images.

YOLOv3-SPP trained using the enhanced images to detect the black rot of grape leaves has significantly better results than the recognition results of the network trained using the unenhanced images. This indicates that the introduction of super-resolution images for grape leaf black rot detection improves the accuracy of the target detectors without reducing the recall rate.

The Detection Effect in the Orchard Environment

The method of super-resolution image enhancement and deep learning can improve the detection effect of grape leaf black rot, which has been proved in the test_pv data set. An additional test set, test_orchard, was used to test the effectiveness of the proposed method in the orchard environment. There are 108 images of grape leaves with 1,275 spots of grape leaf black rot from different orchard environments. The results of spot identification by YOLOv3-SPP were shown in **Figure 12**. It can be seen from **Figure 12** that not only the detection precision of the spot was improved, but also the recall was improved after

enhancing the images using super-resolution. Some undetected spots in the original image were identified on the enhanced images. The statistical data of identification results of the test_orchard was shown in **Table 4**. There are 1,275 spots in the test set, and 1,028 spots were recognized after inputting the original images into the YOLOv3-SPP, of which 186 spots were misidentified. The number of unrecognized spots was 247. The precision of disease spot detection was 84.68% and the recall was 80.63% for the original images of test_orchard. However, a total of 1,049 disease spots were identified for the images after enhancement by super-resolution, of which 161 spots were misidentified. The number of unrecognized spots was 247. The precision of disease spot detection was 86.69% and the recall was 82.27% for the super-resolution images of test_orchard. The number of misidentified and unrecognized spots decreased, and the precision and recall increased 2.01 and 1.64%, respectively after the images were enhanced by super-resolution.

The detection precision and recall of test_orchard were lower than that of test_pv, because the images of test_orchard are from orchards, while the images of test_pv from Plant Village, which photograph indoors. The environment of orchards is complex compared to the indoor. The images of the test_orchard were classified into single-leaf and multi-leaf based on the number of grape leaves in the images, to compare the influence of different image acquisition ways on the detection effect. The detection results of the multi-leaf images were shown in **Figure 13**, and it can be seen that the leaf slits to be misrecognized as disease spots, which reduced the precision. The statistical results of the detection were shown in **Table 5** for the two category images. There are 701 spots in single-leaf images totally, 601 spots were detected, 71 disease spots were wrong identified and 91 spots were missed. The detection precision was 89.57% and the recall was 87.02% for the single-leaf images. A total of 574 disease spots in multi-leaf images and 135 spots were missed detection. Among the identified 439 spots, 90 spots were misidentified. The detection precision was 82.99% and the recall was 76.48% for the multi-leaf images. The detection precision and recall of single-leaf images are 6.76 and 10.54% higher than that of multi-leaf images.

This shows that the acquisition of single grape leaf image is more conducive to detection.

The background of images also affected the detection effect, so the set of test_orchard was divided into two subsets, simple background images and complex background images based on the status of the background. The images are considered to be complex background, which concludes fruits, branches, and soil except for grape leaf, otherwise, they are considered simple background. The detection results of the complex background images were shown in **Figure 14**, and it can be seen that the rotten fruits, gray branches, and soil to be misrecognized as disease

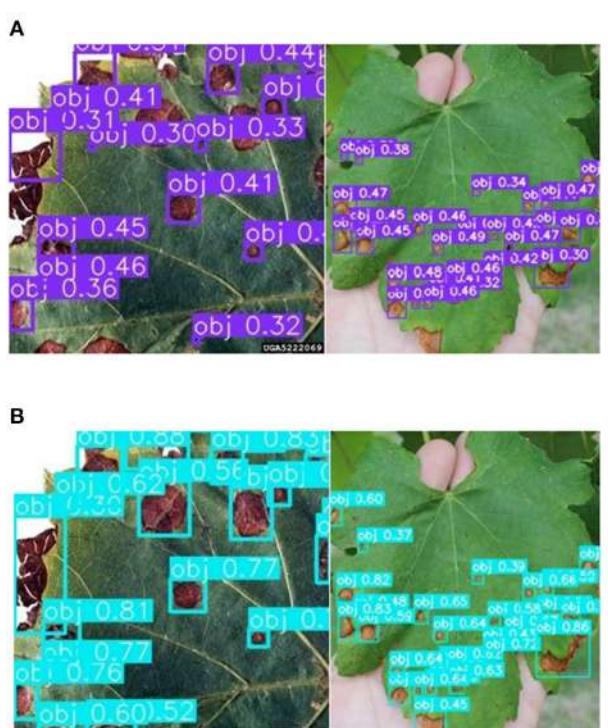


FIGURE 12 | The detection results before and after the data is enhanced for test_orchard. **(A)** The detection results of YOLOv3-SPP trained on the unenhanced images. **(B)** The detection results of YOLOv3-SPP trained on the enhanced images.

TABLE 4 | The detection results on test_orchard set.

YOLOv3-SPP	Objective	TP	FP	FN	Precision	Recall
Original image test_orchard set	1,275	1,028	186	247	84.68%	80.63%
Super-resolution test_orchard set	1,275	1,049	161	226	86.69%	82.27%



FIGURE 13 | Detection results of multi-leaf images.

TABLE 5 | The statistical results of the detection of single-leaf and multi-leaf images for test_orchard.

BL-YOLOv3-SPP	Objective	TP	FP	FN	Precision	Recall
Single-leaf	701	610	71	91	89.57%	87.02%
Multi-leaf	574	439	90	135	82.99%	76.48%

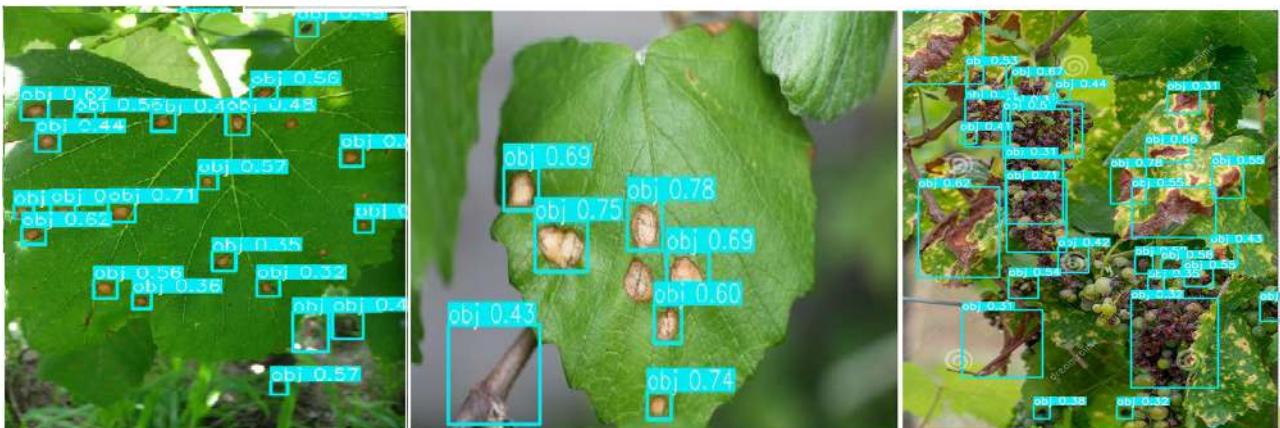


FIGURE 14 | Detection results of grapevine leaf black rot with complex background.

TABLE 6 | The statistical results of the detection of different background for test_orchard.

BL-YOLOv3-SPP	Objective	TP	FP	FN	Precision	Recall
Simple background	712	664	42	48	94.05%	93.26%
Complicated background	563	385	119	178	76.39%	68.38%

spots, which also reduced the precision. The statistical results of the detection were shown in **Table 6** for the test_orchard images in the different backgrounds. There are 712 spots in simple background images totally, 664 spots were detected, 42 disease spots were wrong identified and 48 spots were missed. The detection precision was 94.05% and the recall was 93.26% for the simple background images, which was close to the detection effect of test_pv. A total of 563 disease spots in complex background images and 178 spots were missed detection. Among the identified 386 spots, 119 spots were misidentified. The

detection precision was 76.39% and the recall was 68.38% for the complex background images. The detection precision and recall of simple background images are 17.66 and 24.9% higher than that of complex background images. It can also be seen from the data in **Table 6**, that the influence of background in the image is greater than that of multiple leaves in the image for the grape leaf black rot.

The method proposed in this work can be used for the detection of grape leaf black rot in the natural environment through the test and analysis of the images collected from

orchards, and the detection effect is satisfactory especially in the case of the simple background. At the same time, the analysis results also provide a reference for the field image acquisition, that is, to avoid other objects appearing in the image except for grape leaf.

CONCLUSIONS

In this work, we propose an improved YOLOv3-SPP model for the detection of black rot of grape leaves. This method replaces the loss function in the original YOLOv3 with GIOU. In addition, we also add the SPP module. We enhance the training images of YOLOv3-SPP by using BL super-resolution method. Two test sets from Plant Village dataset and orchards are performed on the model. The results show that the YOLOv3-SPP network performs better for grape leaf black rot detection and has a precision of 95.79% and recall of 94.52% for the test set from Plant Village. For the orchards test set, the precision is 86.69% and the recall is 82.27%, it also has better performs than the original images of the test set. In addition, the precision and recall are improved to 94.05 and 93.26% for those images without fruits, branches, and soil in the background. Moreover, the image enhancement of the training set using the BL method improves the results in terms of precision and recall. The current method requires image enhancement and then trains the deep learning network. In future work, we will attempt to combine these steps.

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DATA AVAILABILITY STATEMENT

The original contributions presented in the study are included in the article/**Supplementary Material**, further inquiries can be directed to the corresponding author.

AUTHOR CONTRIBUTIONS

JZ, MC, and HY: conceived the idea and proposed the method. JZ and QW: contributed to the preparation of equipment and acquisition of data, and wrote the code and tested the method. JZ, QW, and MC: validation results. JZ and HY: wrote the paper. JZ, HY, and ZC: revised the paper. All authors read and approved the final manuscript.

FUNDING

This work was supported by the National Natural Science Foundation of China (Grant No. 32001412) and the Key Research and Development Program of Hebei Province (19227206D).

SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: <https://www.frontiersin.org/articles/10.3389/fpls.2021.695749/full#supplementary-material>

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Conflict of Interest: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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Grape leaf disease identification with sparse data via generative adversarial networks and convolutional neural networks

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Accepted: 20 July 2022 / Published online: 7 August 2022

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Abstract

The main challenge in deep learning related to the identification of grape leaf diseases is how to achieve good performance in the case of available sparse datasets or limited number of annotated samples, small lesions, redundant information and blurred background information in grape leaf disease images. This paper proposes a three-stage deep learning-based pipeline, including a convolutional neural network (Faster R-CNN) for detection of lesions, a generative adversarial network (DCGAN) for data augmentation and a residual neural network (ResNet) for identification of lesions, to solve these problems. Firstly, Faster R-CNN was used to mark the location of grape leaf lesions to obtain lesions dataset for data augmentation and ResNet for identification of lesions. Secondly, leaf lesion images were fed into DCGAN to generate synthetic grape lesion images for identification of lesions. Finally, ResNet trained in the training dataset consisting of real grape leaf lesions and synthetic grape lesion images obtained by DCGAN, was used to identify the grape leaf lesions according to the majority voting principle. The first experimental results showed that Faster R-CNN, DCGAN and ResNet had good performance in each stage. Secondly, the second experimental results showed that the proposed three-stage method is superior to single-stage and two-stage methods in the case of sparse datasets and small lesions. Finally, a generalization experiment was also carried out using 100 images on the internet to verify the generalization of the proposed three-stage method. Experimental results showed that the proposed three-stage method had good generalization ability.

Keywords Grape leaf disease · Faster R-CNN · DCGAN · ResNet

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Introduction

Grapes, as one of the most nutritious crops in the world, are the most important raw materials of wine (Asghari et al., 2013). However, grape leaf diseases, such as viruses, fungi and bacteria, cause considerable grape yield losses and damage to grapes (Compani et al., 2005). Timely and accurate identification of grape leaf diseases is essential to cure and control them. Traditional identification of grape leaf diseases is carried out through on-the-spot investigations by experts but manual identification of grape leaf diseases is typically time-consuming, laborious and inefficient (Bock et al., 2010; Mahlein, 2016). Computer vision-based identification methods using machine learning have been developed for timely and accurate identification of grape leaf diseases to overcome these problems.

In recent years, convolutional neural networks (CNNs) and their modified models have been applied to plant disease identification and provide better performance than the traditional feature extraction method and classification method in the case of large amounts of data for training, since CNNs can learn high-level robust features directly from plant disease images instead of extracting the specific features manually (Brahimi et al., 2017; Geetharamani & Pandian, 2019; Polder et al., 2019; Khan et al., 2018; Fuentes et al., 2017). Nevertheless, when lesions cover a small part of an entire image, or the images contain a lot of redundant information or blurred background information, identification accuracy of grape leaf diseases is not usually satisfactory in the case of image-level classification since deep learning may not be able to extract sufficient detailed appearance features for lesions in an image. Besides, it is difficult and expensive to acquire sufficient grape leaf diseases as a training sample due to the scale of grape orchards and the ever-changing symptoms of grape diseases across temporal and spatial scales. As a result, one of the main challenges in deep learning related to the identification of grape leaf diseases is how to have good generalization ability and prevent overfitting under the condition of available sparse datasets or a limited number of annotated samples.

In order to eliminate the effect of small lesions, redundant information and blurred background information on identification accuracy of grape leaf diseases, object detection methods can be used to locate lesions before identifying grape leaf disease. This operation can utilize maximum information about lesion symptoms and increase the diversity of samples so that identification accuracy is improved. The most intuitive object detection method is to use sliding windows to generate candidate regions, then features can be extracted from these regions and pretrained classifiers can be applied to determine if these regions have certain objects or not. However, region selection strategy based on a sliding window is a brute force method that requires multiple scans of the whole images, resulting in slower generation of the detection regions and large computational cost. Faster R-CNN, as one of ConvNet-based on object (Ren et al., 2016) detection, abandons the traditional sliding window and selective search (SS) method, and directly uses region proposal networks (RPN) to generate the candidate regions, resulting in fast generation speed of the detection regions. Therefore, this study used Faster R-CNN to locate lesions of grape leaf diseases before identifying grape leaf disease.

To tackle the problem of sparse datasets and poor diversity in grape leaf disease identification, data augmentation was widely used to enlarge a grape disease dataset before identifying grape leaf disease, so that this operation can solve the problem of overfitting and improve the accuracy of identification. The researchers attempted to use traditional data augmentation techniques such as flipping, clipping, rotation, Gaussian noise, translation, affine transformation and so on. The essence of this method is to obtain a new image with

the same semantics as the original image without increasing the diversity of the image, so it cannot essentially solve the diversity problem (Jiang et al., 2019). This had motivated the use of generative adversarial networks (GANs) (Mirza & Osindero, 2014), which generate new synthetic grape disease images with the same data distribution as training samples and with different semantics (such as backgrounds, textures and shapes) from training samples, to make the synthetic images more variant and enrich diversity of dataset. However, instability of GAN training, caused by trouble in simultaneous convergence of generator and discriminator, often caused generators to produce meaningless samples. Deep convolutional generative adversarial networks (DCGAN) (Radford et al., 2015), as one of the variants of GAN, combines CNN in supervised learning with GAN in unsupervised learning, so as to solve the problem of instability of GAN training and improve the quality of samples and the speed of convergence. Therefore, this study used DCGAN to generate synthetic images before identifying grape leaf disease.

To solve two problems encountered in identification of grape leaf diseases work: (1) small lesions and redundant or blurred background information in grape leaf disease images; (2) sparse datasets and poor diversity, this study proposed a three-stage accurate deep learning-based pipeline with an automatic detection mechanism to locate grape leaf lesions by Faster R-CNN, a data augmentation network to generate new synthetic grape lesion images by DCGAN and an identification network to identify grape leaf diseases by ResNet (He et al., 2016). At the first stage, Faster R-CNN, which was trained in images manually annotated with bounding boxes, was used to mark the location of grape leaf lesions. At the second stage, DCGAN, which was trained on a grape lesion dataset obtained by Faster R-CNN, was used to generate synthetic grape lesion images for augmentation of training samples. At the last stage, ResNet, which is trained in a training dataset consisting of real grape leaf lesions and synthetic grape lesion images obtained by DCGAN, is used to identify the grape leaf lesions.

Related work

Because deep learning, e.g. convolutional neural networks, could integrate feature learning into the process of establishing a model, deep learning has been successfully applied in grape leaf diseases identification. The studies on disease identification based on deep learning can be divided into two types. The first ones are one-stage methods containing only deep convolutional neural networks (Brahimi et al., 2017; Kamal et al., 2019; Cruz et al., 2017). However, these methods cannot achieve promising results in the case of sparse datasets and small lesions in grape leaf diseases (Sharma et al., 2020; Hu et al., 2019).

The second are two-stage methods, which are divided into two types: one includes a network for detection or segmentation of lesions and a network for identification of grape leaf disease and the other includes a GAN network for data augmentation and a network for identification of grape leaf disease. On the one hand, two-stage methods including detection network and identification network solve the problem of achieving poor results in the case of small lesions, redundant information and blurred background information in images (Sharma et al., 2020; Ghoury et al., 2019; Tassis et al., 2021; Weyler et al., 2021). For example, Sharma et al., 2020 proposed a two-stage method including a segmentation user interface developed by the authors for segmentation of tomato leaf diseases lesions and a novel convolutional neural network architecture for identification to identify tomato leaf diseases. Experimental results showed that the accuracy of 98.6% in lesion-level is

greater than the accuracy of 42.3% in image-level. Besides, Tassis et al. (2021) proposed a two-stage method including fusion of mask R-CNN and UNet for coffee leaf segmentation and ResNet for identification to identify coffee leaf diseases. Experimental results showed that the proposed methods outperformed conventional CNN architectures on identification accuracy. On the other hand, two-stage methods including data augmentation and identification network solved the problem of achieving poor results in the case of sparse datasets and poor diversity in grape leaf diseases images (Han et al., 2018; Zeng et al., 2021; Hu et al., 2019; Liu et al., 2020). For example, Hu et al. (2019) proposed a two-stage method including conditional deep convolutional generative adversarial networks (C-DCGAN) for augmenting tea disease samples and VGG16 (Simonyan & Zisserman, 2014) for identification to identify tea disease. Experimental results showed that an accuracy of 90% by fusion C-DCGAN and VGG 16 was greater than the accuracy of 60% and 41.67% achieved by fusion of VGG16 and traditional augmentation and VGG16 without data augmentation respectively. Liu et al. (2020) proposed a two-stage method including a novel GAN named LeafGAN for augmenting grape leaf disease samples and Xception for identification to identify grape leaf diseases. Experimental results showed that the proposed method can efficiently remedy the existing training disease image shortage for training of grape leaf diseases.

However, when only sparse datasets are available and small lesions simultaneously appear in grape leaf disease images, the aforementioned two-stage methods cannot achieve promising results. Inspired by these analyses, this paper proposed a three-stage pipeline including Faster R-CNN for detection of lesions, DCGAN for data augmentation and ResNet for identification of grape leaf disease to simultaneously solve the two problems mentioned.

Identification of grape leaf disease via fusion of faster R-CNN, DCGAN and CNN

Overview

The scientific hypothesis of this work proposed a three-stage pipeline to identify grape leaf diseases with an automatic detection mechanism to locate grape leaf lesions by Faster R-CNN, a data augmentation network to generate new synthetic grape lesion images by DCGAN and an identification network to identify grape leaf diseases by ResNet. The proposed three-stage method has different processing flows in the training procedure and testing procedure, i.e. practical application of the method. Figure 1 shows the processing flow of the proposed three-stage method. At the first stage, Faster R-CNN was trained to accurately mark the location of lesions with bounding boxes from lesions dataset manually annotated with bounding boxes. Grape leaf disease lesions dataset located by Faster R-CNN were used to train DCGAN for data augmentation and ResNet for identification. At the second stage, DCGAN was trained to generate synthetic lesions from lesions dataset by Faster R-CNN. Synthetic lesions by DCGAN and lesions by Faster R-CNN form final lesions dataset. At the third stage, ResNet was trained to identify grape leaf lesions from final lesions dataset.

Figure 2 shows the processing flow of the proposed three-stage method in a practical application procedure. Firstly, a test grape leaf disease image was input into Faster R-CNN, trained to obtain a few lesions. Then, a few lesions were input into ResNet to determine

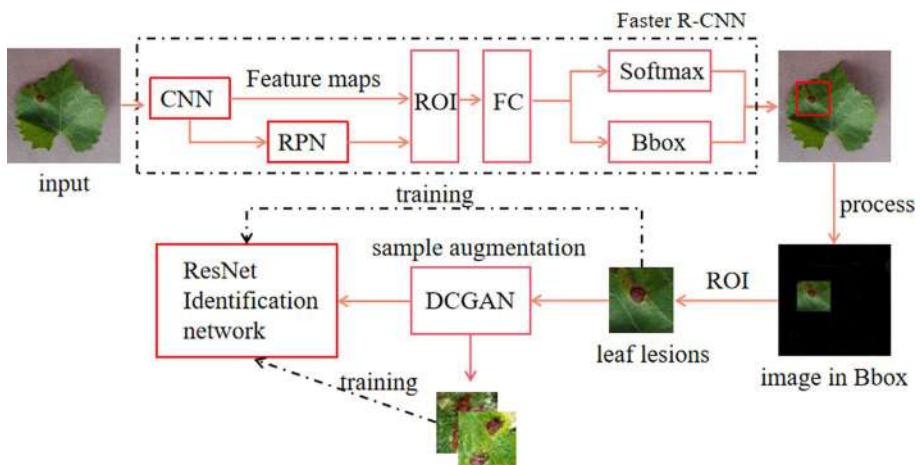


Fig. 1 The processing flow of the proposed three-stage method in training procedure

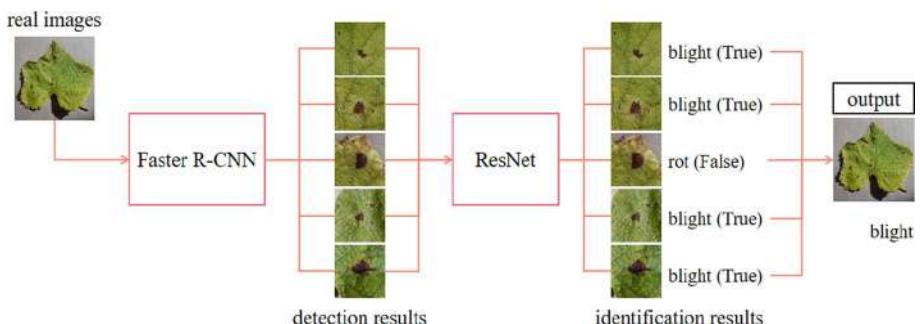


Fig. 2 The processing flow of the proposed three-stage method in practical application procedure

labels of a few lesions. Finally, on the assumption that an image only contains one kind of disease, the testing image was assigned to a class label according to the majority voting principle in the set of lesions that a sample was assigned to the class represented by a majority of labels of n lesions. For example, an image was input into Faster R-CNN, and then five lesions were detected with bounding boxes. After that, these five lesions were input into ResNet to determine labels for each of them. Four lesions were identified to be blight disease and one was identified to be rot disease. According to the majority voting principle, the class of this test grape leaf disease image is blight as shown in Fig. 2.

Detection of lesions by faster R-CNN

Detection of lesions by Faster R-CNN aims to provide lesion datasets for data augmentation and classification of grape leaf disease. Faster R-CNN contains two important components: a feature extraction network and a region proposal network. In this study, ResNet-101 was chosen as the feature extraction network instead of VGG16 to extract features from input grape leaf disease images. The advantage of RPN is that it greatly reduces

the number of regional proposals generated and takes an image of any size as input and outputs a series of rectangular object proposals, in which each one owns an objective score. The procedure of Faster R-CNN for detection of lesions is: Firstly, image size of $m \times n$ is fed into ResNet101 for feature extraction to obtain a feature map. Secondly, k anchor boxes with possible objects are generated around each pixel in a feature map according to the anchor mechanism. Thirdly, the RPN network uses softmax to preliminarily extract positive anchors as the candidate regions (Ren et al., 2015). Next, the candidate regions are fed into the proposal layer to determine region proposals. Then, proposal features are extracted from region proposals by the last convolutional layer in ResNet101. Finally, the probability vector of class and t detection bounding boxes are obtained through the full connect layer and softmax. The processing flow of Faster R-CNN for lesion detection is shown in Fig. 3.

At the stage of training Faster R-CNN for lesion detections, firstly, lesions of images were manually annotated with bounding boxes, which forms a lesion dataset. Then a lesions dataset were used to train Faster R-CNN. At the stage of practical application, an image is fed into Faster R-CNN to obtain a few lesions.

Data augmentation of lesions by DCGAN

Data augmentation with DCGAN aims to provide lesion datasets for classification of grape leaf disease. DCGAN combines CNN and GAN networks whose advantage is that DCGAN's generator and discriminator can learn hierarchy representations in terms of parts of object and scenes. DCGAN uses generator network G and discriminator network D for adversarial training to make the generative model gradually achieve good performance. The generator network maximizes the simulation of the original grape lesion images distribution and generates fake grape lesions. Discriminator network D is trained in real grape lesion dataset by CNN architecture to discriminate whether lesions come from the G or not. The schematic diagram of DCGAN is shown in Fig. 4.

In Fig. 4, z represents Gaussian noise or uniform noise, which is input to the generator network. After the generator G , a fake image is generated— $G(z)$, and $G(z)$ and x are taken as inputs to discriminator D . The output of the final discriminator D represents the probability that the data is real, which ranges from 0 to 1. For discriminator, batch

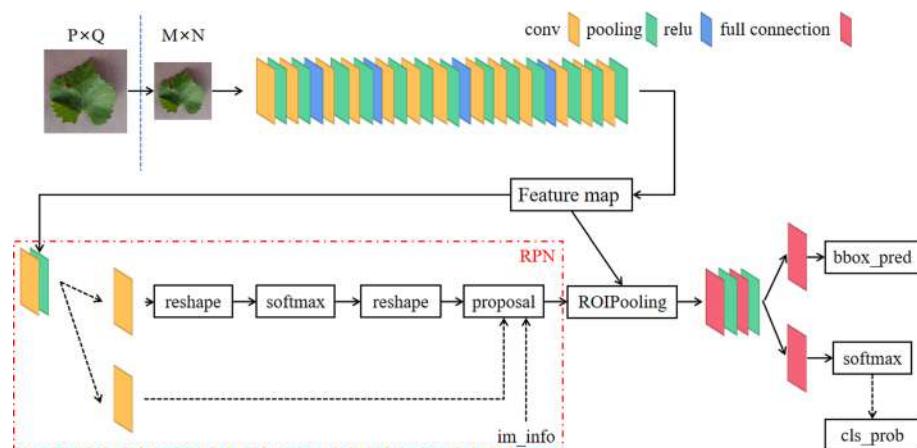


Fig. 3 The processing flow of Faster R-CNN for lesion detection

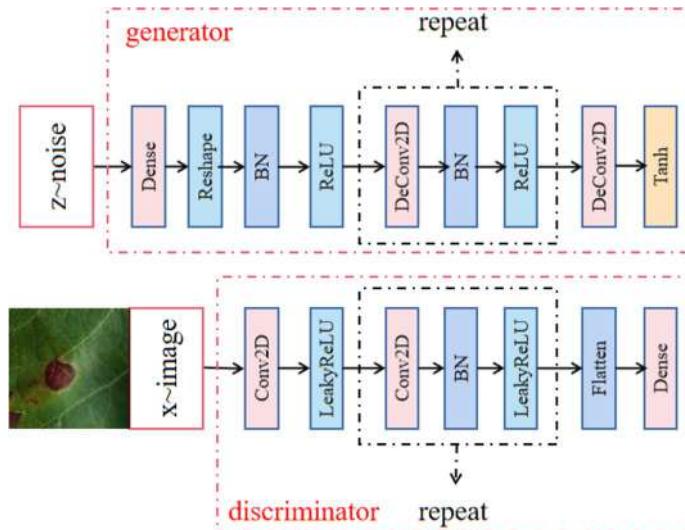


Fig. 4 DCGAN discriminator (left) and generator architecture (right)

normalization (BN) is generally not required after the first layer convolution, and the combination mode of “two-dimensional convolution (conv2D)+BN+leaky rectified linear unit (LeakyReLU)” is always followed. For generator, the first layer is the full connection layer, then the combined mode of “conv2D+BN+rectified linear unit (ReLU)”, and the last layer of convolution is activated by tanh.

At the stage of training DCGAN for data augmentation, the grape lesions dataset obtained by Faster R-CNN were used to train DCGAN to generate synthetic grape lesions. Since the purpose of this stage is data augmentation, this step is not needed in the stage of practical application.

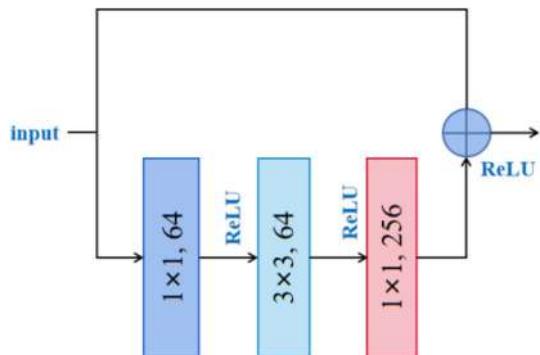
Identification of grape leaf diseases by CNN

ResNet was trained in a lesions dataset containing real lesions obtained by Faster R-CNN and fake lesions generated by DCGAN to identify grape leaf disease lesions and further to identify grape leaf diseases. ResNet is trained by a set of convolution layers, pooling layers and full connection layer so as to identify grape leaf disease lesions into a specific category. The main idea of ResNet is that it adds direct-connect channels to the network and allows a certain percentage of the output of the previous network layer with a non-linear transformation to be retained.

Bottleneck design in ResNet, as the core of ResNet, is shown in Fig. 5, which can reduce the number of parameters. Using 1×1 network in ResNet can greatly reduce the amount of computation. The first 1×1 convolution reduces the 256-dimensional channel to 64 dimensions. The structure of ResNet can accelerate the training of a network very quickly, and the accuracy is also greatly improved. In this work, ResNet-50 is used for training and identifying grape leaf disease lesions.

At the stage of training ResNet for grape lesion identification, it was trained in a grape leaf lesions dataset including real grape lesions and synthetic lesions generated by DCGAN. At the stage of practical application, ResNet was used to identify labels

Fig. 5 Bottleneck building block in ResNet



of a few lesions obtained by Faster R-CNN from an image. The label of this image was determined according to the majority voting principle in the set of lesions.

Experimental setup

Dataset

Considering that the grape leaf disease images are insufficient and difficult to collect in actual situations, 50 images of each class were randomly selected from the PlantVillage (Hughes & Salathé, 2015) as seen in Table 1. Examples of images are shown in Fig. 6. From left to right are healthy leaf, Black Rot Fungus, Black Measles Fungus and Blight Fungus, respectively.



Fig. 6 Examples of grape leaf disease image. (1) Healthy leaf. (2) Black Rot Fungus. (3) Black Measles Fungus. (4) Blight Fungus

Table 1 The number of each class diseases

Disease	Original dataset
Healthy leaf	50
Black Rot Fungus	50
Black Measles Fungus	50
Blight Fungus	50
total	200

Implementation details

In the implementation, Keras and TensorFlow (Abadi et al., 2016) were used as deep learning frameworks for python, using NVIDIA TITAN Xp GPU to build the network model. Dual graphics processing units (GPUs) were used to accelerate the experimental process. Workstation specifications are shown in Table 2.

In order to verify the effectiveness of the proposed three-stage method, three major experiments were carried out. The first experiment was to select the optimal model on each stage. There were three sub-experiments: (i) experiments on detection of lesions by Faster R-CNN, (ii) experiments on data augmentation of lesions by DCGAN and (iii) experiments on identification of lesions by ResNet

During experiments on detection of lesions by Faster R-CNN, 50 grape lesions per category were manually annotated with bounding boxes in 15 images, which formed the 200 grape lesions dataset with label. 160 grape lesions were used to train detection networks and 40 grape lesions to test performance of detection networks. There were two sub-experiments: (a) the first sub-experiment compared Faster R-CNN with ResNet101 with RCNN, Fast R-CNN (Girshick, 2015) and Faster R-CNN with VGG16. The optimization method is stochastic gradient descent (SGD) algorithm with a momentum of 0.9, the initial learning rate is 0.001 and batch size is 16. (b) the second sub-experiment discussed the effect of hyper-parameters on mAP

During experiments on data augmentation of lesions by DCGAN, in the GAN-train experiment, the discriminator was trained by 3200 lesion images and was tested by 200 real lesion images. In the GAN-test experiment, the discriminator was trained by 200 real lesion images and was tested by 200 lesion images generated by GANs. There were three sub-experiments:

- (a) the first sub-experiment compared DCGAN with boundary equilibrium generative adversarial networks (BEGAN) (Berthelot et al., 2017) and fusion of DCGAN with BEGAN. The hyper-parameters were set to default values; the learning rate is 0.0002, the momentum is 0.5 and batch size is 64
- (b) The second sub-experiment visually observed the quality of the lesions generated by DCGAN to analyze the performance of trained DCGAN more comprehensively.
- (c) The third sub-experiment discussed the effect of hyper-parameters on GAN-train and GAN-test.

During experiments on grape leaf disease identification by ResNet, there were two sub-experiments:

- (a) the first sub-experiment compared ResNet with AlexNet, VGG16 and InceptionV3. The hyper-parameters were set to default values; the iteration is 2048 and batch size is 64.
- (b) the second sub-experiment discussed the effect of hyper-parameters on performance.

Table 2 Workstation specifications

Hardware	Software
CPU: Inter Core i7-8700k	Windows10
RAM:32GB	CUDA9.0+CUDNN7.0
GPU: NVIDIA TITAN Xp	Keras Tensorflow

The second experiment was to compare the proposed method with the state-of-the-art for identification of grape leaf disease. In order to verify the generalization performance of the proposed model, the third experiment was to compare the proposed three-stage method with other three-stage methods in the dataset, in which grape leaf diseases come from the internet.

Performance index

In experiments on detection of lesions, mean average precision (mAP) was used to evaluate the performance of Faster R-CNN. The mAP represents a score obtained by comparing the ground-truth bounding box with the detected box. The higher the score is, the more accurate the model is in term of detections.

In experiments on data augmentation, GAN-train and GAN-test (Shmelkov et al., 2018) were used to evaluate the performance of DCGAN. The meaning of GAN-train is to train classifiers based on images generated by GANs and test them on real images to evaluate the diversity and authenticity of GAN generated images. The meaning of GAN-test is to train a classifier based on real images and test them on the generated images to evaluate the authenticity of the generated GAN images.

In experiments on identification of lesions, comparative experiments on the proposed method against the state-of-the-art and generalization experiments, accuracy and confusion matrices were used to evaluate the performance of the proposed three-stage method. Accuracy represents the percentage of predicted correct samples in the total samples. Confusion matrix is a cross table that records the number of occurrences between the true/actual classification and the predicted classification. The columns stand for model prediction whereas the rows display the true classification. Therefore, the correctly classified elements are located on the main diagonal from top left to bottom right.

Results and discussion

Results on each stage in the proposed method

Results on detection of lesions by faster R-CNN

The first sub-experiment showed that Faster R-CNN with ResNet101 achieved mAP of 69.74% for detection of lesions, which was greater than mAP for R-CNN, Fast R-CNN and Faster R-CNN with VGG16, as shown by the dotted line of Fig. 7.

The second sub-experiment discussed the effect of batch size on mAP. The experimental results show that Faster R-CNN with ResNet101 got the best mAP of 71.42% in the case of batch size parameter of 4 for detection of lesions, which is 28.45%, 18.42% and 3.78% greater than the best results for RCNN, Fast RCNN and Faster R-CNN with VGG16 respectively, as shown by the solid line of Fig. 7.

The trained Faster R-CNN above was applied in actual grape leaf disease images to detection lesions, as shown in Fig. 8. In order to subsequently train data augmentation networks of lesions and identification networks of lesions, grape leaf disease lesions dataset including 200 manually annotated lesions with bounding boxes from 60 images and 650 lesions obtained from 140 images by the trained Faster R-CNN, was constructed. Details of grape lesions dataset is shown in Table 3.

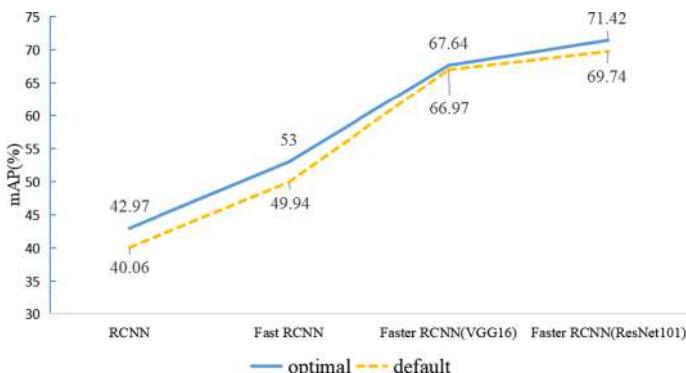


Fig. 7 Results on mAP in grape leaf disease lesions detection by four different detection networks

Fig. 8 Illustration of Detection of lesions in grape leaf disease image by Faster R-CNN

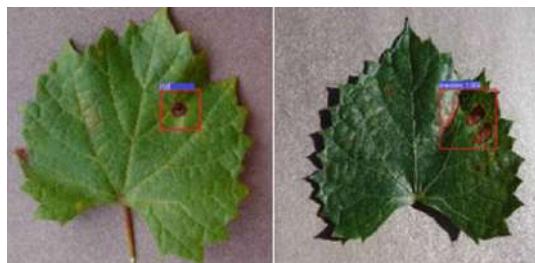


Table 3 Numbers in lesions dataset

Disease	Disease images	Annotated lesions	Disease images	Detecting lesions	Dataset
Healthy	15	50	35	207	257
Black rot fungus	15	50	35	134	184
Black measles fungus	15	50	35	151	201
Blight fungus	15	50	35	158	208
Total	60	200	140	650	850

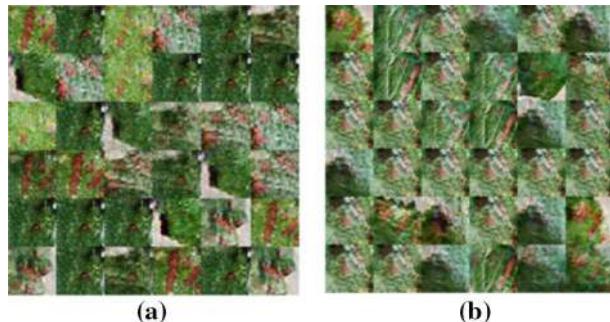
Results on data augmentation of lesions by DCGAN

The first sub-experiment showed that DCGAN achieved GAN-train of 65% and GAN-test of 68%, greater than BEGAN and fusion of DCGAN with BEGAN. Comparative results of DCGAN with BEGAN and fusion of DCGAN with BEGAN in terms of GAN-train and GAN-test are shown in Table 4.

The result of the second sub-experiment is shown in Fig. 9 which represents the generated lesions by DCGAN (left) and the generated lesions by BEGAN (right). Figure 9 showed that lesions generated by BEGAN were more blurred, lower diversity and quality than those generated by DCGAN. Although lesions generated by DCGAN have a lower resolution, they have the same characteristics as the original lesions. At the same

Table 4 GAN-train and GAN-test of different GANs

Model	GAN-train (%)	GAN-test (%)
DCGAN	65	68
BEGAN	34	47.9
DCGAN + BEGAN	56.6	59

Fig. 9 The generated Black measles lesions. **a** Generated Black measles lesions by DCGAN. **b** Generated Black measles lesions by BEGAN**Table 5** Accuracy of identifying lesions generated by DCGAN in the case of different hyper-parameters

	Learning rate	Momentum	Batch size	Accuracy (%)
0.02	0.5	16	88.33	
	0.5	36	91.67	
	0.9	16	85.83	
	0.9	36	84.17	
0.002	0.5	16	90.83	
	0.5	36	91.67	
	0.9	16	90	
	0.9	36	89.17	
0.0002	0.5	16	96.67	
	0.5	36	97.5	
	0.9	16	93.3	
	0.9	36	92.5	

Bold values are the best result obtained in the test experiments

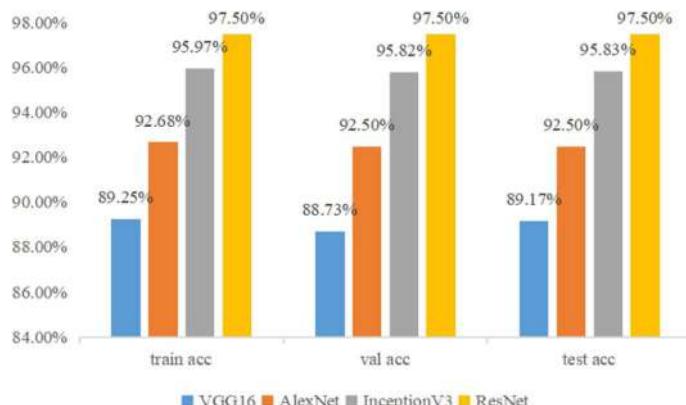
time, lesions generated by DCGAN avoid the interference of background information and edge information. Lesions generated by DCGAN have different features of different classes, so they can be used to train identification networks of grape leaf disease lesions.

The third sub-experiment achieved different accuracies in the case of different hyper-parameters by feeding 240 real lesions into trained ResNet in 4000 lesions partially generated by DCGAN as shown in Table 5. From Table 5, the highest accuracy of 97.5% was obtained, in the case of optimal hyper-parameters combination, with a learning rate of 0.0002, a momentum of 0.5 and a batch size of 36.

In order to subsequently train lesions identification networks, the trained DCGAN above was used to augment lesions. Note that, in this study, in order to make the number of samples of each class highly balanced, different numbers of samples were augmented for each class. Finally, the total number of augmented data and original data for each class is 1000,

Table 6 Numbers in lesions dataset including 3390 grape lesions generated by DCGAN

Disease	Real lesions	Augmented lesions	Dataset	Training	Validation	Test
Healthy	257	803	1060	800	200	60
Black rot fungus	184	876	1060	800	200	60
Black measles fungus	201	859	1060	800	200	60
Blight fungus	208	852	1060	800	200	60
Total	850	3390	4240	3200	800	240

**Fig. 10** Identification accuracy of the different architectures for grape lesions identification

which had met the quantitative requirements for training such as VGG16 networks (Du et al., 2018). 3390 lesions were generated by the trained DCGAN from 850 real lesions obtained by manual annotation and Faster R-CNN. Thus, grape lesions dataset contains 4240 grape lesions as shown in Table 6.

Results on identification of lesions by ResNet

3200 grape lesion images were used to train ResNet for grape disease lesions, 800 and 240 grape lesions were regarded as validation samples and test samples respectively as shown in Table 6. In the first sub-experiment, comparative results of ResNet with AlexNet, VGG16 and InceptionV3 in terms of accuracy are shown in Fig. 10, which showed that ResNet achieves accuracy of 97.5%, greater than AlexNet, VGG16 and InceptionV3.

Comparative results of ResNet with AlexNet, VGG16 and InceptionV3 in terms of confusion matrices are shown in Fig. 11. In Fig. 11, label1 to label4 represent Blight Fungus, healthy, Black Measles Fungus and Black Rot Fungus, respectively. Figure 11 showed that ResNet achieves accuracy of 100%, 100%, 93% and 97% of each class better than that of AlexNet, VGG16 and InceptionV3 respectively. In addition to AlexNet, the other three models can easily distinguish blight fungus and healthy images, but black measles and black rot fungus can easily be misclassified due to the similar pathological characteristics between black measles and black rot fungus.

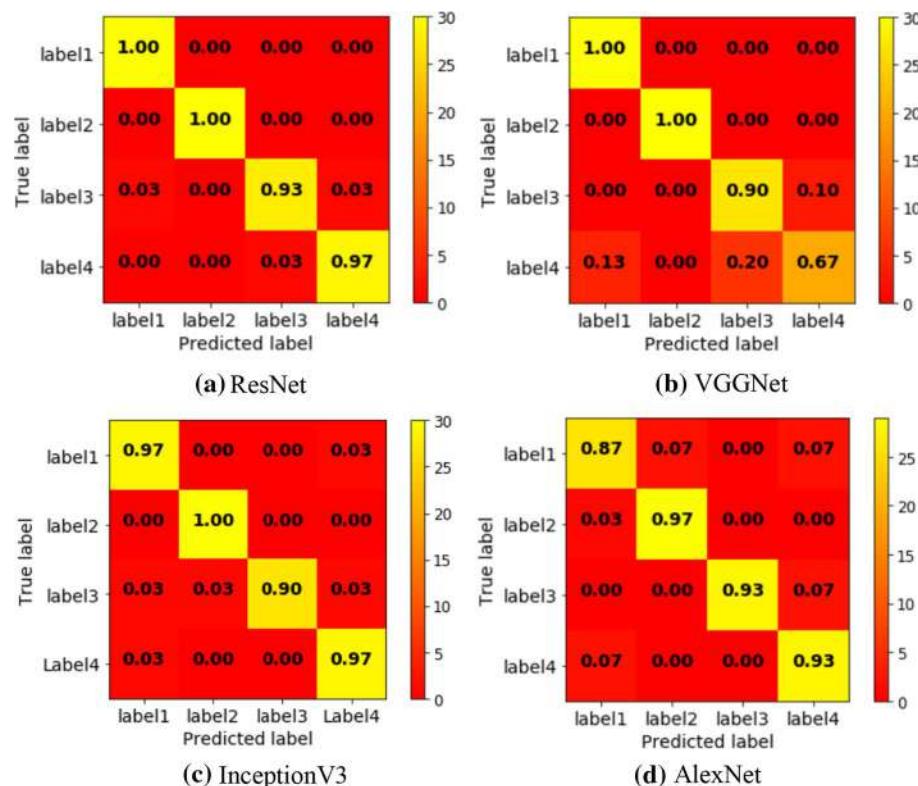


Fig. 11 Confusion matrices of four network architectures for identification of grape lesions

Table 7 Accuracy of identifying lesions in the case of different hyper-parameters

	Iterations	Batch size	Accuracy (%)
512	512	16	92.5
		32	91.67
		64	93.3
1024	1024	16	95
		32	95.83
		64	94.17
2048	2048	16	96.67
		32	97.5
		64	96.67

Bold values are the best result obtained in the test experiments

In the second sub-experiment, different accuracies were achieved in the case of different hyper-parameters by feeding 240 real lesions into trained ResNet as shown in Table 7 where the highest accuracy of 97.5% was obtained in the case of optimal hyper-parameters combination with an iteration of 2048 and a batch size of 32.

Results on comparing the proposed method with the state-of-the-art methods

The proposed three-stage method was compared with the state-of-the-art methods, which consist of single-stage methods and two-stage methods for identification of plant leaf disease as shown in Table 8. Agarwal et al. (2019) proposed a novel CNN architecture to identify grape leaf diseases. Their proposed method, belonging to a single-stage method, was trained on 3251 images from the publicly available PlantVillage dataset and achieved an accuracy of 99%. Ji et al., (2020) merged three deep learning to form a new framework named UnitedModel to identify grape leaf diseases. Their proposed method belonging to a single-stage method was trained in 1619 grape leaf images and achieved an accuracy of 98.57%. Zhu et al. (2019) proposed an automatic method for grape leaf diseases based on back-propagation neural network (BPNN). Their proposed method belonging to a single-stage method was trained in 240 grape leaf images and achieved an accuracy of 91%. Liu et al., (2020) proposed a novel GAN named LeafGAN for augmenting grape leaf disease samples and Xception for identification to identify grape leaf diseases. Their proposed method belonging to a two-stage method was trained in 4062 grape leaf images and achieved an accuracy of 98.7%. In the authors' previous work, a two-stage method was proposed using DCGAN for tomato leaf disease augmentation and GoogLeNet for tomato leaf disease identification. The previous method belonging to a two-stage method was trained in 1500 tomato leaf images and achieved an accuracy of 94.33% (Wu et al., 2020). In order to maintain the same experimental conditions, the previous method, named as DCGAN + GoogLeNet also used 200 images, which is the same as the number of training samples in the proposed three-stage method.

In the single-stage methods, although Agarwal et al. (2019) and Ji et al. (2020) achieved an accuracy of 99% and 98.57%, higher than that of the proposed method, they used sufficient images to train networks, which cannot solve the problem of sparse data. In addition, Although Zhu et al. (2019) used only 240 grape leaf images to train BPNN, the accuracy of identification was low because of the shallow network. Similarly, in the two-stage method, although Liu et al. (2020) achieved an accuracy of 98.7%, they used 4062 images instead of sparse data. The proposed two-stage method in previous work (Wu et al., 2020) achieved

Table 8 Results on comparing our proposed method against the state-of-the-art methods

Study	Classification method	Dataset	Accuracy (%)
Agarwal et al. (2019)	CNN	3251 images	99
Zhu et al. (2019)	BPNN	240 images	91
Ji et al. (2020)	UnitedModel (CNN)	1619 images	98.57
Liu et al. (2020)	LeafGAN + Xception	4062 images	98.7
Wu et al. (2020)	DCGAN + GoogLeNet	200 images	88.75
Proposed method	Faster R-CNN + DCGAN + ResNet	200 images	97.5

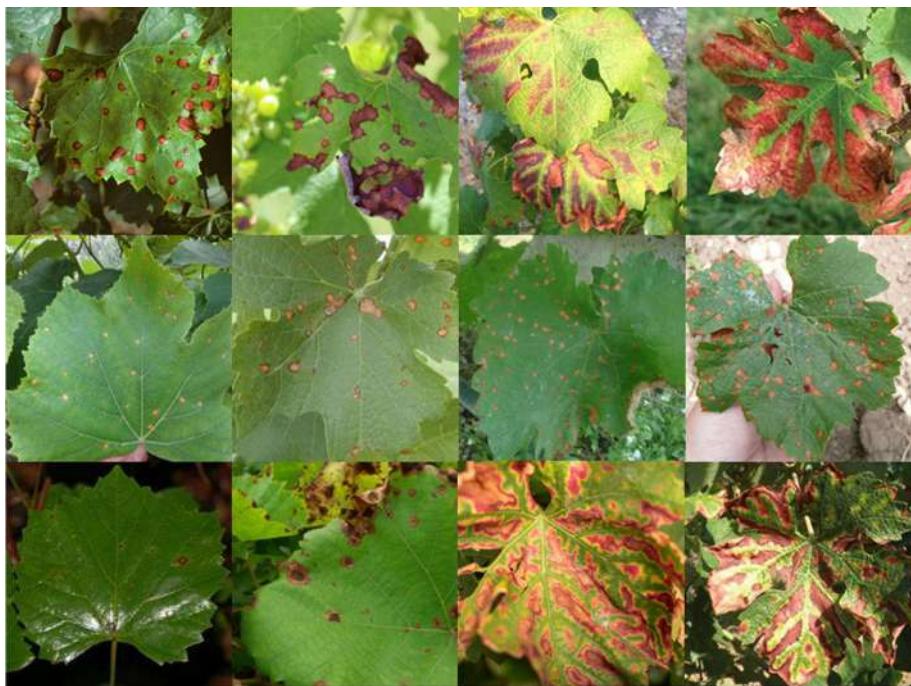


Fig. 12 Grape leaf images from the Internet

Table 9 generalized results of the proposed three-stage method

Model	Accuracy (%)
Faster R-CNN + traditional augmentation + ResNet	67
Faster R-CNN + DCGAN + ResNet	88

an accuracy of only 88.75%. In summary, the proposed three-stage method is superior to single-stage and two-stage methods in the case of sparse datasets and small lesions.

Results on generalization experiments

In the real grape field, the quality of the collected images is mostly affected by the growing environment, the shape of the lesions, lighting, shooting angle, shooting skills and many other factors, which may have an impact on the accuracy of recognition. In order to verify the generalization ability of the proposed method, this experiment used ResNet trained in the grape lesions by Faster R-CNN and DCGAN to identify 100 labeled images randomly selected from the Internet as shown in Fig. 12. Besides, this experiment compared DCGAN with traditional data augmentation method. The result was shown in Table 9. It showed that the proposed three-stage method, named Faster R-CNN + DCGAN + ResNet, achieved an accuracy of 88%, higher than that of the other

three-stage method named Faster R-CNN + Traditional augmentation + ResNet. Experimental results show that the proposed three-stage method has good generalization ability.

Conclusions

This work proposed a three-stage learning-based pipeline with an automatic detection mechanism to locate grape leaf lesions by Faster R-CNN, a data augmentation network to generate new synthetic grape lesion images by DCGAN and an identification network to identify grape leaf diseases by ResNet to solve two problems encountered in identification of grape leaf diseases: (1) small lesions and redundant or blurred background information in the images; (2) sparse datasets and poor diversity. In the lesion detection stage, Faster R-CNN with ResNet101 achieved mAP of 69.74% for detection of lesions, which was greater than mAP of R-CNN, Fast R-CNN and Faster R-CNN with VGG16. In the data augmentation stage, DCGAN achieved GAN-train of 65% and GAN-test of 68%, greater than BEGAN and fusion of DCGAN with BEGAN. In the disease identification stage, ResNet achieved an accuracy of 97.5%, greater than AlexNet, VGG16 and InceptionV3. Compared with the previous single-stage and two-stage method, it has been proved that this three-stage method using leaf lesions as the research object in the disease identification stage is better than that using whole leaves. When tested with images from the internet, the identification accuracy reached 88%, which proved that the method has good generalization.

Acknowledgements This work was supported by the Public Welfare Industry (Agriculture) Research Projects Level-2 under Grant 201503116-04-06; Postdoctoral Foundation of Heilongjiang Province under Grant LBHZ15020; Harbin Applied Technology Research and Development Program under Grant 2017RAQXJ096 and National Key Application Research and Development Program in China under Grant 2018YFD0300105-2.

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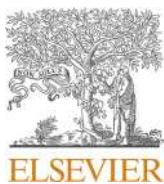
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Diagnosis of grape leaf diseases using automatic K-means clustering and machine learning

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ARTICLE INFO

Keywords:

Artificial intelligence
Deep learning
Disease classification
Grape diseases
Machine vision

ABSTRACT

Plant diseases often reduce crop yield and product quality; therefore, plant disease diagnosis plays a vital role in farmers' management decisions. Visual crop inspections by humans are time-consuming and challenging tasks and, practically, can only be performed in small areas at a given time, especially since many diseases have similar symptoms. An intelligent machine vision monitoring system for automatic inspection can be a great help for farmers in this regard. Although many algorithms have been introduced for plant disease diagnosis in recent years, a simple method relying on minimal information from the images is of interest for field conditions. In this study, a novel image processing algorithm and multi-class support vector machine (SVM) were used to diagnose and classify grape leaf diseases, i.e., black measles, black rot, and leaf blight. The area of disease symptoms was separated from the healthy parts of the leaf utilizing K-means clustering automatically, and then the features were extracted in three color models, namely RGB, HSV, and $l^*a^*b^*$. As an efficient classification method, SVM was used in this study, where principal component analysis (PCA) was performed for feature dimension reduction. Finally, the most important features were selected by the relief feature selection. Gray-level co-occurrence matrix (GLCM) features resulted in an accuracy of 98.71%, while feature dimension reduction using PCA resulted in an accuracy of 98.97%. The proposed method was compared with two deep learning methods, i.e., CNN and GoogleNet, which achieved classification accuracies of 86.82% and 94.05%, respectively, while the processing time for the proposed method was significantly shorter than those of these models.

1. Introduction

Agriculture is the primary source of national income for many countries, including Iran. Crop diseases are serious causes of reducing the quantity and quality of production; therefore, identifying plant diseases are of great importance. Disease symptoms can occur in different parts of the plant; however, plant leaves are commonly used to diagnose diseases [1,2]. Early and accurate diagnosis is a critical first step in mitigating losses caused by plant diseases. An incorrect diagnosis can lead to improper management decisions, such as selecting the unsuitable chemical application, potentially resulting in further health loss and yield reduction [3,4]. The unaided eye method is a traditional method of identifying diseases that requires enormous manpower and is prone to human error, time-consuming, and not applicable for large fields [5]. In addition, it is costly as it requires continuous monitoring by experts. Intelligent disease detection techniques can be beneficial in

detecting a plant disease at the initial growth stages [6].

As a reliable prediction methodology, machine learning can detect various fungal, bacterial, and viral diseases [7,8]. Intelligent detection of plant diseases by utilizing machine learning algorithms is an essential research topic as it may prove advantageous in monitoring large fields and automatically detecting diseases based on symptoms appearing on plant leaves. Advanced technologies can be used to reduce the adverse effects of plant diseases by diagnosing them in early development stages. The application of artificial intelligence and computer vision for the automatic diagnosis of plant diseases is now widely studied because human monitoring of plant diseases is tedious, time-consuming, and challenging [9].

In recent years, there has been a lot of research in the field of machine vision in agriculture, including fruit maturity classification and quality rating [10,11,12], fruit disease diagnosis [13,14], plant pest diagnosis [15–17], plant species classification [18,19], fruit

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	Black measles	Black rot	Leaf blight	Healthy leaf
Leaf image				
Disease symptoms	The symptoms can be identified on the leaves as they take on a tiger-stripe pattern.	Spots on leaves appear as small, tan to reddish-brown circular lesions.	First, it appears as red spots on the upper leaf surface. These circular spots enlarge and become tan to light brown with distinct, dark borders.	No symptoms
Number of images in the dataset	1309	1105	1058	413

Fig. 1. Dataset of healthy and diseased grape leaves and their symptoms.

identification in harvesting robots [20], weed control and recognition [21,22], and disease diagnosis and classification in plant organs [23]. Machine vision can include a variety of sensors, such as color, multi-spectral, and hyperspectral cameras. In typical machine vision applications, illumination used and captured by the sensor is in the visible spectral range.

Al Bashish et al. [24] proposed a framework for detecting and classifying RGB images of leaf and stem diseases for pepper. Their method was investigated for five diseases: early scorch, cottony mold, ashen mold, late scorch, and tiny whiteness. First, a color transformation was conducted, and then, *K*-means clustering was used for segmentation. The color co-occurrence method was applied for feature extraction, and finally, an artificial neural network (ANN) classifier was employed. Ratnasari et al. [25] proposed a system for sugarcane leaf disease detection utilizing RGB images. The proposed system has been verified only on three diseases: rust spot, ring spot, and yellow spot. A combination of color and texture features was used in feature extraction, while SVM was used for classification. In the SVM classifier, four kernel types were tested: linear, quadratic, radial basis function, and polynomial, among which linear kernel provided better results than the others. However, because of the limitations of the segmentation method, only an accuracy of 80% has been achieved. Rastogi et al. [26] developed a machine vision-based technology for maple and hydrangea leaf disease detection and grading. First, preprocessing was performed on leaf RGB images, then segmentation was applied using *K*-means clustering and the Euclidean distance technique. In feature extraction, the GLCM matrix is considered in which contrast, energy, homogeneity, and correlation have been calculated. In this study, ANN has been used for classification. For grading, using total leaf area (AT) and disease area (AD), the percentage of infection has been calculated. After calculating

the percentage of infection, grading has been applied by using fuzzy logic.

Recently, due to the advancement in computing, a large number of artificial neurons are stacked in a specific architecture that forms deep neural networks, and these are capable of learning the features automatically, contrary to the previous approach. These features are used for image classification (in different domains), and this is popularly known as deep learning. One of the deep learning approaches, namely convolutional neural network (CNN), is widely used for image classification [27]. Different CNN-based architectures, i.e., AlexNet, GoogLeNet, ResNet50, etc., have been developed to solve disease classification in various crops [28,29,30,31]. The training from scratch approach requires a large dataset for training as it is a data-driven technique that poses a significant challenge to the researchers. In several studies, authors have used their own developed datasets to classify various crop diseases [32,33]. Cruz et al. [34] presented a novel algorithm for framing a convolutional neural network (CNN) by fusing data at different levels of abstraction to improve the system's performance, which achieved a true positive rate of $98.60 \pm 1.47\%$. They utilized this method for detecting olive quick decline syndrome in olive leaves. Ferentinos [35] adopted a CNN model for disease diagnosis on an open database containing RGB images of 25 different plants. They achieved a 99.53% accuracy in identifying plant diseases. Through testing, Cruz et al. [36] evaluated six ANN architectures showing great potential for image analysis for RGB images of the grapevine yellow disease. They proved that deep learning offers 35.97% and 22.88% better predictive values for recognizing the disease from a baseline system without deep learning and trained humans, respectively.

Generally, it is difficult to compare studies that present emerging techniques for crop disease detection, mainly because they use different

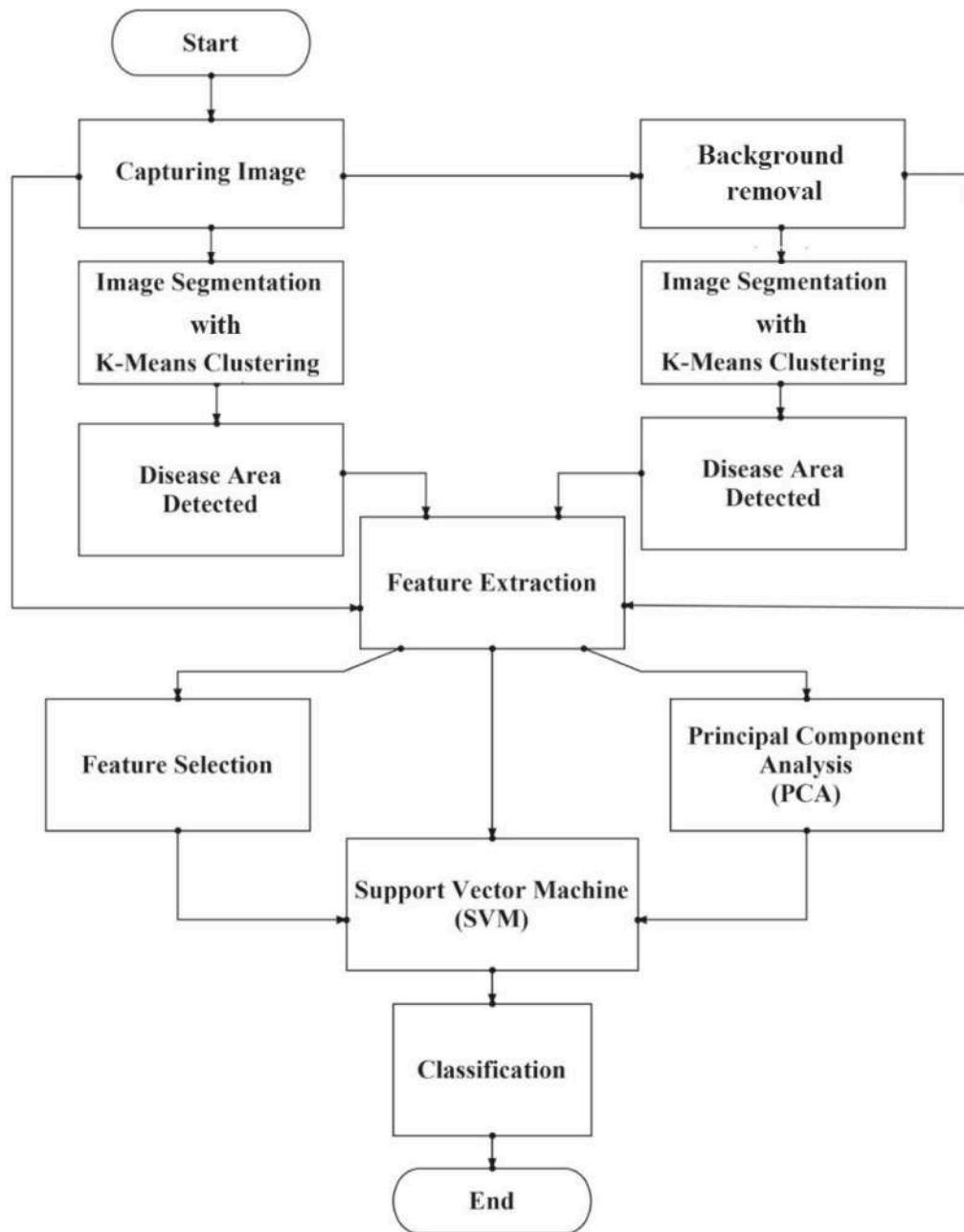


Fig. 2. Flowchart of the proposed methodology for disease detection and classification.

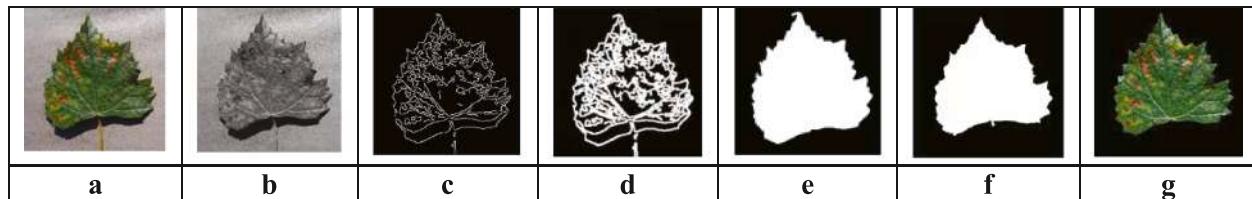


Fig. 3. (a) Image with shadow, (b) extracting green color band from the image, (c) edge detection, (d) morphological dilation to connect edges, (e) filling in the blanks in the edge image, (f) shadow removal based on thresholding, and (g) final image.

sensing systems, datasets, and evaluation metrics (Zhang et al., 2018). One of the limitations when using machine learning models for disease detection is the large and high-quality dataset required for model training and testing. Another challenge is the clustering sensitivity required to diagnose the diseased area(s) for accurate symptom-based

disease detection. This means detecting the region of interest (ROI) requires high precision and sensitivity to achieve the required application and accuracy. In previous research, to separate the diseased area from the leaf, it was necessary to determine the number of clusters before implementing the *K*-means clustering algorithm. Thus *K*-means divides

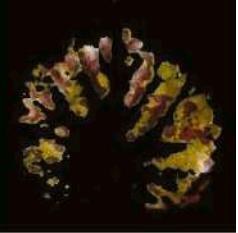
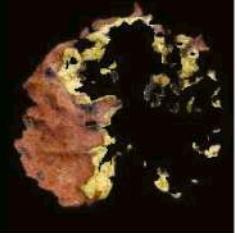
Disease type	Captured image	<i>K</i> -means clustering of the captured image	Removed Background	<i>K</i> -means clustering of the DA with removed background
Black measles				
Black rot				
Leaf blight				
Healthy				

Fig. 4. Preparing and separating the image from the background and detecting the DA.

the data set into a number of predefined clusters. Finding the optimal number of clusters is also a challenging task. Most current machine learning methods are not yet accurate, precise, and robust enough to be adopted for diagnosing plant diseases in the field and point-of-care situations. They also require a long time to diagnose leaf disease due to not separating either the diseased part or the background from the original image.

Furthermore, most machine learning and deep learning methods introduced cannot determine the most effective features extracted from images of diseased crops for disease classification. In fact, the machine learning and deep learning models are somehow black-box [37], and there is no clear explanation for better classification accuracies achieved when different methods/models are used [38,39]. One of the most critical challenges in disease detection is classifying a plant infected with multiple diseases (or disorders). Another challenge is identifying and classifying diseases with similar symptoms, especially in early disease development stages [40]. Therefore, it seems that a comprehensive

system should be developed to extract features for accurate disease diagnosis and classification, especially when comparing diseases and disorders with similar symptoms. This study aims to address this challenge by developing a methodology to classify multiple grape leaf diseases (black measles, black rot, leaf blight, and healthy leaves) utilizing RGB image processing-based feature extraction and multi-class SVM classification. The performance of the proposed method was compared with two well-known deep learning algorithms, i.e., CNN and GoogLeNet, to investigate the efficiency of the method.

2. Material and methods

In order to develop accurate image classifiers to diagnose plant diseases, a large verified data set of images of diseased and healthy plants is required. Until very recently, such a dataset did not exist, and even smaller datasets were not freely available. So, researchers had to create datasets by themselves [41]. In this study, the PlantVillage dataset, as a

Table 1

Description of the extracted features for disease detection and classification.

Feature	Description	Formula	Reference
Contrast	The measure of the difference between the brightness of the objects or regions and other objects within the same field of view	$\sum_{ij} i - j ^2 p(i, j)$	Haralick et al. [46]
Correlation	The measure of degree and type of relationship between adjacent pixels	$\frac{\sum_{ij} (i - \mu_i)(j - \mu_j)p(i, j)}{\sigma_i \sigma_j}$	Haralick et al. [46]
Energy	The sum of squared elements in the gray level co-occurrence matrix	$\sum_{ij} p(i, j)^2$	Haralick et al. [46]
Homogeneity	the closeness of the distribution of elements in the GLCM	$\sum_{ij} \frac{p(i, j)}{1 + i - j }$	Haralick et al. [46]
Mean	The measure of the average intensity value of the pixels present in the region	$\frac{1}{n} (\sum_{i=1}^n X_i)$	Haralick et al. [46]
Standard Deviation	The measure of how much the gray levels differ from the mean	$\sqrt{\frac{1}{n} (\sum_{i=1}^n (X_i - \bar{X})^2)}$	Haralick et al. [46]
Entropy	The measure of differences in gray levels	$E = \sum(p_i * \log_2(p_i))$	Haralick et al. [46]
Root Mean Square (RMS)	The measure of root mean square value of an image	$X_{RMS} = \sqrt{\frac{1}{N} \sum_{n=1}^N X_n ^2}$	Haralick et al. [46]
Variance	The measure of variance value of an image	$\frac{1}{n} (\sum_{i=1}^n (X_i - \bar{X})^2)$	Haralick et al. [46]
Smoothness	A measure of relative smoothness of intensity in a region	-	Haralick et al. [46]
Kurtosis	A measure of peaks distribution related to the normal distribution	$K = \frac{E(x - \mu)^4}{\sigma^4}$	Haralick et al. [46]
Skewness	A measure of asymmetry in a statistical distribution	$S = \frac{E(x - \mu)^3}{\sigma^3}$	Haralick et al. [46]
Inventive Design Method (IDM)	The measure of the closeness of the distribution of GLCM elements to the GLCM diagonal	-	Haralick et al. [46]
Local binary patterns (LBP)	measure and extract the local texture information of images	$\sum_{i=0}^{p-1} s(n_i - G_C) 2^i$ $sx = \begin{cases} 1 & x > 0 \\ 0 & \text{otherwise} \end{cases}$	Sairamya et al. [47]
Histogram of Oriented Gradients (HOG)	histograms of edge orientation	-	Zhou et al. [48]
Harris	An algorithm for extracting corners and inferring features of an image	-	Gong et al. [49]
Binary Robust Invariant Scalable Keypoints (BRISK)	An algorithm for feature point detection and description algorithm with scale invariance	-	Kashif et al. [50]

Table 1 (continued)

Oriented FAST and Rotated BRIEF (ORB)	and rotation invariance	-	Ma et al. [51]
MSER	An algorithm for extracting the number of co-variant regions in an image	-	Fouad et al. [52]
Hough	An algorithm to find imperfect instances of objects within a certain class of shapes by a voting procedure	-	Kazhagamani et al. [53]

freely-available dataset, was used. The present study involved three types of plant diseases in addition to healthy leaves, which made four classes in total (Fig. 1).

2.1. Proposed algorithm

The proposed methodology applied in this work is depicted in Fig. 2. It includes (1) background removal, (2) image segmentation for detecting the disease symptoms (i.e., DA) using K -means clustering, (3) feature extraction, (4) feature selection, (5) feature dimension reduction, and finally, (6) multi-class SVM classification. The proposed methodology is described below in detail. This process was performed for two datasets, i.e., without background and with background, to check the classification accuracy and processing time. This operation was performed to determine the importance of the presence or absence of seismicity in image classification and reliable disease identification. For this purpose, the background will first be removed from the leaf to obtain two sets of data.

Background removal. This step involves removing the background to prevent any possible bias in the extracted properties and the trained framework. Color cast removal is performed by normalizing the gray values of three-color channels separately. The background removal task needs to be performed automatically, free from any human influence to increase its usability. It can be performed in two ways: pixel clustering and edge detection. In this study, a combination of both methods was used: gray-level thresholding for pixel clustering and the Canny method for edge detection. A critical challenge that occurs in images in real and natural conditions is the presence of shadows [42]. Fig. 3(a) shows a leaf with a shadow and a background. In the plant leaf images, the green color band is often dominant, so by extracting the green band, Fig. 3(b) can be obtained. Edge detection was then performed using the Canny algorithm, and then the pixel size of the edges was morphologically dilated to connect the borders. Figs. 3(c) and 3(d) show the edges extracted from the image. In the next step, the empty spaces in the image were filled. As shown in Fig. 3(e), the resulting image still had a shadow. In this step, by removing the shadow color pixels using gray-level thresholding, the shadow was omitted (Fig. 3f). The final image of a leaf without a background is shown in Fig. 3(g).

Image segmentation. Image segmentation is the process of dividing an image into several parts. There are various methods for image segmentation, ranging from simple thresholding methods to advanced color and frequency-domain image segmentation methods [6,43]. The Otsu algorithm and K -means method are among the reliable image segmentation processes for image thresholding due to their simple calculation process and methodology [44].

K -means clustering. The K -means clustering is used to classify objects based on a set of features into K number of classes. The classification of objects is done by minimizing the sum of the squares of the distance between the object and the corresponding cluster. The

Table 2

Grape disease classification results of the SVM method.

	Input images	Features	Color bands	SVM Kernel Function			
				Linear	Polynomial	Radial Basis Function	Sigmoid
1	Captured image	GLCM	RGB-HSV-L*a*b	0.9472	0.5984	0.8553	0.779
2	K-means clustering of the captured image			0.9678	0.7082	0.9142	0.8848
3	Images without background			0.9781	0.7006	0.9168	0.8012
4	K-means clustering of DA without background			0.9871	0.7425	0.9197	0.8922
5	Captured image	HOG	RGB-HSV-L*a*b	0.7622	0.4677	0.6134	0.5367
6	K-means clustering of the captured image			0.7931	0.3501	0.6803	0.5776
7	Images without background			0.7815	0.5284	0.6862	0.5696
8	K-means clustering of DA without background			0.8860	0.3719	0.8422	0.7979
9	Captured image	LBP	RGB-HSV-L*a*b	0.8345	0.3640	0.6525	0.5683
10	K-means clustering of the captured image			0.6008	0.3467	0.4605	0.3964
11	Images without background			0.8595	0.4098	0.6891	0.6422
12	K-means clustering of DA without background			0.7107	0.3411	0.4618	0.4698
13	Captured image	Harris, BRISK, ORB, MSER, Hough (line length and point number) and Histogram	RGB-HSV-L*a*b	0.3254	0.3254	0.3254	0.3254
14	K-means clustering of the captured image			0.3045	0.3045	0.3045	0.3045
15	Images without background			0.2937	0.2937	0.2937	0.2937
16	K-means clustering of DA without background			0.2965	0.2965	0.2965	0.2965

algorithm for K -means clustering can be described by these steps: (1) picking the center of K -th cluster either randomly or based on some heuristics; (2) assigning each pixel to a cluster that minimizes the distance between the pixel and the cluster center; (3) computing the cluster centers by averaging all the pixels in the cluster; and finally, (4) repeating steps 2 and 3 until convergence is obtained [45]. Generally, in the mentioned steps, the selection of the value of K and the selection of ROI are performed manually, which depends on the user's skill, and sometimes ROI might not be selected correctly by the user. This means that for each number of images in the database, the ROI number must be manually selected to determine the desired area of the disease, so this is very time-consuming and error-prone. Therefore, automatic clustering can be useful for the automatic diagnosis of the disease area in the plant leaves. In this study, K -means clustering was used to automatically separate the disease symptoms from the "healthy" areas of a leaf. Therefore, the ROI in the K -means clustering, which had to be selected by the user in other methods, was determined automatically. This was done by thresholding between the color of the disease area (i.e., symptoms) and the color of the healthy leaf area. For this purpose, in the leaf image, the pixels in which the red color is less than the blue and green values were masked out. Therefore, in the rest of the image, only the diseased area of the leaf will remain. Fig. 4 shows the steps of preparing and separating the image from the background and detecting the DA of grape leaves.

Feature extraction. An image contains a remarkable amount of information, and usually, only some information is needed to distinguish objects in images, for example, texture, color, and shape [5]. In this study, several features such as gray-level co-occurrence matrix (GLCM), local binary patterns (LBP), histogram of oriented gradients (HOG), Harris corner detection, binary robust invariant scalable key-points (BRISK), oriented fast and rotated BRIEF (ORB), maximally stable external regions (MSER), Hough transform data, in three bands, i.e., RGB, HSV, and L*a*b were extracted. Color bands vary in color, brightness, and composition. The algorithms used in the field of machine vision are different in that they are based on the properties of color,

brightness, and composition. For example, an image-based algorithm distinguishes between different sections and thresholds based on color values; therefore, in this research, the three color bands of RGB, HSV, and L*a*b have been used. A description of the extracted features is given in Table 1.

The features were categorized into four groups: (1) GLCM; (2) HOG; (3) LBP; and (4) Harris, BRISK, ORB, MSER, and Hough (line length and point number). The features were extracted from four groups of images, including the captured image (Group 1), K -means clustering of the captured image (Group 2), images without background (Group 3), and K -means clustering of the DA without background (Group 4) (Fig. 4). Finally, each group of features that were extracted was examined more carefully and the most important and best features will be selected from that group.

Principal component analysis (PCA). PCA is a dimensionality reduction that is often used to reduce the dimension of the variables of a larger dataset that is compressed to the smaller one, which contains most of the information to build an efficient model. The justification behind the use of PCA is its versatility and simplicity in real-time implementations. PCA helps to efficiently remove correlated features in a dataset, resulting in the components being independent of one another, which further reduces training time when subjected to machine learning algorithms. Also, since the most significant features are selected efficiently, PCA reduces the chances of overfitting. The high dimensional dataset is converted into low dimensions when PCA is used, and hence, it becomes easy to visualize its nature in a 2D plot and derive inferences [54,55]. Therefore, the data were analyzed in two stages: one after feature extraction and the other after feature selection so that the results can be compared.

Feature selection. Feature selection aims to better classification results by listing significant features, which helps in reducing computational overload. The reason behind the feature selection is that classifiers trained on reduced feature space are more robust and reproducible than classifiers constructed on the original large feature space. In feature selection, the most important feature(s) for predicting a

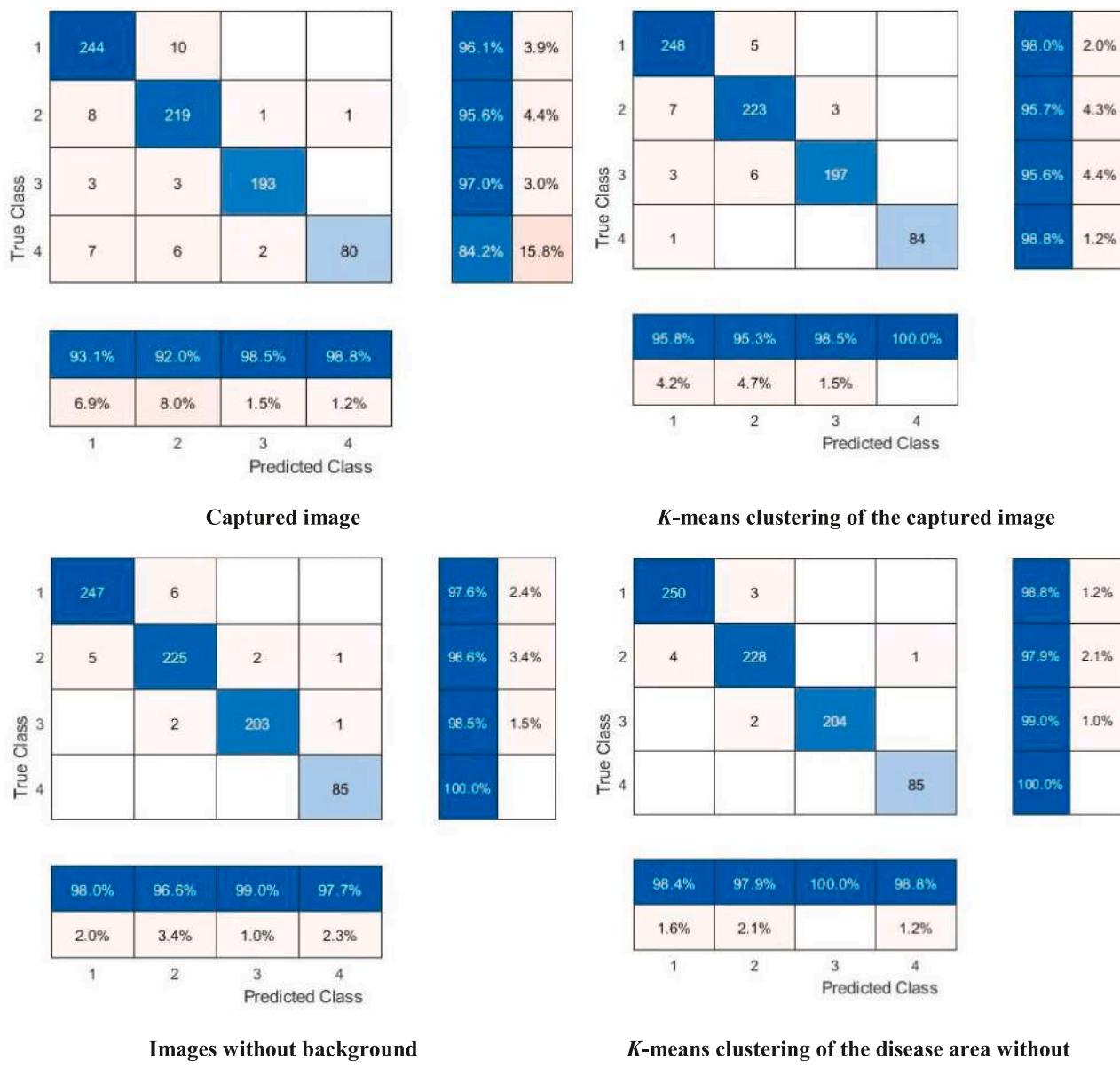


Fig. 5. Confusion matrix for grape leaf disease detection utilizing SVM linear kernel function.

variable (e.g., disease, yield, etc.) is identified [56]. The features which do not provide helpful information are called irrelevant features, and the features which do not provide more information than the currently selected features are called redundant features [57]. The features that are unrelated or uncorrelated to class variables are called noise, introducing bias in prediction and reducing classification performance. Hence, noise should be handled to improve prediction performance, and it can be made possible with dimensionality reduction. It can be achieved by either feature extraction or feature selection [58]. Many feature selection methodologies have been proposed, and research continues to support the claim that there is no universal “best” method for all tasks [54]. In this research, the Relief feature selection method was used to select the best and essential features for diagnosing grape leaf diseases.

Relief feature selection. In the Relief feature selection method, at each step and randomly, a sample is selected from the samples in the data set. Then, the degree of relevance of each feature is updated based on the difference between the selected sample and the two neighboring samples. If one of the selected sample properties differs from a similar

feature in the neighboring sample of the same class (hit sample), the score of this feature decreases. On the other hand, if the same feature in the selected instance differs from the similar feature in the neighboring instance of the opposite class (miss sample), the score of this feature increases.

Support Vector Machine (SVM). Various machine learning approaches, e.g., neuron-based and kernel-based methods, help predict and classify various diseases from the input plant leaf images of different plants [59]. SVM is a widely used supervised learning classification algorithm that utilizes various types of kernel functions. In this study, several kernel functions such as linear, polynomial, radial basis function (RBF), and sigmoid functions were investigated to diagnose and classify diseased and healthy leaves, and a confusion matrix was created for each result. Finally, the best algorithm was selected in terms of efficiency and accuracy for the diagnosis and classification of grape diseases.

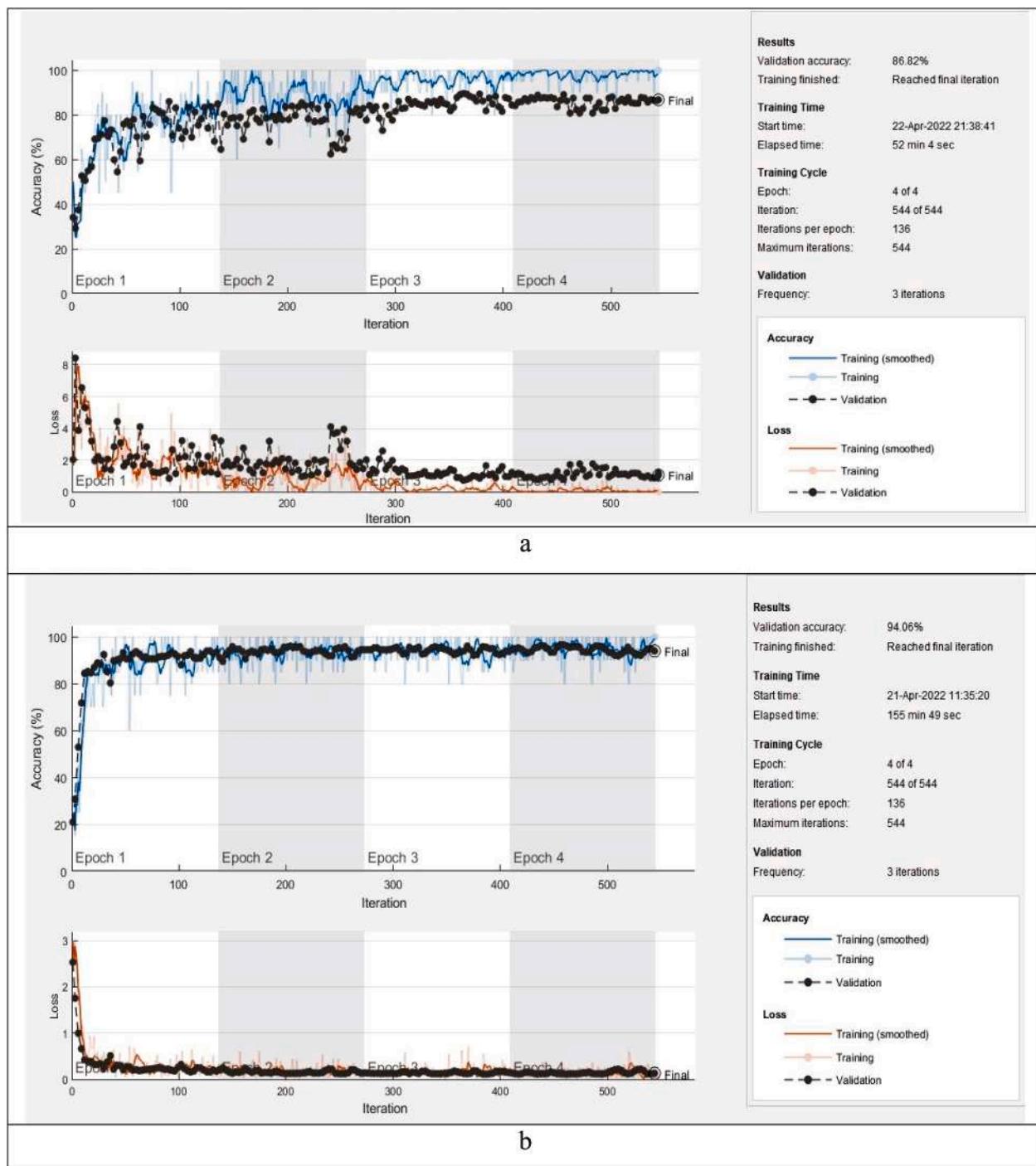


Fig. 6. Training plot for (a) CNN; (b) GoogleNet.

2.2. Deep learning methods

In this study, the proposed machine learning method was compared with two deep learning-based classifiers, i.e., CNN and GoogleNet, in terms of classification accuracy and duration of disease diagnosis. CNN and GoogleNet are freely accessible on the GitHub website (www.github.com). They implemented in MathWorks MATLAB R2010b programming environment considering the default values for the parameters of learner layers.

2.3. Performance evaluation indicators

Confusion matrices of the prediction process were used to evaluate the success and efficiency of disease diagnosis systems. A confusion matrix is a summary of prediction results on a classification problem. The number of correct and incorrect predictions are summarized with count values and broken down by each class. In this study, accuracy was used to evaluate the performance of models. The accuracy of a classification method on test data is the percentage of observations of the test set that is correctly categorized by the model used (Eq. (1))



Fig. 7. Confusion matrix of deep learning methods (a) CNN, (b) GoogLeNet.

$$\text{Accuracy} = \frac{(TP + TN)}{(TP + TN + FP + FN)} \quad (1)$$

where TP is the number of true positives, TN is the number of true negatives, FP is the number of false positives, and FN is the number of false negatives. The processing time reported in this study was based on the time consumed for five-fold cross-validation.

3. Results

3.1. Classification results using support vector machine

After extracting the features for four groups of images, including captured image, K-means clustering of the captured image, images without background, and K-means clustering of the disease area without background, the results of Table 2 were obtained using SVM. In this table, for the GLCM feature, a feature group (contrast, correlation, energy, homogeneity, mean, standard deviation, entropy, RMS, variance, smoothness, kurtosis, skewness, and IDM) was extracted from each group of images. Moreover, another group of features, including LBP and HOG features, and finally, Harris, BRISK, ORB, MSER, and Hough (line length and point number) feature groups were extracted from the images. In order to classify with the SVM, four kernel functions (linear, polynomial, radial basis function, and sigmoid) were used to obtain the classification accuracy for each of the feature groups.

According to Table 2, the highest accuracies were obtained for the GLCM features and the SVM with linear kernel function, which were 0.9472, 0.9678, 0.9781, and 0.9871 for the raw captured image, K-means clustering of the captured image, Images without background, and K-means clustering of DA without background, respectively (first to fourth rows of Table 2). The processing time for training of these algorithms were 365.22, 337.68, 267.78, and 187.8 s, respectively. The processing time obtained shows that the algorithm, after separating the background and the disease area from the original image, can achieve high leaf disease detection accuracy in a very short time. It can also be observed that removing the background from the raw image increases the algorithm's accuracy. This might be due to the fact that using K-means clustering increased the ability to diagnose the disease. The

highest accuracy was achieved by the "K-means clustering of DA without background" algorithm (Row 4 in Table 2), which removes both the background and the DA from the leaf. The processing time of disease diagnosis in this algorithm (187.8 s) was significantly less than the others (267-365 s).

Fig. 5 depicts the confusion matrices of this classification. In this matrix, the rows represent the true class of the samples, while each column represents the predicted classes. The diagonals show the number of samples which have been classified correctly. The class numbers for Black measles, Black rot, Leaf blight diseases were 1, 2 and, 3, respectively, and for Healthy leaves were 4. In this experiment, 2,861 images were used for training and 1024 images for testing.

3.2. Classification results with Convolutional Neural Network (CNN) and GoogleNet

To classify the three groups of disease and healthy leaf data, two deep learning classification method was used to be compared with the method introduced in this study. The prediction accuracy using these deep learning models, i.e., CNN and GoogleNet, were 0.8682 and 0.9405, respectively. The learning rate remained constant for the entire training of all the models. The training plot for the two models is shown in Fig. 6. The time taken for the training of the dataset using CNN and GoogleNet were approximately 53 and 156 min, respectively. Fig. 7 depicts the confusion matrices of the deep learning models in the classification task. According to the results, not only the prediction accuracy of deep learning methods was not favorable, but they are also highly time-consuming.

3.3. Result of feature dimension reduction

In this study, the PCA and SVM methods were used to classify grape leaf diseases based on the extracted color features, shape features, and texture features from disease images and their combined features. After reducing the dimensions of the data using PCA, acceptable prediction accuracies for image recognition could be obtained using the SVM as a classifier. Table 3 shows the results of the PCA of the classified output of grape leaves using SVM. The highest accuracies were obtained for the GLCM features, which were 0.9601, 0.9704, 0.9871, and 0.9897 (first to

Table 3

Grape disease classification result of the PCA and SVM combination.

Number	Input images	Features	Color Bands	Kernel Function
1	Captured image	GLCM	RGB-HSV-1*a*b	Linear 0.9601
2	K-means clustering of captured image			0.9704
3	Images without background			0.9871
4	K-means clustering of the disease area without background			0.9897
5	Captured image	HOG	RGB-HSV-1*a*b	0.8077
6	K-means clustering of the captured image			0.8208
7	Images without background			0.8237
8	K-means clustering of the disease area without background			0.8891
9	Captured image	LBP	RGB-HSV-1*a*b	0.8486
10	K-means clustering of the captured image			0.6564
11	Images without background			0.8620
12	K-means clustering of DA without background			0.6577
13	Captured image	Harris, BRISK, ORB, MSER, Hough (line length and point number), and Histogram	RGB-HSV-1*a*b	0.4604
14	K-means clustering of the captured image			0.2942
15	Images without background			0.3318
16	K-means clustering of the disease area without background			0.3326

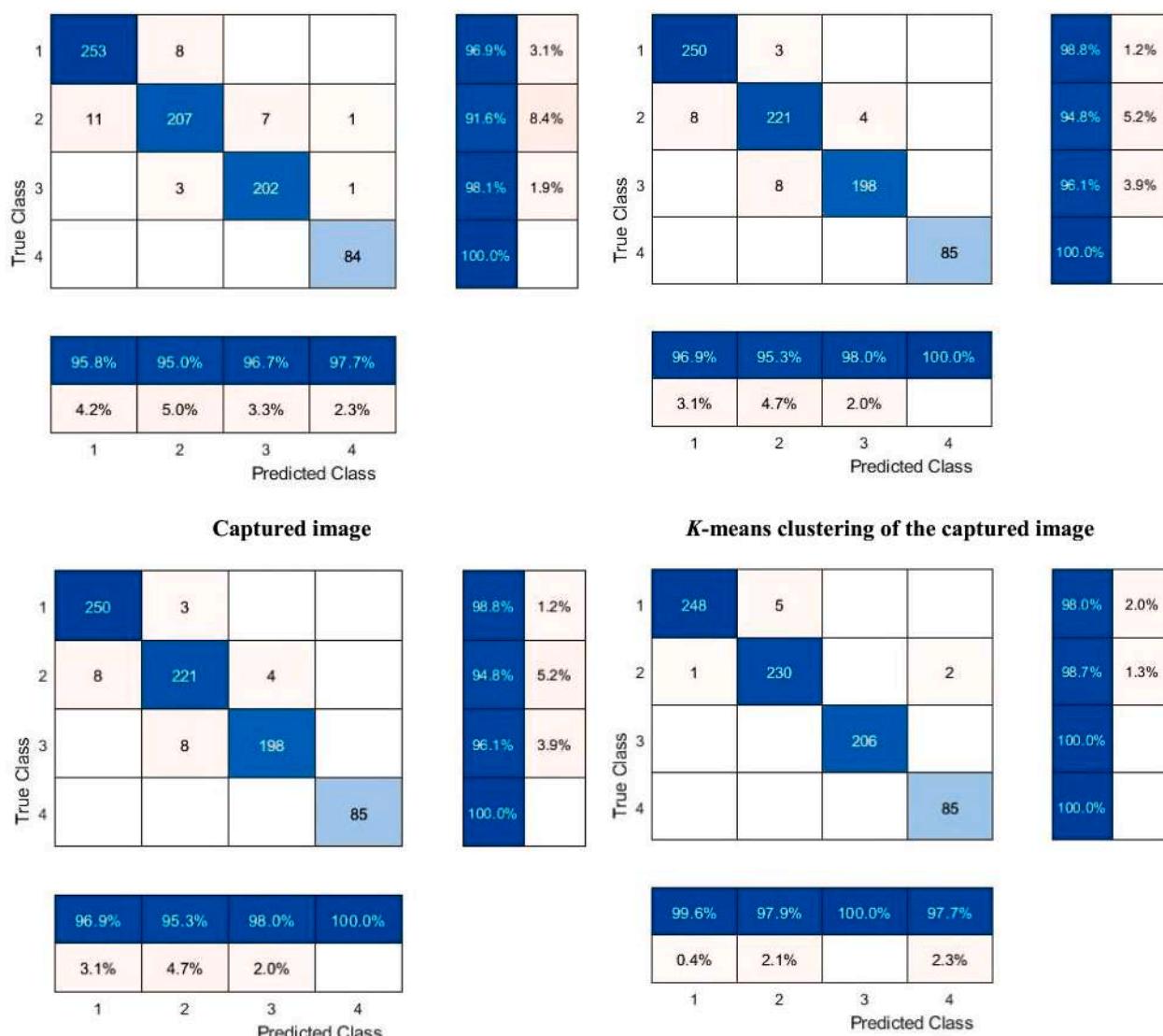


Fig. 8. Confusion matrix for grape leaf diseases detection utilizing PCA and SVM linear kernel function.

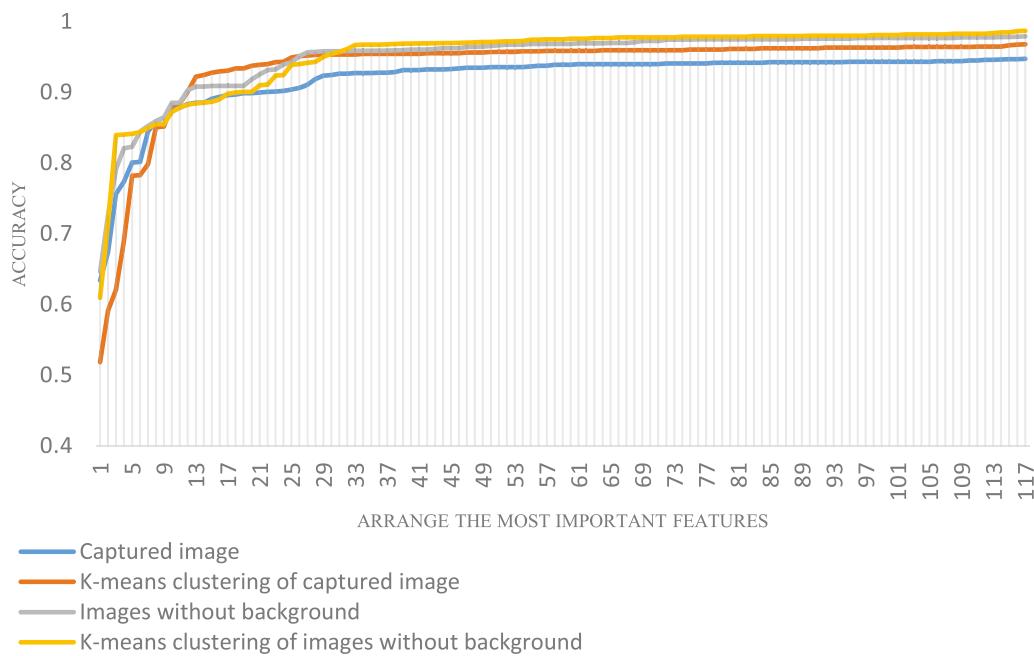


Fig. 9. The order of the selected features for various image groups for disease detection.

fourth rows of Table 3), with processing times of 351.02, 260.28, 120.69, and 96.38 s, respectively. Fig. 8 depicts the confusion matrices of the classification. As the results showed, reducing the dimensions of the feature data extracted from the images of grape leaf diseases could reduce the running time of the classification, and acceptable detection results could be obtained. In the practical application, PCA could be used to reduce the dimensions of the data extracted from the leaf disease images, and then SVM classification could be constructed for leaf disease detection. The method used in this study could also be used for the image recognition of other plant leaf diseases.

3.4. Results of the feature selection

As can be seen in Table 3, the highest accuracy for diagnosing and classifying grape leaf diseases belongs to the use of the GLCM features group. Therefore, in this section, the most effective/important features for disease classification are presented. Among the 117 features extracted from the images in four groups, the most effective/important features that played a role in diagnosing the disease were selected by the Relief method. Then, SVM was used again for disease detection using only the important features. Fig. 9 shows the order of the selected features. The accuracy of the algorithms that used *K*-means clustering is higher than the other algorithms. It was also found that the algorithm which removes the background of the leaf image and can separate the DA from the leaf was more accurate. In the next step, some of the most important features were selected. The number of these features was obtained based on reaching a prediction performance with a maximum of 2% difference from the highest accuracy. Table 4 lists the number of these features for each group, as well as the accuracy of diagnosing the disease for the same number separately. For groups 1, 3, 2 and 4 the accuracies were 0.9282, 0.9484, 0.9585, and 0.9673, respectively. The estimated time to reach the accuracy of 0.9673 using the most important features shown in Table 4 was 54.6 s, representing a 60% reduction in time compared to the use of all 117 extracted features. An essential advantage of this technique, compared to previous studies, is that by developing an automatic clustering algorithm and also by removing the

background from the original image, the algorithm was able to accurately diagnose the disease in less time. This can be seen in the yellow line compared to other lines (Fig. 9). This diagram shows that the proposed algorithm with a lower number of features has the ability to diagnose the disease with high accuracy in a faster time.

4. Discussion

Non-destructive methods, such as image processing, are emerging solutions for the intelligent diagnosis and classification of plant diseases. Although biochemical methods at the molecular level can accurately detect plant diseases, they are extremely labor- and time-consuming [60–62]. When evaluating disease classification techniques, the type and number of diseases that can be detected and the ability to diagnose diseases with similar symptoms should be considered. Since the goal of a disease detection algorithm is to identify a pattern for achieving the highest possible classification rate for disease diagnosis, factors such as the accuracy of diagnosis and classification of diseases, the shortest possible time to diagnose a disease (for real-time applications), and the determination of the important features, extracted from the collected images, for disease detection should be compared and discussed too. Table 5 compares several previous methods with this study for grape leaf disease detection, presenting detection accuracies and limitations. According to the table, limitations such as low accuracy and long diagnosis time, the number of diseases classified, uncommonness and similarity of diseases, the uncertainty of the extracted features, and selection of the most important features can be seen in previous research. Although deep learning techniques, which are black-box methods (the inputs and operations are not visible to the user), might result in promising performance, they require a high number of training samples, and the effective features for disease diagnosis are not specified [63]. Therefore, an accurate deterministic algorithm is considered in this study for diagnosing and classifying diseases with similar symptoms in grapes. The proposed novel algorithm was compared with two deep learning methods, CNN and GoogleNet, which are widely used methods in the classification of plant leaf diseases, and the results showed that the algorithm proposed

Table 4

The best and most important selected features for the four groups of algorithms.

Number	Feature	Color Band	Feature	Captured image		K-means clustering of the captured image	Image without background	K-means clustering of the disease area without background
				Accuracy	0.9282			
1	Energy Homogeneity	HSV (H)	Skewness	l^*a^*b (a)	Energy	HSV (H)	Skewness	l^*a^*b (a)
2		HSV (H)	Standard Deviation	l^*a^*b (a)	Entropy	HSV (H)	Kurtosis	l^*a^*b (a)
3	Kurtosis	l^*a^*b (a)	Entropy	l^*a^*b (a)	Homogeneity	HSV (H)	Standard Deviation	l^*a^*b (a)
4	Standard Deviation	l^*a^*b (a)	Mean	l^*a^*b (a)	Kurtosis	RGB (R)	Correlation	l^*a^*b (b)
5	Variance	l^*a^*b (a)	Variance	l^*a^*b (a)	Variance	l^*a^*b (a)	Correlation	RGB (B)
6	Contrast	l^*a^*b (b)	Skewness	l^*a^*b (b)	Kurtosis	RGB (B)	Variance	l^*a^*b (a)
7	Variance	HSV (H)	Energy	HSV (S)	Contrast	l^*a^*b (a)	Correlation	RGB (G)
8	Entropy	HSV (S)	Energy	HSV (H)	Skewness	RGB (B)	Correlation	RGB (R)
9	Mean	l^*a^*b (a)	Contrast	l^*a^*b (l)	Skewness	RGB (R)	Correlation	HSV (V)
10	Mean	HSV (H)	Contrast	HSV (H)	Kurtosis	l^*a^*b (a)	Contrast	l^*a^*b (a)
11	Contrast	HSV (H)	Contrast	l^*a^*b (a)	Standard Deviation	l^*a^*b (a)	Smoothness	l^*a^*b (a)
12	Energy	HSV (S)	Kurtosis	l^*a^*b (a)	Kurtosis	l^*a^*b (b)	Skewness	RGB (R)
13	Entropy	l^*a^*b (b)	Energy	l^*a^*b (b)	Kurtosis	RGB (G)	Skewness	HSV (V)
14	Contrast	l^*a^*b (a)	Homogeneity	l^*a^*b (l)	Kurtosis	l^*a^*b (l)	Mean	l^*a^*b (a)
15	Homogeneity	l^*a^*b (a)	Standard Deviation	l^*a^*b (b)	Kurtosis	HSV (V)	Smoothness	RGB (R)
16	Standard Deviation	HSV (H)	Entropy	HSV (H)	Correlation	RGB (R)	Smoothness	HSV (V)
17	Skewness	l^*a^*b (b)	Homogeneity	l^*a^*b (a)	Standard Deviation	HSV (H)	Homogeneity	l^*a^*b (b)
18	Kurtosis	l^*a^*b (b)	Skewness	HSV (S)	Skewness	l^*a^*b (b)	Skewness	RGB (B)
19	RMS	HSV (H)	Standard Deviation	HSV (S)	Variance	HSV (H)	Energy	HSV (H)
20	Entropy	l^*a^*b (a)	Entropy	l^*a^*b (B)	Standard Deviation	HSV (S)	Smoothness	RGB (B)
21	Energy	HSV (H)	Mean	HSV (H)	Correlation	l^*a^*b (a)	Skewness	RGB (G)
22	Energy	l^*a^*b (b)	Energy	l^*a^*b (a)	Mean	l^*a^*b (a)	Smoothness	HSV (H)
23	Correlation	HSV (S)	IDM	l^*a^*b (a)	Kurtosis	HSV (S)	Correlation	l^*a^*b (a)
24	Correlation	l^*a^*b (l)	Kurtosis	l^*a^*b (b)	Energy	l^*a^*b (a)	Kurtosis	HSV (S)
25	Kurtosis	RGB (B)	Correlation	HSV (S)	Contrast	l^*a^*b (b)	Homogeneity	l^*a^*b (l)
26	Skewness	RGB (B)	-	-	IDM	l^*a^*b (a)	Kurtosis	RGB (R)
27	Homogeneity	l^*a^*b (b)	-	-	Homogeneity	HSV (V)	Kurtosis	HSV (V)
28	Entropy	RGB (B)	-	-	Standard Deviation	RGB (B)	Energy	l^*a^*b (a)
29	IDM	l^*a^*b (a)	-	-	Homogeneity	RGB (R)	Entropy	l^*a^*b (b)
30	Correlation	l^*a^*b (a)	-	-	Homogeneity	RGB (G)	Skewness	HSV (H)
31	Kurtosis	HSV (S)	-	-	-	-	Standard Deviation	RGB (R)
32	IDM	HSV (H)	-	-	-	-	Smoothness	HSV (S)
33	Skewness	HSV (S)	-	-	-	-	Kurtosis	HSV (H)
34	-	-	-	-	-	-	Skewness	HSV (S)

in this study had a higher detection accuracy with a less processing speed. The advantages of the proposed algorithm are as follows:

- using the automatic ROI selection to cluster the disease area, there is no need for user input at the time of segmentation. The proposed method is fully automated, while other methods require user input to select the best input image segmentation;
- increasing the classification accuracy using the proposed algorithm;

- having the ability to develop detection algorithms for more diseases as well as classifying diseases accurately with similar symptoms;
- identifying the most effective features in diagnosing and classifying diseases;
- reducing the time for algorithm training;
- achieving higher accuracy and reduced classification time compared to the CNN and GoogleNet deep learning methods;
- and reducing the diagnosis time using the proposed algorithm.

Table 5

A comparison of the methods, accuracy, and limitations of previous research and the present study for grape leaf diseases.

Diseases	Methods	Accuracy	Limitation	Reference
Downy, Powdery	K-Means Clustering - SVM Classifier	88.89%	Low number of diseases, low detection accuracy, does not extract all the features from the image, does not select the most effective features, common diseases in grape leaves have not been studied	Padol et al. (2016)
Black Rot, Black Measles, and Leaf Blight	SVM Classifier	93%	It does not extract all the features from the images, does not select the most effective features	Jaisakthi et al. (2019)
Black Measles	SVM Classifier	97. 2%	A low number of diseases does not extract all the features from the image and also does not specify the most effective features extracted	Singh et al. (2020)
Black Rot, Black Measles, and Isariopsis	AlexNet GoogLeNet ResNet-18	95.65% 92.29%	Using a black-box method, being time-consuming, does not select the most effective features	Lauguico et al. (2020)
Anthracnose, Brown Spot, Mites, Black Rot, Downy Mildew, and Leaf Blight	DICNN - CNN	89.49% 97.22%	Using a black-box method, being time-consuming, does not select the most effective features	Liu et al. (2020)
Black rot, Esca measles, Leaf spot	GAN - CNN	98.70%	Using a black-box method, being time-consuming, not select the most effective features	Liu et al. (2020)
Black Rot, Esca and Isariopsis Leaf Spot	UnitedModel - CNN	99.17%	Using a black-box method, being time-consuming, not selecting the most effective features	Ji et al. (2020)
Black Rot, Black Measles, Leaf Blight, and Mites	DR-IACNN	81.1%	Low detection accuracy, uses a black-box method, being time-consuming, does not select the most effective features	Xie et al. (2020)
Black Rot, Black Measles, and Leaf Blight	AlexNet MobileNet MobileNet ShuffleNet ShuffleNet	99.01% 95.34% 96.69% 97.79% 94.8%	In some cases, it uses a black-box method, being time-consuming, does not select the most effective features	Tang et al. (2020)
Black Rot, Black Measles, and Leaf Blight	K-Means Clustering - GLCM Feature Extraction- SVM Classifier-PCA- Relief feature selection CNN GoogleNet	98.97% 86.82% 94.05%	Compared to other methods used, the algorithm method used in this research includes the following advantages: Accurate diagnosis of the disease area Use automated clustering (ROI) Low operating time for diagnosis and classification of diseases Identify the best and most important features to diagnose the disease High accuracy for diagnosing and classifying diseases Higher accuracy for classification compared to CNN and GoogleNet deep learning methods	This Study

5. Conclusion

In this study, to diagnose and classify grape leaf diseases, a new technique is proposed. Features of grape images, categorized in different groups, have been extracted and compared with each other for disease detection. The SVM classifier with linear kernel and using only the GLCM features resulted in the highest accuracy of 0.9472, 0.9678, 0.9781, and 0.9871 for the captured image, K-means clustering of the captured image, images without background, and K-means clustering of images without background, respectively. After using PCA for the feature dimension reduction of the same input images, the accuracy reached 0.9601, 0.9704, 0.9871, and 0.9897, respectively. In order to find the most effective features to diagnose the diseases, the Relief feature selection method showed that about thirty basic features are among the most important features. The proposed technique was compared to two deep learning methods (i.e., CNN and GoogLeNet), which achieved lower classification accuracies of 0.8682 and 0.9405, respectively. The results show that the algorithm developed in this study can detect plant leaf diseases in grapes with high accuracy in a short time.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Plant Disease Detection using CNN Model and Image Processing

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Abstract— The rate of plants and crops cultivation rates growing rapidly with the increment of human and animal demands all over the world. The agricultural science invented lots of authentic techniques to use in cultivation sector for improve the production rate. During cultivation, farmers faced lots of challenges to protect their plant from different diseases and insects which make their production lower and they faced much financial losses. Form decades, agricultural scientists tried hardly to invent a quick medication system for detect plant disease quickly and gives treatment immediately. But the identification techniques of fetal abnormalities of plant are manual and it takes huge time. For reducing detection time and increasing efficiency of plant disease detection lots of new technologies introduced with cultivation system. In this work we introduced a model with the help of computer science and engineering using machine learning specially deep learning for detecting the leaf disease by the image of "Corn", "Peach", "Grape", "Potato" and "Strawberry". In Bangladesh, Mize and Potato is very popular food item and Strawberry is also very appealing for all aged people. Peach and Grape is not so popular cultivation in our country but their attraction in fruit market skyrocketed. The farmer who is interested and involved to cultivate corn, peach, grape, potato and strawberry faces lots of disorder and attract of insects and huge loss faced by the farmer. For prevent these losses and provide immediate cure, in this paper uses image processing, CNN (Convolutional Neural Network) model for training the dataset. Our system provides accuracy rate 94.29% successfully. The universal cultivator can get assistance from our research work for growing the production rate of crops and fruits and alleviate the plant disease and insect attract.

Keywords— Machine learning, CNN, Image Processing, Computer Vision.

I. INTRODUCTION

Bangladesh is an agricultural country. Around 80 percent people directly or indirectly related with the agronomical services. Bangladeshi economy extremely depends on agricultural department and large portion of economy in Bangladesh comes from this sector. Our financial status is moved forward by cultivating crops and fruits yearlong. In Bangladesh numerous crops are cultivated over the country and among all the crops and fruits rice, wheat and potato touched the height position of their popularity. The plantation of Maize, Peach, Grape and Strawberry shows increasing pattern and the invitation of this cultivation enhance rapidly. So the interest of farmer for cultivating these sorts of crops and fruits shows higher than any preceding decay.

Zea mays is known as the scientific name of Maize and it's another name is corn or mielie. Around the world the corn is the most cultivated crops and for numerous uses corn cultivated commercially almost every country. People of different culture and nature are enjoyed corn as food and the

maize act as a good source of minerals, dietary fiber and vitamins. There exist different types of corn for instance pop corn, dent corn, flour corn, sweat corn and flint corn. Spring season consider as the best time period for maize plantation and the corn is unable to tolerate coolness. The plant grows rapidly with the moisture soil. The cultivator faced different types of critical challenges for protecting maize from different types of disease which reduces the production rate. There are lots of maize diseases for example Anthracnose, Black bundle and Late wilt, Charcoal-Rot, Common Rust, Downy mildews, Cercospora leaf spot, Common sumt (Boil sumt, Blister sumt), Giberella stalk and ear rot, Northern leaf blight, Southern corn leaf blight, Bacterial leaf blight, Bacterial leaf streak, Bacterial stalk rot, Goss's bacterial blight, Holcus spot, Stewart's walt, Maize dwarf mosaic, pythium root rot, slugs, Aphids, Corn earworm, Cutworms, Fall armyworm, Flea beetles, Thrips, Root knot nematode, Spider mites and so on. During Black bundle and Late wilt disease, the infected plant shows symptom after reaching tassel state. When this disease started its attack the top leaves whose color is dull green and losing its color gradually and finally dry. This disease can be controlled by altering the crops, treatment the seed and reducing water stress. The top and bottom part of leaves become golden brown powdery color in common rust diseases and this disease can be controlled by hybrid the plant. At the time of growing, the leaves shows yellow rings brown spot in cercospora leaf spot and the disease can be reduced by rotate and hybrids the plant.

The peach is very popular fruits and very testy for eating containing vitamin A. The peach grows in warmer temperature in the hemispheres of Northern and Southern region. Peach is first invented in China after that it spreads Asia, Europe, Spain, Mexico and United States. Peach (*Prunus persica*) fruit tree size is very short. The peach's cultivator faced different types of disease which reduced the peach production rate and causes huge losses. There are numerous diseases such as Bacterial canker (*Pseudomonas syringae*), Bacterial spot (*Xanthomonas campestris*), Crown gall (*Agrobacterium* spp), Scab (*Cladosporium carpophilum*), Brown rot (*Monilinia fructicola*), Rust (*Tranzschelia discolor*), Short hole disease (*Wilsonomyces carpophilus*), Silver leaf disease (*Chondrosterum pupureum*), Leaf curl (*Taphrina deformans*), Plum pox virus (PPV), Fruit tree leafroller (*Archips argyropila*), Oriental fruit moth (*Grapholita molesta*) and so on. During Bacterial spot disease leaves under side become purple color with shot hole at the center and drop out the leaf from the tree. When peach faced Scab disease the fruits surface introduce small circular spot with green color and gradually its size rising become dark produced yellow

halo. In Brown rot disease the skin and tissue of fruits losses its color. The peach upper and lower side shows angular shape yellow green spots. The young leaf turn into red color from yellow color and the leaf raised irregularly is known as leaf curl disease.

Grapes is very testy fruits with green, red, purple color, seedless grapes, jelly grapes, jam grapes, grapes juice and so on. Grapes holds lots of vitamin A and B. Grapes can be eaten as cure of different jeopardy diseases such as Diabetes, eye problems, cardiovascular disease, cancer, heart disease, high blood pressure and so on. During cultivation grapes lots of disease are faced by the plant and fruits such as Powdery mildew (*Uncinula necator*), Downy mildew (*Plasmopara viticola*), Anthracnose (*Elsinoe ampelina*), Black rot (*Guignardia bidwellii*), Bacterial canker (*Xanthomonas campestris* pv. *Viticola*), Brown leaf spot, Rust, *Coniothyrium* blight, *Alternaria* blight, *Drechslera* leaf spot and so on. Powdery mildew is very dangerous disease. This disease attacks the vines and aerial part of the plant and firstly cluster and berry infection arrives. The leaf experienced circular spot which is brown color known as Black rot disease and the disease can be controlled by separating attacked fruits. The gray mold or bunch rot disease attacked the flowers and ripen fruits. Potato is very popular food item around the world and it act as vegetable. It has large leaf of small plant and the potato produces under the soil. Potato can be grown in high and cool region. Potato is helpful for different disease like blood pressure, brain functioning and nervous system, immunity, inflammation, digestion, heart health, skin care, cancer risk and so on. Potato production are reduced by different types of diseases such as Common scab, Powdery scab, Rhizoctonia, Silver scurf, Bacterial spot rot, Blackleg, Early blight, Freezing and chilling injury, Fusarium dry rot, Late blight, leak, Mechanical injury and cracking, Pink rot, Ring rot, Root knot nematode, Blackheart, Black spot, Fusarium wilt, Net necrosis, Verticillium wilt and so on.

Strawberry is very popular and testy fruit all over the world and its family is Rosaceae, genus *Fragaria*. Strawberry is cultivated all over the world and mostly grew in the Northern Hemisphere temperate regions. Strawberry is first invented in Europe then it is spreads all over the world and it's commercial production have two format for consumption immediate and processing. Strawberry is available during summer and it is popular nutritious fruits with antioxidant content. Strawberry can prevent lots of disease such as Heart disease, stroke, cancer, Blood pressure, Constipation, Diabetes. Strawberry is full of vitamin C, potassium, fiber and foli acid. Strawberry plant and fruits are attacked by numerous diseases for instance Angular leaf spot (*Xanthomonas fragariae*), Leaf scorch (*Diplocarpon earlianum*), Anthracnose (*Colletotrichum fragariae*), Gray mold (*Botrytis cinerea*), Leaf spot (*Mycosphaerella fragariae*, *Phomopsis* leaf blight (*Phomopsis obscurans*), Powdery mildew (*Spaerotheca macularis*), Red stele or Red core (*Phytophthora fragariae*), Slugs, Aphids, Armyworm, Japanese beetle, Loopers and so on. During Angular leaf spot disease the lower side of leaves show little water soaked which become large gradually and turn onto dark green color or angular spots. For protecting this

disease need to crop rotation, avoiding over irrigation, controlling over chemical use. The upper leaf side introduced dark or brown spot due to leaf scorch disease. This diseases can be controlled by renewing regular plants, well air circulating area choose for plantation, well drainage system ect.

In Bangladesh major portion of cultivator are illiterate and they are unable to detect disease using recent technologies. In our country, the new invented algorithm CNN (Convolutional Neural Network) is not used by our farmer. Our cultivator is used hand-made, non-scientific techniques for harvesting crops and detection of diseases. For protecting these diseases they preferred to use pesticides without appropriate scale which damages natural ecosystem. Most of them are largely depend on eye view or blind guesses for disease detection whereas USA, China developed country used various modern technologies like CNN, AI and mostly image processing techniques to detect or harvest their crops. In our research work we developed a model using machine learning so that our farmer can easily use this technique to identify and give appropriate cure. For training and testing our dataset through developing model here used CNN algorithm.

II. LITERATURE REVIEW

Before doing this work, we read and try to understand some source paper work so that we can do our work accurately. The paper which we read before starting this work is introduced here as literature review. During reviewing these papers it is clear that for disease detecting, classifying and surveying different types of authentic model is introduced by researcher. For plant disease detection, classification and surveying properly lots of innovative techniques are established by researcher and their work summery is included in this section.

Esker published a conference paper for detecting Stewart's disease on corn whose scientific name is "Pantoea stewartii subsp" in 2006 [1]. They used three predictor model for identify the stewartia corn disease and these three model name are "Stevens", "Stevens-boewe" and "Iowa state". Among these three models "Stevens-boewe" finds the Stewart's disorder leaf blight phase. Umair Ayub published a international conference paper in Pakistan for finding crop disorder dealing with Data Mining, 2018[2]. In this research work they mainly introduced losses which are faced by Pakistani farmer and theses losses appear due to crops diseases which is occurred by the attack of insects. For analyzing the disorder properly they used several data mining model for instance Neural Network, Supporting Vector Machine, Decision Tree and K Nearest Neighbors ect. James rethinks feature of Transgenic crops in 2002 and the requirement of maize over the world [3] and here introduced that the corn approximate requirement id 852 million at 2020. The financial losses is caused by the heavy uses of pesticides in corn is given by the Craig Osteen in the Economic Threshold Concepts [4]. Ravi introduced a clear concept of the origination of peach, its biological action and Morphology using Medical Phytochemicals [5]. Here they mainly focused on the use of peach fruits according to medicine and the use of different betterment of human being. Naeem identify and

manages fungal post-harvest pathogens of peach using morphological model [6]. They mainly characterize the fungal by morphological model and verified motive of postharvest rot of peach. In this work mainly focused on the detection of plant diseases and provides appropriate cure instantly. For doing this work here used image processing and authentic technologies like CNN so that the illiterate farmer can get immediate result with high accuracy.

III. PROPOSED METHODOLOGY

In our proposed model image processing method is used for the construction of system through which leaf disorder is detected if any distorted picture is supplied with in very short time. As a result a farmer without sufficient sense disease detection knowledge, modern techniques and software can be effortlessly applied this system. The dataset which is used as input is mixed of healthy and distorted images and after completing the action of input dataset the system output provides the affected and healthy leaves. A chart is introduced below as the proposed methodology. Figure 1 is that flowchart.

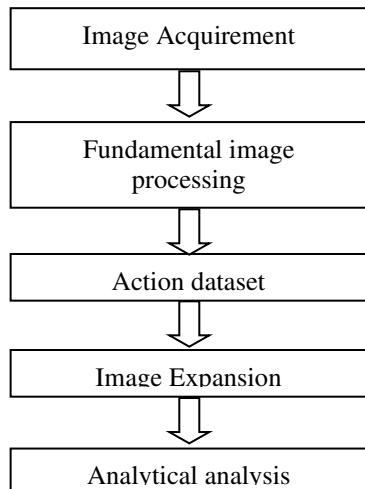


Fig.1 Methodology Flow Chart

A. Image Acquirement

When one wants to start a research work his primary responsibility is to gather and process as many data as he capable because in research work dataset contribute vital action. For obtaining perfect result and excellent exactness and getting powerful research work need to collect adequate data. During our research work we are able to collect around 13000 corn, peach, grape, potato and strawberry leaf images. Major part of our dataset is collected from corn, peach, grape, potato and strawberry harvesting field and the remainder data set has obtained from Google and public source of GitHub [7]. For making the spontaneous process system we can take lots of image format such as .gif, .bmp, .jpg and so on. .

B. Fundamental Image Processing

Form total collected data we have elected around 10000 valid data and the dataset separated into several folders. The dataset which is selected as training and testing and its ratio is 80 percent and 20 percent respectively. The testing section have been selected 103 images for the disease of Foliar fungal, 239 images for Gray_leaf_spot, Rust disease select 239 images, 233 images for Common_rust_corn, maize healthy

images 233, sort hole disease select 459 images, peach healthy image number is 72, Alternaria_blight disease select 80 images, Anthracnose select 80 images, for downy mildew 94 images 80 healthy images, powdery mildew select 80 images, Black_rot uses 233 images. During training portion of the research work Foliar_Fungal uses 410 images, select 953 images as Gray leaf spot disease, Rust disease collect 929 images, 929 maize healthy images, Short_hole disease elected 1838 images, peach fruits use 288 healthy images. The dataset which is collected before starting the research work is reshaped duo to match the picture size with each other and set the pixel size as 265×256. In order to increase the image proficiency the operation of image quality enhancement is received. The example of our selected dataset which occur before our research work starting is given below as Fig.2.



Fig.2. Accumulated Dataset

C. System Architecture

The scheme is created using CNN Convolutional Neural Network) multi-level model. The first convolutional layer include the ReLu activation function “1”, image input shape is (256, 256, 3), 64 used as filter_size, Kernel_size (8×8), “SAME” Padding and the Strides is (1×1). The second convolutional layer display the equivalent shape of the first layer and the additional feature is Max_Pool_size (2×2) and strides is (2×2).

$$\text{ReLU}(X) = \text{MAX}(0, X) \quad (1)$$

In the third and forth convolutional layer ReLu activation function “1”, image input_shape is (128, 128, 3), 32 used as

the filter_size, Kernel_size is (5×5) , “SAME” Padding and the strides is (1×1) . The forth layer used Max_Pool_size (2×2) and strides is (2×2) . In the fifth and sixth convolutional layer ReLu activation function “1”, image input_shape is $(64, 64, 3)$, 16 used as the filter_size, Kernel_size is (5×5) , “SAME” Padding and the strides is (1×1) . The sixth layer used Max_Pool_size (2×2) and stride is (2×2) . In the seventh and eighth convolutional layer ReLu activation function “1”, image input_shape is $(32, 32, 3)$, 8 used as the filter_size, Kernel_size is (3×3) , “SAME” Padding and the strides is (1×1) . The sixth layer used Max_Pool_size (2×2) and stride is (2×2) . The flatten layer usage 512 units of the dense layer and among them 50 percent is dropped by the ReLu activation function [10]. The utmost output tier used 5 units with softmax activation function “2”.

$$\sigma(z) = \frac{e^{x_i}}{\sum_{j=1}^k e^{x_j}} \text{ for } i = 1, \dots, k \quad (2)$$

0.001 used as the learning rate used in our proposed model as the optimization of ADAM [9].

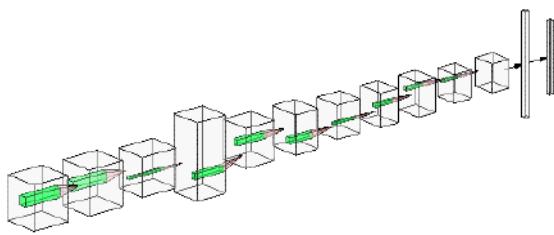


Fig.3. Proposed Convolutional Neural Network

D. Optimization and Learning Rate

The optimization algorithm is selected for confirming the sufficient variation of the result of deep learning and computer vision. The evaluation of various subsamples data is done in the Esoteric Adam paper. Various motive functions are stabilizing in this paper. In the gradient steps the efficiency is shown enhancement pattern by the optimization algorithm [11]. Different types of application like NLP (Natural Language Processing) and computer vision shows perfect adaption with the optimization algorithm in the modern world. The optimization technique is efficient for individual learning rate estimation dealing with numerous parameters from the 1st and 2nd moment of gradient. The model which is introduced here using 0.001 as the learning rate in the ADAM “3” optimization amidst.

$$v_t = (1 - \beta_2) \sum_{i=1}^t \beta_2^{t-i} \cdot g_i^2 \quad (3)$$

The neural network and cross entropy function provides acceptable output in the modern work of classification and prediction and this result is more grantable than MSE (mean square error). Usually, the training is not stalled out due to disable of getting sufficient minor using Cross-entropy error

and weighting change. In our research work the categorical cross entropy is used as the loss function “4”.

$$L_i = \sum_j t_{i,j} \log(p_{i,j}) \quad (4)$$

E. Image Expansion

The image partitioning work is taken place in the procedure of image expansion. The image expansion provides some motive and the main motive of the image expansion is:

- To represent the image through simplifying and alternating pattern.
- Changing the image shapes and angle for producing superfluous data.
- Using maximum image rotation range is 40, the width and height shifting range is 0.2, rescaling value is 1/155, shearing and zooming range is 0.2. During the expansion the horizontal flip act as True. For obtaining the greatest accuracy the nearest model is given in fig.4.

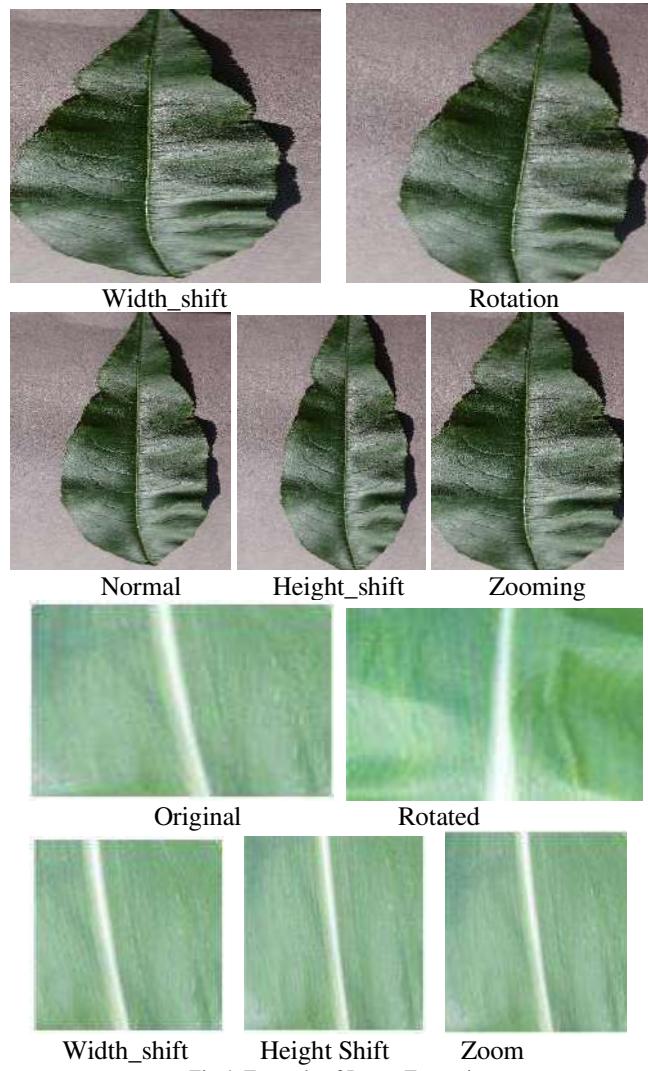


Fig.4. Example of Image Expansion

- The angle of the image is rotated counter clockwise which is controlled by the sheer range and allow our images to be sheared.
- The image is “Rescale” by multiplying the image data with numeric value at the initial state of the image processing. The coefficient range of the image is 0-255 and it is known as RGB image. But the range of the image is very high in our proposed model. As a result the range of our target value is one and zero and that value acquired by scaling the images with 1/255.

F. Training the Model

Numerous validation and training dataset is used for training the model with the batch_size 30. At the time of operation, the validation and reduction accuracy rate is supervised using learning rate reduction method. When 30 epochs is completed the supervision is worked manually among the validation accuracy and reduced learning rate. Then our model process 15-20 epochs and in a certain time set causal learning rate.

G. Layer Visualization

The gradual change of image is symbolized by layer visualization. The visual change of image in multiple layers is given below.

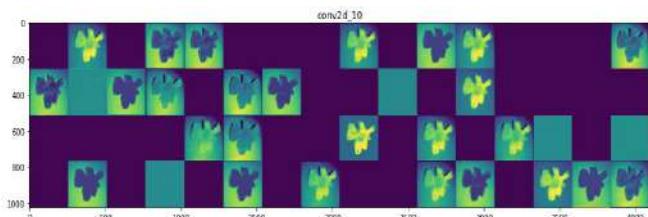


Fig.5. Layer visualization using 3x3 matrix

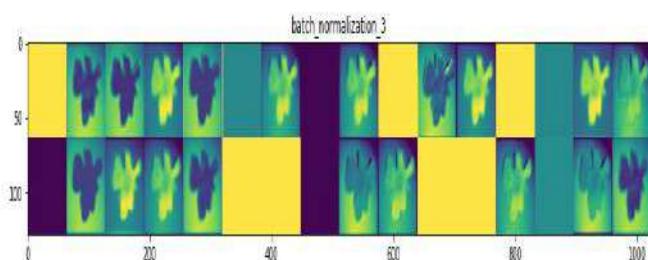


Fig.6. Final layer visualization using 2x2 matrix format

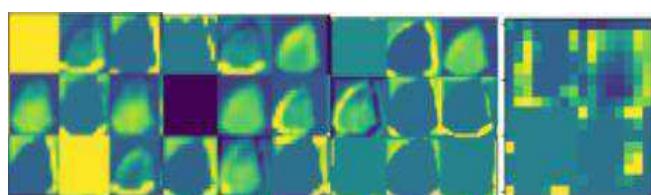
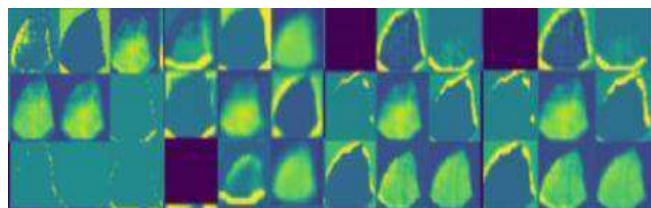


Fig.7. Layer visualization using kernel size (3,3)

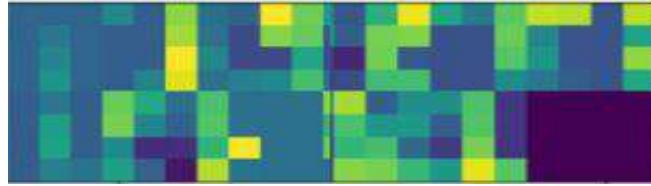
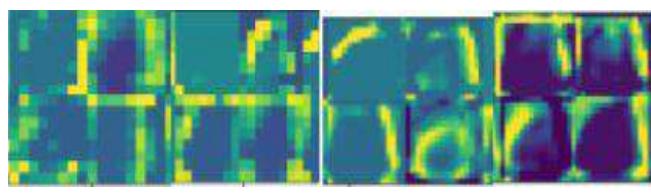


Fig.8. Layer visualization using kernel size (2,2)

IV. RESULT AND DISCUSSION

In our research work, the proposed model is provided expected output after completing the training, testing and validation using various dataset. The detail description about this model output is given below.

A. Analytical Analysis

The training and validation accuracy is obtained through this model 77.99% and 34.17% respectively. With time, after each run the model experienced trained and the exactness of the result improved as well. After completing 10 runs the training and validation accuracy become 89.56% and 61.91% respectively and the learning rate decreased at .0005. When the successful run is counted 30 the training and validation accuracy reached to 93.8% and 95.8% respectively and the learning rate decreased at 3.124e-05. After completing final run the height accuracy is obtained and the value for training and validation accuracy is 94.29% and 96.28% respectively.

B. Accuracy Graph

The term over fitting is used for describing and referring a model and this appear during capturing noise of the data. So the indication is that the perfect fitting of model or algorithmic data occur over fitting. The term under fitting is introduced during showing the lacking of capturing insufficient underlying data. The model which we introduced here shows absence of over or under fitting. The graph for training and validation accuracy and loss of our model is shown in Fig 9.

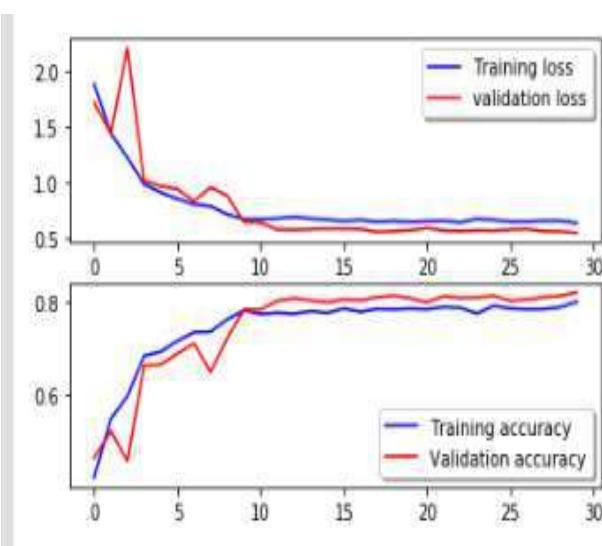


Fig.:-9 Training and validation accuracy and loss graph.

C. Confusion Matrix

The performance of the model is shown by the specific error table known as confusion or error matrix. Among total 67 images true image is 67 and false image is 0 only for Alternaria blight, for Anthracnose true images is 41 and false image is 45 among total approximate image 86, The Dwny mildew shows 91 true and 3 false image among 94, For Powdery mildew consider total 80 images where 44 images are true and the remain 36 is false. In Healthy, among 70 image 59 detected as true and 11 is false. Finally for Black rot, among total 80 images 58 shows true and 22 is false. The values introduced in diagonal position of the confusion matrix are bigger than others. The values in diagonal position used (4×4) shape is showing their best performance comparing to the other position and this part maximizing the data and that's why its color is deep blue. Fig.10. Shows confusion matrix and Table 1 shows classification report of our model.

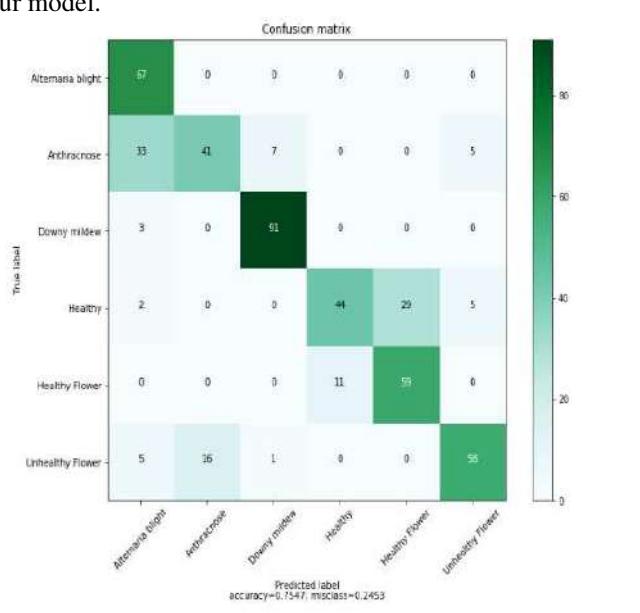


Fig.10. Confusion Matrix

TABLE I. CLASSIFICATION REPORT

Disease	precision	recall	F1-score	support
Alternaria blight	0.78	1.00	0.76	67
Anthracnose	0.97	0.86	0.91	86
Downy mildew	0.92	0.97	0.94	94
Healthy leaf	0.80	0.89	0.92	80
Healthy flower	0.88	0.84	0.84	70
Unhealthy flower	0.94	0.95	0.96	80
Gray_leaf_spot	0.97	0.94	0.96	102
Common_Rust	0.99	0.99	0.99	238
Healthy_corn	0.99	0.99	0.99	232
Bacterial_spot	0.98	0.98	0.98	458
Healthy_peach	0.97	0.98	0.97	72
Micro avg.	0.92	0.92	0.92	1204
Macro avg.	0.92	0.92	0.92	1204
Weighted avg.	0.94	0.94	0.94	1204

D. Result Analysis of Different Model

Some research papers are analyzed by our self which are related to our research work. We compared our model with other researchers model and found that the model which we proposed provide best result shown in Table 2

TABLE II. ACCURACY COMPARISON BETWEEN MODELS

Work	Accuracy (%)	work	Accuracy (%)
Sharada et al. [12]	85.53	s.phadikar et al. [15]	79.50
Prem et al. [14]	89.93	Jyoti and tanuja [16]	93.00
Proposed model	94.29	Naik Durgesh et al. [17]	94.00

E. Result Analysis and Variation Accuracy

This proposed model worked well for the separate dataset of corn and peach, shown in (Table 3).

TABLE III. SEPERATE RESULT RATION IN OUR DATASET

Dataset	Validation accuracy	Training accuracy	Validation loss	Training loss
Maize	98.23	98.23	0.0122	0.0210
Peach	97.53	96.98	0.0196	0.0204
Grape	98.89	98.92	0.0201	0.0310
Potato	96.90	96.96	0.0198	0.0217
Strawberry	84.89	85.85	0.0268	0.0271
Mixed Dataset	94.87	95.98	0.0189	0.0321

V. CONCLUSION

This work provides an authentic notion for detecting the attacked leaf ('Grape', 'Potato' and 'Strawberry') and the farmer who works for produce these fruits gets remedy so that they can enhance the production in agricultural industry. Specialist who works in agriculture department accepts quick disease detection process by image processing technique as a result Image Processing technology touch it's milestone within very short time. The transited portion of leaf easily segments and analyzes using CNN model and this model provides best possible result instantly. As a result the farmer who detects plant disease manually can save their time and diminish suspicion on possibilities of wrong detection. Our future goal is to develop an open multimedia system and make a software which automatically detect plant disease and provide their solution.

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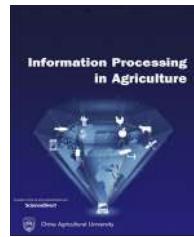
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INFORMATION PROCESSING IN AGRICULTURE 7 (2020) 418–426

journal homepage: www.elsevier.com/locate/inpa



Automatic grape leaf diseases identification via UnitedModel based on multiple convolutional neural networks



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ARTICLE INFO

Article history:

Received 17 April 2019

Received in revised form

11 October 2019

Accepted 15 October 2019

Available online 23 October 2019

Keywords:

Grape leaf diseases

Identification

Multi-network integration method

Convolutional neural network

Deep learning

ABSTRACT

Grape diseases are main factors causing serious grapes reduction. So it is urgent to develop an automatic identification method for grape leaf diseases. Deep learning techniques have recently achieved impressive successes in various computer vision problems, which inspires us to apply them to grape diseases identification task. In this paper, a united convolutional neural networks (CNNs) architecture based on an integrated method is proposed. The proposed CNNs architecture, i.e., UnitedModel is designed to distinguish leaves with common grape diseases i.e., black rot, esca and isariopsis leaf spot from healthy leaves. The combination of multiple CNNs enables the proposed UnitedModel to extract complementary discriminative features. Thus the representative ability of UnitedModel has been enhanced. The UnitedModel has been evaluated on the hold-out PlantVillage dataset and has been compared with several state-of-the-art CNN models. The experimental results have shown that UnitedModel achieves the best performance on various evaluation metrics. The UnitedModel achieves an average validation accuracy of 99.17% and a test accuracy of 98.57%, which can serve as a decision support tool to help farmers identify grape diseases.

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1. Introduction

Grapes, as one of the most commonly cultivated economical fruit crops throughout the world, are widely used in the production of wine, brandy or nonfermented drinks and are eaten fresh or dried as raisins [1]. However, grapes are vulnerable to various different types of diseases, such as black rot,

esca, isariopsis leaf spot, etc. It is estimated that losses caused by grape diseases in Georgia, USA in 2015 were approximately \$1.62 million. Around \$0.5 million was spent on diseases control and the rest was the loss caused by the diseases [2]. Thus, early detection of grape diseases can potentially cut losses and control costs and consequently can improve the quality of products.

For decades, the diseases identification is mostly performed by human. The process of recognition and diagnosis is subjective, error-prone, costly and time-consuming. In addition, new diseases can occur in places where they were

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Peer review under responsibility of China Agricultural University.

<https://doi.org/10.1016/j.inpa.2019.10.003>

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previously unidentified and, inherently, where there is no local expertise to combat them [3]. As a result, an automatic identification method for grape disease identification is in urgent demand.

The development of sophisticated instruments and fast computational techniques have paved the way for real-time scanning and automatic detection of anomalies in a crop [4]. Although traditional machine learning methods have gained some valuable experience in identification and diagnosis of crop diseases, they are limited to following the pipelined procedures of image segmentation (such as clustering method [5], threshold method [6], etc.), feature extraction (such as shape, texture, color features, etc. [7]), and pattern recognition (such as k-nearest neighbor method (KNN) [8], support vector machine (SVM) [1], back propagation neural network (BPNN) [9], etc.). It is difficult to select and extract the optimal visible pathological features and thus highly skilled engineers and experienced experts are demanded, which is not only to a considerable extent subjective but also leads to a great waste of manpower and financial resources. In contrast, deep learning techniques can automatically learn the hierarchical feature of pathologies and do not need to manually design the feature extraction and classifier. Deep learning method has so excellent generalization ability and robustness that it excels in many areas: signal processing [10], pedestrian detection [11], face recognition [12], road crack detection [13], biomedical image analysis [14], etc. In addition, deep learning techniques have also achieved impressive results in the field of agriculture and benefit more smallholders and horticultural workers, including diagnosis of crop diseases [15], recognition of weeds [16], selection of fine seeds [17], pest identification [18], fruit counting [19], research on land cover [20] etc, which has contributed to dealing with image classification of areas of interest. Furthermore, some applications focused on predicting future parameters, such as crop yield [21], weather conditions [22] and soil moisture content in the field [23]. Inspired by the great success of CNN-based methods in image classification, we propose an integrated model, denoted UnitedModel, for automatic grape leaf disease identification.

The rest of this paper is organized as follows. [Section 2](#) starts with an overview of related works. [Section 3](#) introduces dataset as well as data preprocessing and covers details of the proposed UnitedModel. In [Section 4](#), we conduct all the experiments, discuss the limitation of the proposed UnitedModel and prospect the future work. In [Section 5](#), we conclude this paper.

2. Related works

Machine learning techniques were applied widely in plant disease classification in the early stage. Li et al. [24] proposed a method based on K-means clustering segmentation of the grape disease images and a SVM classifier was designed based on thirty-one effective selected features to identify grape downy mildew disease and grape powdery mildew disease with testing recognition rates of 90% and 93.33%, respectively. Significant progress has been made in the use of image processing approaches to detect various diseases in crops.

Athanikar and Badar [9] applied Neural Network to categorize the potato leaf image as either healthy or diseased. Their results showed that BPNN could effectively detect the disease spots and could classify the particular disease type with an accuracy of 92%. The deployment of deep CNNs has especially led to a breakthrough in plant disease classification, which can find very high variance of pathological symptoms in visual appearance, even high intra-class dissimilarity and low inter-class similarity that may be only noticed by the botanists [25]. Lee et al. [26] proposed a CNN approach to identify leaf images and reported an average accuracy of 99.7% on a dataset covering 44 species, but the scale of datasets was very small. Zhang et al. [27] used GoogLeNet to address the detection of cherry leaf powdery mildew disease and obtained an accuracy of 99.6%. Their results also demonstrated transfer learning can boost the performances of deep learning model in crop disease identification. Mohanty et al. [15] fine-tuned deep learning models pre-trained on ImageNet to identify 14 crop species and 26 diseases. The models were evaluated on a publicly available dataset including 54,306 images of diseased and healthy plant leaves collected under controlled conditions. They achieved the best accuracy of 99.35% on a hold-out test dataset.

Although the basic CNN frameworks, such as AlexNet [28], VGGNet [29], GoogLeNet [30], DenseNet [31] and ResNet [32] have been demonstrated effective and widely used in crop diseases classification, most previous works had troubling boosting up the classification accuracy rate to some extent. As a matter of fact, a single model can't meet the further requests in terms of precision. In large machine learning competitions, the best results were usually achieved by the integration of multiple models rather than by a single model. For instance, the well-known Inception-ResNet-v2 [33] was born out of the fusion of two excellent deep CNNs, as the name suggests. Inspired by network in network concept [34], we think that integration is the most straightforward and effective way when the basic models are significantly different. We propose the UnitedModel in this study. The UnitedModel is a integration of the powerful and popular deep learning architectures of GoogLeNet and ResNet. We also take advantage of transfer learning to boost accuracy as well as reduce the training time.

3. Materials and methods

3.1. Dataset and preprocessing

Our dataset comes from an open access repository named PlantVillage which focuses on plant health [35]. The dataset used for evaluating the proposed method is composed of healthy (171 images) and symptom images including black rot (pathogen: *Guignardia bidwellii*, 476 images), esca (pathogen: *Phaeomoniella spp*, 552 images) and isariopsis leaf spot (pathogen: *Pseudocercospor a-vitis*, 420 images) (see [Table 1](#)). The identification of grape diseases is based on its leaf, not flower, fruit or stem. For one thing, the flower and fruit of grape only appear in a limited time while the leaf presents most of the year. For another thing, the stem of grape can hardly present the symptoms of the diseases timely, while

Table 1 – Introduction of grape leaf dataset.

Label	Category	Number	Data augmentation			Leaf symptoms	Illustration
			Training samples	Validation samples	Test samples		
1	Black rot	476	288	72	116	Appear small, brown circular lesions	See Fig. 1 first row
2	Esca	552	288	72	192	Appear dark red or yellow stripes	See Fig. 1 second row
3	Isariopsis leaf spot	420	288	72	60	Appear many small rounded, polygonal or irregular brown spots	See Fig. 1 third row
4	Health	171	96	24	51	–	See Fig. 1 fourth row
Total samples		1619	960	240	419	–	–

**Fig. 1 – The grape leaf images after data augmentation.**

the leaf is generally sensitive to the state of plants, whose shape, texture and color usually contains richer information.

The raw images are divided into training dataset and test dataset. 360 Symptom and 120 healthy images are selected for training and the rest images are used for testing. To prevent over-fitting, the training dataset is further split into training (80%) and validation data (20%). Thus the training dataset is 960 samples in total, validation dataset is 240 samples in total and test dataset is 419 samples in total [36]. The original images in the PlantVillage dataset are RGB images of arbitrary size. Data preprocessing is necessary and all the images are resized to the expected input size of the respective networks, i.e. 224×224 for VGGNet, DenseNet and ResNet, and 229×229 for GoogLeNet. Model optimization and prediction are both performed on these rescaled images. To avoid over-fitting and to boost the generalizability of the CNNs, data augmentation techniques which include rotating, flipping, shearing, zooming and colour changing are randomly performed in training phase as shown in Fig. 1.

Considering that the number of healthy samples in our work is relatively small with 171 samples in total, the proportion between healthy samples and diseased samples is set to 1: 3 while the *class_weight* ratio of them is set to 3: 1. By this way, the loss function can be adjusted in the training process and healthy samples can obtain more attention.

3.2. Identification model of grape leaf diseases

In this paper, the grape leaf diseases identification can be formulated as a multi-class classification problem. The classification process of this work can be described as follows (Fig. 2). Assuming a mapping function from grape leaf images to corresponding predicted labels (i.e. “Label”, “Label2”, “Label3” and “Label4”) $f : X \rightarrow Y$. Then the grape leaf training dataset is denoted as $(x_1, y_1), (x_2, y_2), \dots, (x_n, y_n)$. The training dataset is the input of the CNN model A. During training, the weights of A are updated continuously to minimize the average loss function which is defined as:

$$J(\omega) = -\frac{1}{n} \sum_{i=1}^n y_i \log(h_\omega(x_i)) \quad (1)$$

where x is the training sample, n is the number of input data, y_i is the true label and $h_\omega(x_i)$ is the predicted label of the CNN model A given current weights ω . Then, the end-to-end optimization can be performed using the stochastic gradient descent (SGD) method. The gradient of the loss function can be computed with the following equation:

$$\omega_{t+1} = \mu \omega_t - \alpha \nabla J(\omega_t) \quad (2)$$

where μ is the momentum weight for the current weights ω_t and α is the learning rate. Noted that the iterative operation

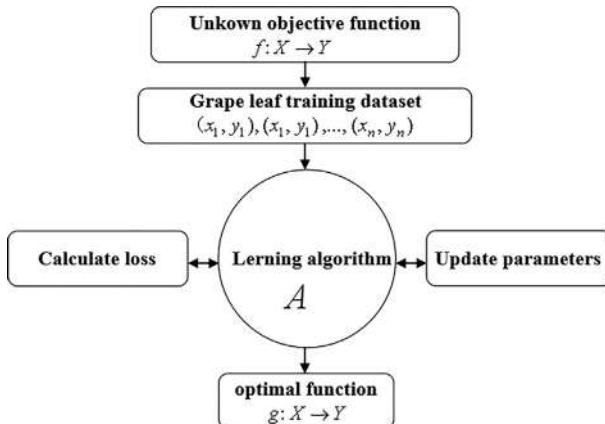


Fig. 2 – The mathematical model of grape leaf disease identification.

of ω is limited in added layers because all parameters in convolutional layers are set to the pre-trained network weights and fixed. After a series of epochs, an optimal function $g : X \rightarrow Y$ is obtained, which is the final hypothesis. Then we can input the test dataset into A and get the corresponding predicted labels.

3.3. Architecture of UnitedModel

The UnitedModel proposed for grape leaf disease identification is based on two popular deep learning architectures i.e., GoogLeNet and ResNet. GoogLeNet, the winner of ILSVRC 2014, was precisely aimed to reduce the computational cost and complexity. The whole architecture of GoogLeNet is stacked by inception modules that combine multi-scale feature extraction and dimension reduction layers based on the Hebbian principle and embedding learning. In our work,

InceptionV3 is selected as one component of the UnitedModel. ResNet won the first place in ILSVRC 2015 and COCO 2015 classification challenge with error rate of 3.57%, which introduced residual units for addressing the degradation problem of CNNs. ResNet is stacked by many residual units. Given the size of the dataset used in this work, ResNet50 becomes our first choice to be another basic network of the UnitedModel, which also has high performance in classification tasks. Given sufficient data, the most straightforward way of improving the performance of CNNs is increasing their parameters. In this study, GoogLeNet increases its width: the number of units at each layer while ResNet increases the depth: the number of network layer. The integration is most effective when the basic models are significantly different because their combination will enable the integrated network to capture more distinguishing feature information, thereby improving identification accuracy.

An illustration for the workflow of the proposed method is shown in Fig. 3. Given a testing image, the well-trained UnitedModel extracts two different feature sets by using GoogLeNet and ResNet and then performs the prediction based on the combined feature sets. In Fig. 4, we show the detailed structure of the UnitedModel. Considering that our dataset is relatively small, direct training from scratch on the dataset of grape leaf diseases will result in over-fitting. And thus transfer learning is adopted. The training phase is as follows: Firstly, the input image is resized to the expected input size of the respective networks and propagated forward to each basic single model, i.e. InceptionV3 and ResNet50. The feature maps are extracted by multi-type convolution filters arranged in InceptionV3 and ResNet50. And then through global average pooling (GAP), the feature maps extracted from convolution layers will be output in the form of two-dimensional matrix and then merged operation concatenation (Fig. 3). After that, a dropout layer, a fully connected layer, an another dropout layer, a classification layer (Fig. 4) are added. Within

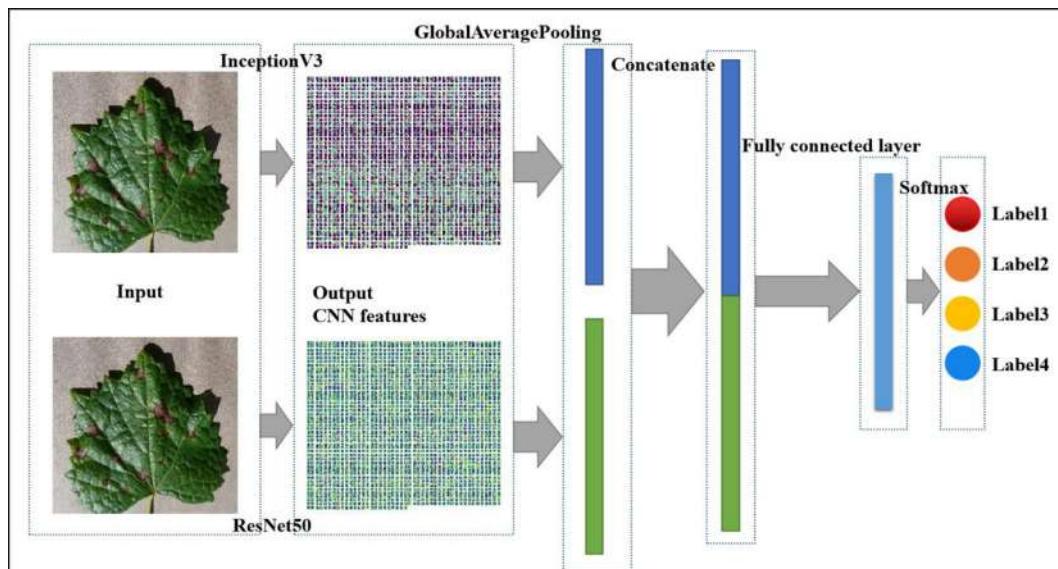


Fig. 3 – An illustration for the workflow of the proposed method.

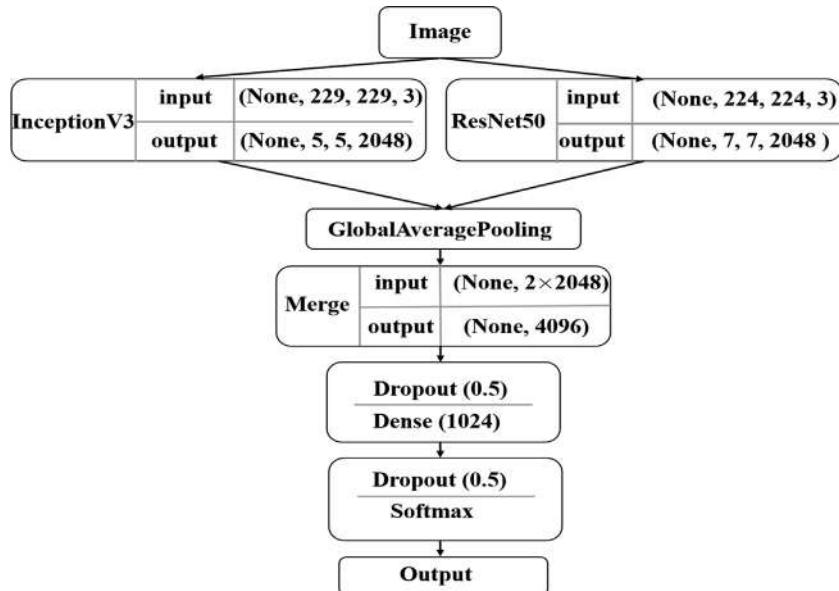


Fig. 4 – Structure of UnitedModel.

the classification step, each neuron in fully-connected layers provides a full connection to all learned feature maps. Accordingly, the united two-dimensional feature matrix combines freely with each other, generating different feature maps and thus improving the flexibility and characterization ability of the model [37]. Since the abundant training parameters and complex structures in the proposed UnitedModel easily cause over-fitting, dropout layers are used with rate 0.5. The softmax classifier is used as the final classification layer to obtain the classification results.

3.4. Experimental environment

The proposed model is built using the open source Keras framework on top of TensorFlow. All experiments are conducted on a system with the specifications in Table 2.

The original architectures of VGGNet, GoogLeNet, DenseNet and ResNet are trained as the control experiments of UnitedModel to explore whether the integrated approach can improve the performance in the grape diseases identification task and where the improvement is significant. To enable a fair comparison between the results of all the experimental configurations, all the hyper-parameters are standardized. The SGD algorithm is used to learn the best set of weights and biases of the neural networks that minimize the loss function. While learning, the SGD algorithm works by randomly choosing a small number of training inputs referred to as batch size which is set to 16. The learning rate is set to 0.001. It is the rate at which a function moves through the search space. A small learning rate leads to more precise results but it requires more training time. The momentum is an additional factor to determine how fast the SGD algorithm converges on the optimum point. It is set to 0.9. Early stopping mechanism is used to deal with the problem of over-fitting and speed up the training process. The training ends when

Table 2 – Experimental environment.

Hardware	Software
CPU: Intel Core i7-6700HQ	Windows10
RAM: 8 GB DDR4	CUDA9. 0+CUDNN7.0
GPU: NVIDIA GEFORCE GTX 960M	Keras, Tensorflow

the network does not significantly improve its validation performance after 3 epochs.

3.5. Evaluation metrics

The evaluation of the different experimental configurations is based on a train-validation-test scheme. The actual training is carried-out on the training dataset while the validation dataset is used to avoid over-fitting. The performance of each model is assessed on the test dataset. Precision, recall and average F1-score are used as evaluation metrics. Experimental results are reported across all our experimental configurations. Due to its increased sensitivity to imbalances among the classes, the overall accuracy is also computed [38]. The precision, recall and F1-score are expressed in the following:

$$\text{precision}_c = \frac{\text{TP}_c}{\text{TP}_c + \text{FP}_c} \quad (3)$$

$$\text{recall}_c = \frac{\text{TP}_c}{\text{TP}_c + \text{FN}_c} \quad (4)$$

$$\text{F1-score} = \frac{2}{4} \sum_{c=1}^4 \frac{\text{recall}_c * \text{precision}_c}{\text{recall}_c + \text{precision}_c} \quad (5)$$

where TP is true positive, FP is false positive, FN is false negative, c is the class of grape diseases and healthy type is included. For a more detailed comparison at different operating points, confusion matrix analysis for VGGNet, GoogLeNet, DenseNet, ResNet and UnitedModel is also performed.

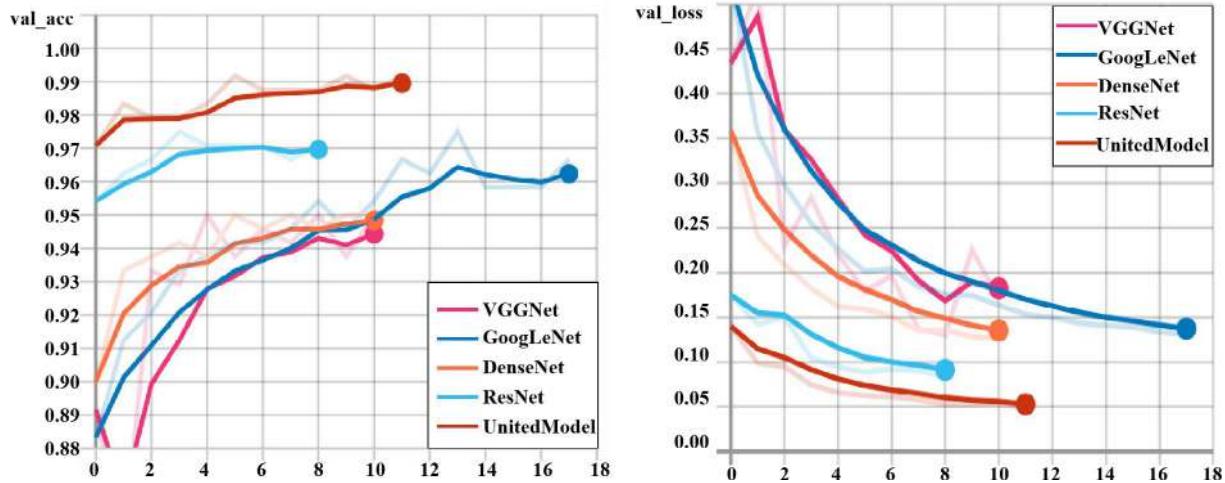


Fig. 5 – Validation accuracy and validation loss of various architectures are compared and the number of epoch is varied in the case of early stopping mechanism. VGGNet, GoogLeNet, DenseNet, ResNet and UnitedModel stop training with the epoch 11, 18, 11, 9 and 12, respectively.

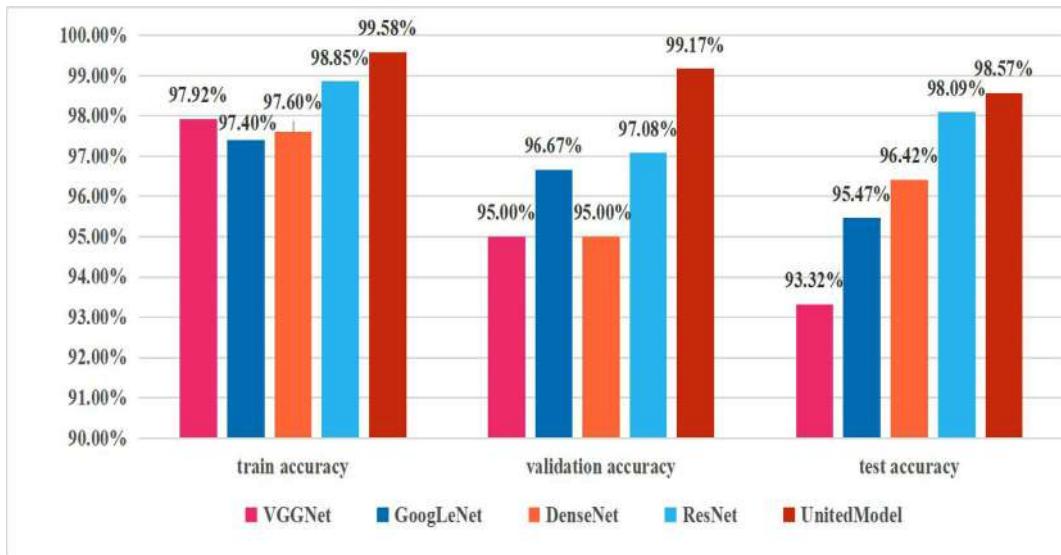


Fig. 6 – Comparison of the average accuracy for the different architectures.

4. Results and discussion

As illustrated in Fig. 5, UnitedModel has a tendency to consistently improve in accuracy with growing number of epochs, with no signs of performance deterioration. On the other hand, loss curve of UnitedModel converges rapidly and has a big gap with other single models in terms of error rate. Consistent with Fig. 6, the performance of GoogLeNet, VGGNet, DenseNet and ResNet is similar and all inferior to UnitedModel.

As we can see in Table 3, the average precision (99.05%), recall (98.88%) and F1-score (98.96%) of UnitedModel are the highest among all these models. And scores of VGGNet are the lowest with precision (94.16%), recall (93.32%) and F1-

score (94.40%), which once again proves the superiority of integrated CNNs.

The confusion matrices of different models on test dataset are shown in Fig. 7. The threshold is set to 0.5 and the fraction of accurately predicted images for each class is displayed in detail. The performance of VGGNet is poor. VGGNet tends to distinguish diseased samples as healthy, which is extremely harmful in actual agriculture produce. All the models except VGGNet can distinguish label3 and label4 easily, but label1 and label2 are prone to be misclassified. The large green area of healthy leaves and the golden appearance of leaves infected with isariopsis leaf spot disease make them easier to be distinguished. Meanwhile, the confusion between label1 and label2 is due to their similar pathological features.

Table 3 – Precision, recall and F1-score for the corresponding experimental configurations (best overall performance is displayed in boldface).

Architecture	Criterion	Label Support	Label1 116	Label2 192	Label3 60	Label 4 51	Total/Average
VGGNet	Precision		0.8699	0.9514	0.9828	0.9623	0.9416
	Recall		0.9224	0.9167	0.9500	1.0000	0.9332
	F1-score		0.8954	0.9337	0.9661	0.9808	0.9440
GoogLeNet	Precision		0.9076	0.9577	1.0000	1.0000	0.9663
	Recall		0.9310	0.9427	1.0000	1.0000	0.9684
	F1-score		0.9191	0.9501	1.0000	1.0000	0.9673
DenseNet	Precision		0.9642	0.9784	1.0000	1.0000	0.9722
	Recall		0.9655	0.9427	1.0000	1.0000	0.9771
	F1-score		0.9372	0.9602	1.0000	1.0000	0.9744
ResNet	Precision		0.9737	0.9742	1.0000	1.0000	0.9870
	Recall		0.9569	0.9844	1.0000	1.0000	0.9853
	F1-score		0.9652	0.9793	1.0000	1.0000	0.9861
UnitedModel	Precision		0.9825	0.9794	1.0000	1.0000	0.9905
	Recall		0.9655	0.9896	1.0000	1.0000	0.9888
	F1-score		0.9739	0.9845	1.0000	1.0000	0.9896

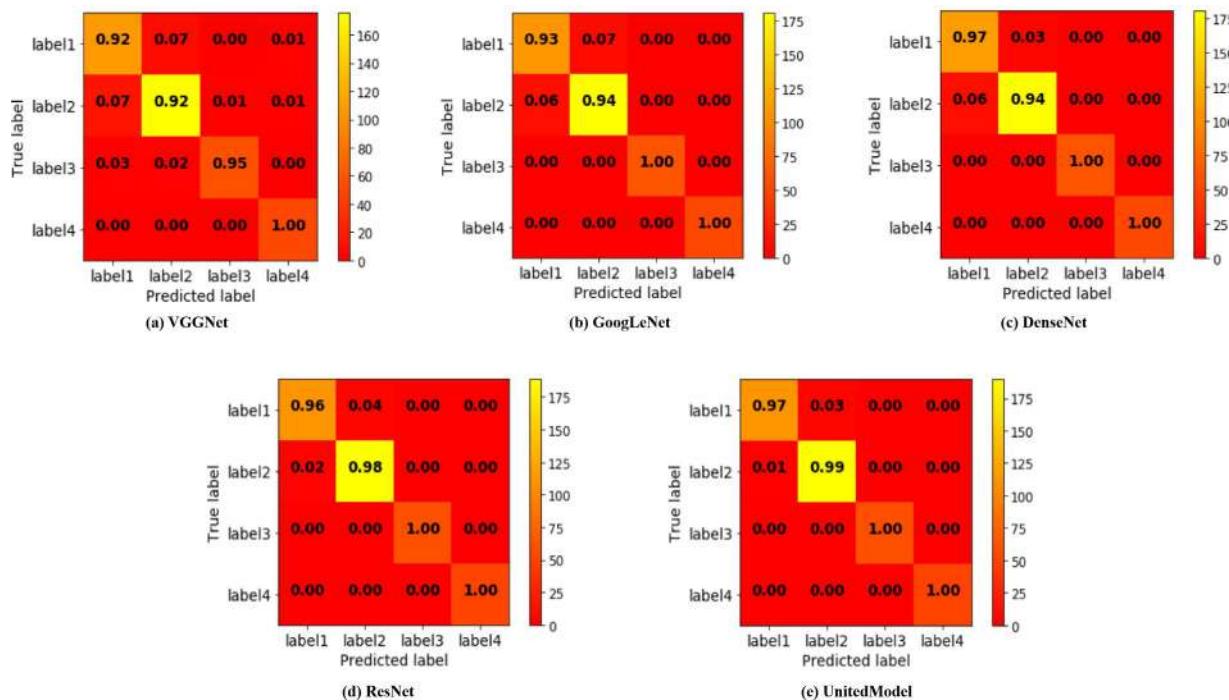


Fig. 7 – Confusion matrices for the grape diseases dataset are presented with an overall accuracy associated for individual classes. The confusion matrices are given in terms of percentages, not absolute numbers.

However, UnitedModel improves the test accuracy of label1 (97%) and label2 (99%). The UnitedModel is a combination of InceptionV3 and ResNet50 and can improve the representative capability by enriching features using multi-network integration method. In this study, we conjecture different CNN models to generate complementary features and we boost the performance by combining the complementary features. In addition, the use of transfer learning makes this process more concise and efficient.

The loss and accuracy curves of the UnitedModel during training phase are presented in Fig. 8. The green and black curves are the loss function values on the training dataset and validation dataset, respectively. The two curves drop rapidly in the first two epochs and start to converge after around 6 epochs. And then, the training loss continues to descend slightly until roughly the final epoch while validation loss is no longer significantly reduced. The red and blue curves represent the training accuracy and validation

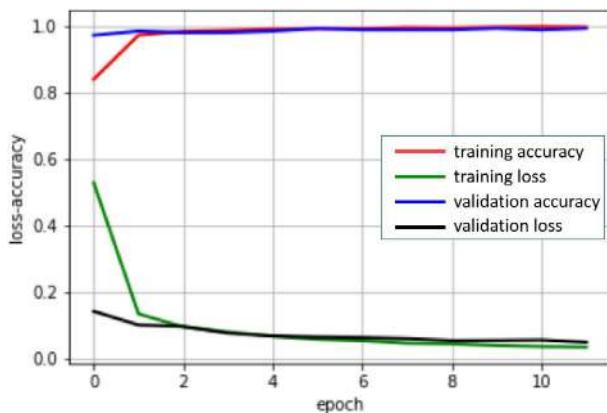


Fig. 8 – The trend of train accuracy, validation accuracy, train loss and validation loss of the UnitedModel.

accuracy, respectively. In Fig. 8, we can observe that after a few epochs they overlap almost completely, showing that UnitedModel gets sufficiently trained.

Experimental results have shown that the proposed UnitedModel integrating InceptionV3 and ResNet50 can achieve promising results for the grape leaf diseases identification task. However, since the training dataset used in our work is composed of samples in a simple background scene, the trained model cannot be applied for real-time diagnosis of grape leaf diseases in the complex background. One direction of future work is to create datasets under un-controlled scenario which can be used for training model to improve the generalizability. Thus the proposed model can be used for the development of mobile systems and devices. Another direction of future work is to compress the model while keeping the same performance. The proposed UnitedModel is a combination of two popular models and is of huge number the parameters. The training of the UnitedModel is great computational cost. It is important to find out an effective pruning mechanism for model compression to reduce computational resources.

5. Conclusions

In this work, we have developed an effective solution to automatic grape diseases identification based on CNNs. We have proposed the UnitedModel which is a united CNNs architecture based on InceptionV3 and ResNet50 and can be used to classify grape images into 4 classes, including 3 different symptom images i.e., black rot, esca, isariopsis leaf spot, and healthy images. UnitedModel takes advantage of the combination of InceptionV3's width and ResNet50's depth and thus can learn more representative features. The representational ability of UnitedModel is strengthened by way of high-level feature fusion, which makes it achieve the best performance in the grape diseases identification task. The experimental results demonstrate that our model can outperform the state-of-the-art basic single CNNs including VGG16, InceptionV3, DenseNet121 and ResNet50. The proposed UnitedModel achieves an average validation accuracy of 99.17% and a test accuracy of 98.57% and thus can serve as a decision

support tool to help farmers identify the grape diseases. We also provide a practical study for dealing with the insufficiency and unbalance of dataset. The methods of data augmentation techniques, early stopping mechanism and dropout are used to improve the generalization ability of model and reduce the risk of over-fitting. In addition, we have proposed an effective multi-network integration method which can be used to integrate more state-of-the-art CNN models and can also be easily extended to other plant disease identification tasks.

Declaration of Competing Interest

We declare that we have no financial and personal relationships with other people or organizations that can inappropriately influence our work, there is no professional or other personal interest of any nature or kind in any product, service and company that could be construed as influencing the position presented in, or the review of, the manuscript entitled "Automatic Grape Leaf Diseases Identification via UnitedModel Based on Multiple Convolutional Neural Networks".

Acknowledgements

This work was supported by the Public Welfare Industry (Agriculture) Research Projects Level-2 under Grant 201503116-04-06; Postdoctoral Foundation of Heilongjiang Province under Grant LBHZ15020; Harbin Applied Technology Research and Development Program under Grant 2017RAQXJ096 and National Key Application Research and Development Program in China under Grant 2018YFD0300105-2.

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Grape Leaf Multi-disease Detection with Confidence Value Using Transfer Learning Integrated to Regions with Convolutional Neural Networks

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Abstract—Identifying variant diseases in leaves is a significant method for optimizing food production. As the global population continues to arise and agricultural space continues to decline, every possible way of increasing the supply of food in any given condition and limited resources will address the above-mentioned problems. This study proposes a way for detecting three different diseases from grape leaves apart from the healthy leaves and considers the confidence value of the system in correctly identifying the classes. The diseases are namely: Black Rot, Black Measles, and Isariopsis. The system conducted a comparative analysis to determine which among the three pre-trained networks, AlexNet, GoogLeNet, and ResNet-18 will be the most suitable network to be integrated with Regions with Convolutional Neural Networks (RCNN) in performing multiple object detection in a given image. The data used in training the models comprised of annotated image data represented as a ground truth table with image files and their corresponding bounding boxes coordinates. The models evaluated resulted to AlexNet being the best pre-trained network to be working on the RCNN with an accuracy of 95.65%. The other two models from GoogLeNet and ResNet-18 only obtained accuracies of 92.29% and 89.49% respectively.

Keywords—alexnet, confidence value, deep learning, disease detection, googlenet, regions with convolutional neural network, resnet-18, transfer learning

I. INTRODUCTION

Trend development on international agricultural resources trading has effected to the contagious spread of plant viruses among involving countries [1]. These plant viruses initiated to a new environment paved way for these diseases to mutate to new strains and to remodel to new hosts [2], causing tremendous impacts on variety of plant species. The diseases in these plants can cause multiple losses in terms of ecological, economic, and social attributes [3]. Thus, they are not only a cause for environmental issues, but can result to inefficient food production as well.

An assessment of overall yield and morphology of okra conducted proved that there is a huge reduction in growth and yield due to leaf curl disease [4]. A study on Taro leaf blight further proved that leaf diseases can contribute to food insecurity [5]. Instability in the food supply according to a study [6], can also be caused by fungi, specifically the Botrytis Cinerea that infect 230 plant species worldwide. With the presented problems, it is evident that plant diseases need to be addressed and controlled to preserve availability of food globally [7]. Leaf disease detection is one of the recent advances being focused on for addressing the concerns on food scarcity [8]. Several studies to be discussed in the literature discuss the continuous improvement of such systems in different plant species.

The importance of recognizing leaf diseases that can later contribute on determining the necessary actions for disease prevention and control influenced the objective of this study. The system aims to determine an appropriate model that can accurately identify and detect three grape leaf diseases given simulated images that contain multiple diseases. This will be specifically done by comparing analytically three pre-trained networks to be integrated with Regions with Convolutional Neural Networks to determine which can train the best-fitting model. Confidence values will be integrated as well to determine how convinced and certain the system is in providing the appropriate disease classification.

II. RELATED STUDIES

Leaf disease detection models have been widely implemented in numerous studies. Mostly, these applications utilize machine vision algorithms to extract variety of features such as color [9], shape [10], texture [11], venation [12], and morphology [13] to classify diseases. The use of Regions with Convolutional Neural Network has been recently integrated in these applications to support the classification with detection by the use of regression algorithms embedded in these networks to provide the necessary bounding boxes along with

the classification [3]. Shown in Table 1 are the use of deep learning models in detecting existing diseases in the leaves of different plant species.

TABLE I. RELATED STUDIES ON PLANT DETECTION

Leaf Disease Detection		
References	Pre-trained networks	Plant species to detect
De Luna et al. 2018 [14]	Alexnet and Faster RCNN	Tomato leaf
Amara et al. 2017 [15]	LeNet	Banana leaf
Mishra et al. 2019 [16]	CNN-integrated model	Corn leaf
Singh 2019 [17]	AlexNet, VGG16, VGG19, Densenet201, GoogLeNet, Inception-ResNet-v2, Inception-v3, ResNet-18, ResNet-50, ResNet-101, XceptionNet	Rice leaf
Ozguven and Adem 2019 [18]	CNN and Faster RCNN	Sugar beet leaf
Sorte et al 2019 [19]	CNN-based model	Coffee leaf
Barbedo 2019 [20]	GoogLeNet and CNN	14 plant leaf species
Geetharamani and Arun 2019 [21]	Deep CNN model	38 plant leaf species
Ghoury et al. 2019 [22]	Faster RCNN and SSD MobileNet	Grape leaf
Wagh et al. 2019 [23]	CNN-based model	Grape leaf

The presented papers in the table mostly focused on detecting a single variant of disease existing in a single leaf. Though the papers presented classification of multiple variants of diseases, the conducted studies are limited to detection of the disease variants in different leaves. However, a single leaf can also carry multiple diseases.

III. METHODOLOGY

The methods of this research follow the structure presented in the system architecture shown in Figure 1. Image dataset of grape leaves with different diseased was acquired and was created to sets of montage images. These montage images were then annotated to be used for training a network for detecting multiple objects in a single image simulated for having multiple diseases. Hyperparameter and algorithm setup were pre-determined before training the model for classifying diseases and predicting the coordinates of the bounding boxes.

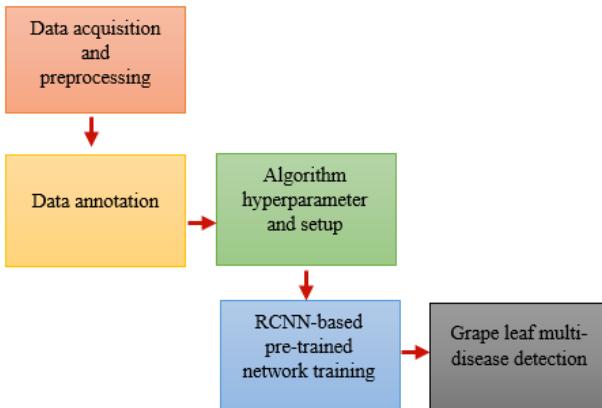


Fig. 1. System Architecture

Further detailed and technical discussions are presented in the four following subsections of Section 3.

A. Data Gathering and Preprocessing for Multi-disease Simulation

Image datasets of grape leaves with variety of diseases were gathered from Kaggle.com by Abdallah Ali [24]. Presented in Figures 2 to 5 are three samples of each of the image dataset variety.



Fig. 2. Black Rot Grape Leaf Disease



Fig. 3. Black Measles Grape Leaf Disease



Fig. 4. Isariopsis Grape Leaf Disease

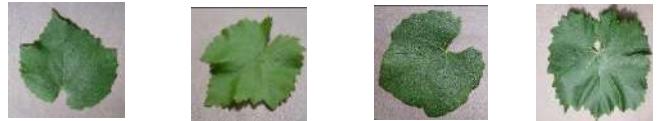


Fig. 5. Healthy Grape Leaves

Since there are no image data on which a single contains leaf multiple variety of diseases, montage of nine images randomly selected from the dataset were created to represent a single image which contains the three different diseases and the healthy leaves. This therefore produces an image simulation of multiple classes present in one image.

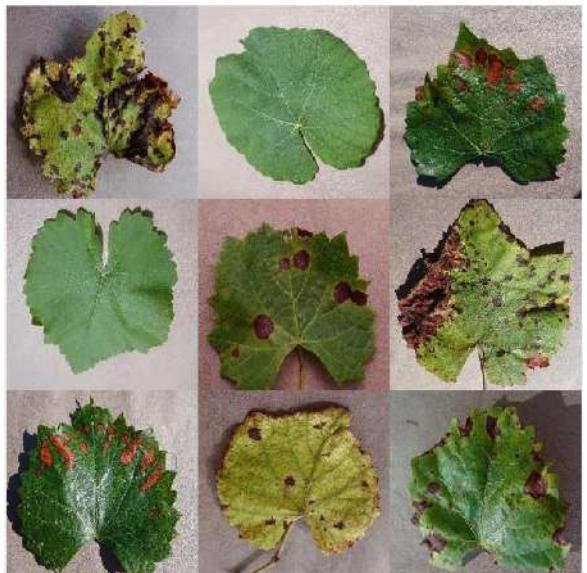


Fig. 6. Sample Montage of the Image Dataset for Multi-disease Leaf Simulation

It can be seen from the montage in Figure 6 that there are two leaves with Black Rot located at rows 2 and 3 at columns 2 and 3 respectively. There are two leaves black measles located at rows 1 and 3 at columns 3 and 1 respectively. There are three leaves with Isariopsis at rows 1, 2, and 3 at columns 1, 3 and 2 respectively. For the healthy leaves, they are located at rows 1 and 2 at columns 2 and 1 respectively. This brings a total of nine images preprocessed to be a single montage image consisting of four varieties of objects to be detected. 100 montage images were produced selecting 900 raw dataset images for annotation.

B. Data Annotation

Data annotation was done through the image labeler app of MATLAB R2020a. The montage created were uploaded in the application and a disease detecting session were developed. Four labels were set, namely: Isariopsis, Black_Measles, Black_Rot, and Healthy; with the corresponding color of rectangle bounding boxes as follows: purple, light blue, orange, and red. Each of the montage was annotated manually by selecting the regions to be detected in a single image. Shown in Figure 7 is a sample montage annotated for the diseases to be detected.

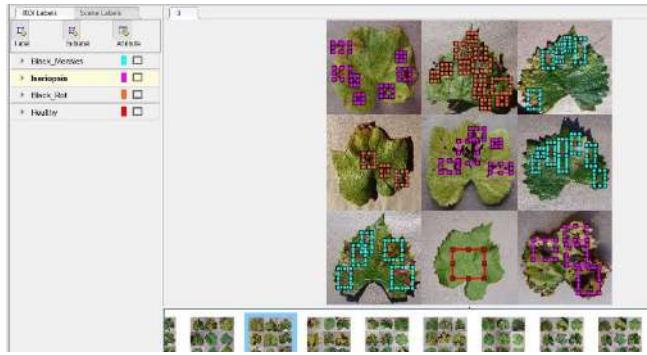


Fig. 7. Data Annotation Using MATLAB Image Labeler Application

After annotating the montage images, a ground truth table was exported to the MATLAB workspace to be used for training the model. Resizing of images to be compatible with the pre-trained networks was not considered because RCNN is already capable of resizing the montage images according to the image input size of the pre-trained networks.

C. Algorithm and Hyperparameter Setup

The algorithm created starts with the ground truth table being arranged so that the first column of the table consists of image files and directories of the montage located in a local folder. The second, third, fourth and fifth columns of the ground truth table were arranged so that they contain the four coordinates of the classes corresponding the montage file in column one. Two Directed Acyclic Graph Networks (DAG) were created with the GoogLeNet and ResNet-18 on which their last fully connected layers were replaced with a new one designated for four classifications added with one more as recommended. Their last layers, which is the classification layer was replaced as well. For the AlexNet, no DAG network was created and the network itself was used for training with the Regions with Convolutional Neural Network (RCNN).

These networks were chosen as the result of preliminary evaluations on which the three pre-trained networks provided the highest accuracies when re-trained by RCNN for obtaining

the objectives of this study. Specifically, AlexNet has proved to be one of the simplest networks yet can be trained to perform with high accuracy in detection applications. AlexNet is a pre-trained eight layer CNN architecture composed of five convolution and three fully-connected layers [25]. This network uses non-linear Rectified Linear Unit (ReLU) instead of the commonly used hyperbolic tangent function for activation and over pooling for reducing the pooling by 0.5%. GoogLeNet, also known as Inception-v1, utilizes CNN on which its architecture is composed on inception modules. Convolutional and pooling layers comprise these modules [26], on which a 1x1 convolution is at the middle of the network while the global average pooling is at the tail end of the network. ResNet in general is a pre-trained network that introduced the skipping of one or more layers known as “identity shortcut connection” as proven [27] that stacking layers would not diminish the performance.

Training options were predetermined and set before training the model. The parameters and their values are as follows:

1. Optimizing algorithm – Stochastic Gradient Descent with Momentum
2. Mini Batch Size – 32
3. Initial Learning Rate – 0.000001
4. Maximum Epochs – 10

These training options were utilized together with the three different pre-trained networks to be re-trained by the RCNN. Other options were not considered as the training resulted to high-performing models.

D. Model Training

Shown in Figure 8 is the last few iterations of the model training plot having RCNN to retrain GoogLeNet. The plot is represented in a table form having the Epoch column end at 10 as predetermined in the training options. The training took slightly over 9670 iterations stopping at 81.25% mini-batch accuracy and at 0.4712 mini-batch loss with a constant learning rate of 0.000001.

Epoch	Iteration	Time Elapsed	Mini-batch Accuracy	Mini-batch Loss	Base Learning Rate
10	8850	04:54:53	75.00%	0.7870	1.0000e-06
10	8900	04:56:27	81.25%	0.7244	1.0000e-06
10	8950	04:58:04	68.75%	1.0849	1.0000e-06
10	9000	04:59:43	68.75%	0.8010	1.0000e-06
10	9050	05:01:19	68.75%	0.8919	1.0000e-06
10	9100	05:03:06	62.50%	0.7845	1.0000e-06
10	9150	05:04:42	71.88%	0.7195	1.0000e-06
10	9200	05:06:23	65.75%	0.9373	1.0000e-06
10	9250	05:08:05	75.00%	0.8574	1.0000e-06
10	9300	05:09:54	71.00%	0.9437	1.0000e-06
10	9350	05:11:37	78.13%	0.8015	1.0000e-06
10	9400	05:13:20	68.75%	0.9599	1.0000e-06
10	9450	05:14:57	65.63%	0.9519	1.0000e-06
10	9500	05:16:30	71.88%	0.9532	1.0000e-06
10	9550	05:18:12	81.25%	0.5865	1.0000e-06
10	9600	05:19:47	73.00%	0.7272	1.0000e-06
10	9650	05:21:25	75.00%	0.7552	1.0000e-06
10	9670	05:22:02	81.25%	0.4712	1.0000e-06

Network training complete.
-> Training bounding box regression models for each object class...100.00%...done.
Detector training complete.

Fig. 8. Last Portion of Training Plot Using RCNN to Re-Train GoogLeNet for Disease Detection

Figures 9-11 are the architecture of the three pre-trained network re-trained by the RCNN.

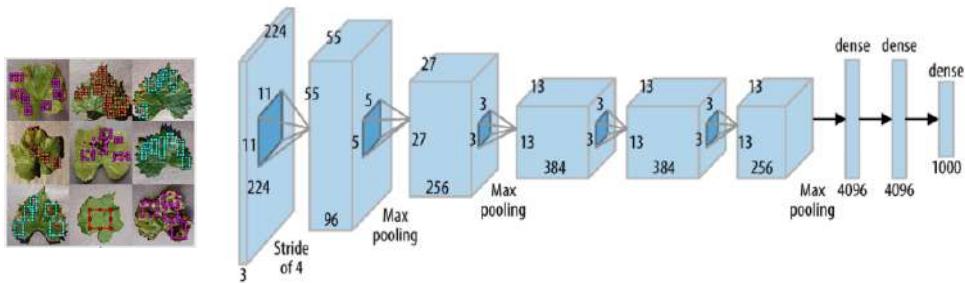


Fig. 9. AlexNet Architecture Used for Multi-disease Detection [28]

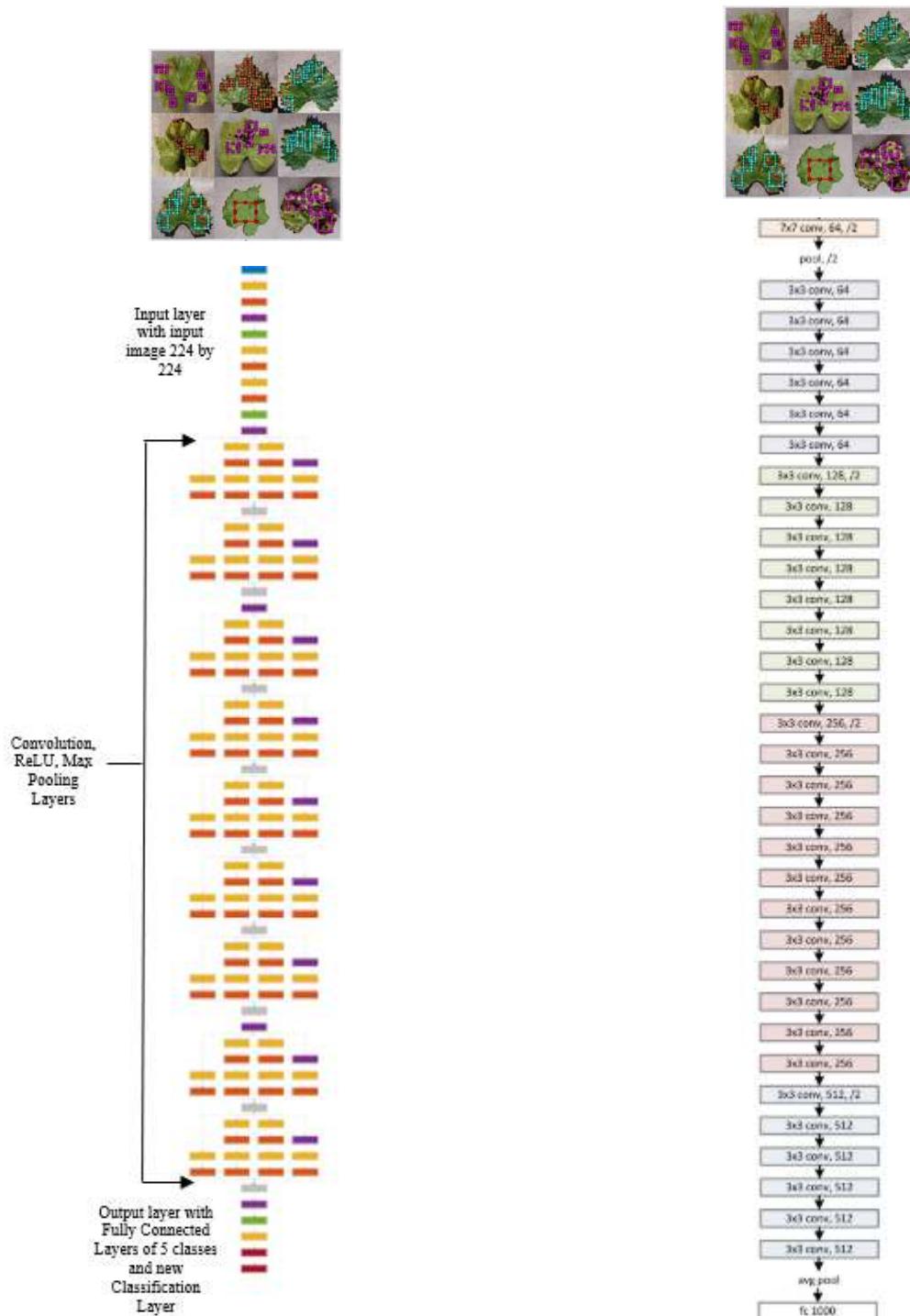


Fig. 10. GoogLeNet Architecture Used for Multi-disease Detection

Fig. 11. ResNet Architecture Used for Multi-disease Detection [29]

Regions with Convolutional Neural Network has been widely used in high-performing object detection applications [30] [31] as it is based on CNN capable of performing both classification and regression simultaneously to classify the objects and regress the coordinates of the bounding boxes to the objects to be detected.

IV. RESULTS AND DISCUSSION

After RCNN training, evaluations were done using new sets of montage images that were not yet seen by the model. Each of the three pre-trained networks were given test montage images consisting of nine leaves with four variant classes similar to the training data. Using the models as detect function, bounding boxes, confidence values, and labels were produced and then inserted to the testing data as object annotations. The results were limited to one bounding box for each leaf to avoid overcrowding of labels and confidence values. The healthy leaves are left unbounded. Figures 12 to 14 are one of the 10 resulting examples for each of the RCNN re-trained transfer learning networks.

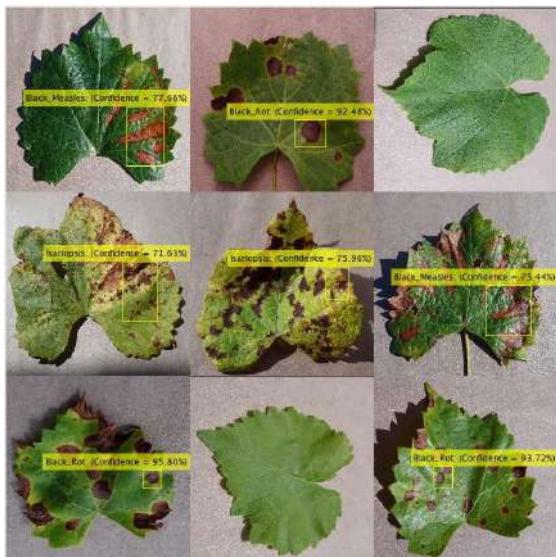


Fig. 12. RCNN-Trained AlexNet Sample Result

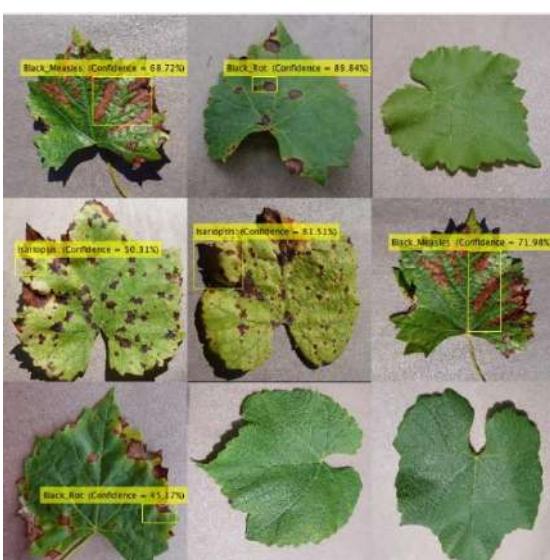


Fig. 13. RCNN-Trained GoogLeNet Sample Result

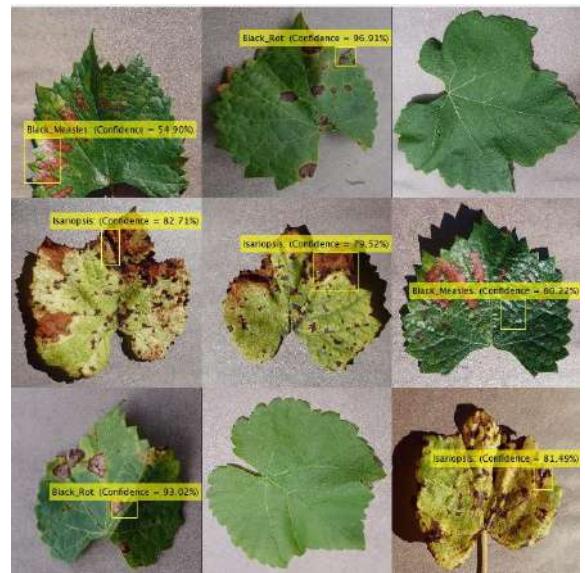


Fig. 14. RCNN-Trained ResNet-18 Sample Result

Confusion matrices were used to evaluate the overall performances of the models as well as in determining the accuracy in terms of classifying each disease for a montage image. The overall accuracies were computed by averaging the accuracy derived from each classification of all trained models. AlexNet obtained an accuracy of 95.65%, 92.29% accuracy for GoogLeNet, and ResNet-18's accuracy was 89.49%.

It can be analyzed from Tables II to IV that Isariopsis is the easiest disease to detect in a single montage image with an accuracy of 100% for all three models. Black Rot comes second with average accuracy of 92.75% for all models, 89.86% for Black Measles, and 87.30% for Healthy. However, to optimize performance ResNet-18 can be used to detect Black Rot for 100% accuracy, and AlexNet for Black Measles and Healthy with 95.65% and 100% accuracy respectively.

TABLE II. CONFUSION MATRIX OF ALEXNET DETECTION

Actual Values	Predicted Values			
	Black Rot	Black Measles	Isariopsis	Healthy
Black Rot	20	0	0	0
Black Measles	1	22	0	0
Isariopsis	0	0	23	0
Healthy	2	1	0	21
Accuracy	86.96%	95.65%	100.00%	100.00%

TABLE III. CONFUSION MATRIX OF GOOGLENET DETECTION

Actual Values	Predicted Values			
	Black Rot	Black Measles	Isariopsis	Healthy
Black Rot	21	2	0	1
Black Measles	0	19	0	0
Isariopsis	1	0	23	0
Healthy	1	2	0	20
Accuracy	91.30%	82.61%	100.00%	95.24%

TABLE IV. CONFUSION MATRIX OF RESNET-18 DETECTION

Actual Values	Predicted Values			
	Black Rot	Black Measles	Isariopsis	Healthy
Black Rot	23	2	0	6
Black Measles	0	21	0	1
Isariopsis	0	0	23	0
Healthy	0	0	0	14
Accuracy	100.00%	91.30%	100.00%	66.67%

V. CONCLUSION

The study conducted was able to produce three high performing models for detecting multi-disease in a single montage image using transfer learning and RCNN. The models can also suggest which among the models can be best used for a specific classification. Overall, re-training the pre-trained AlexNet through the RCNN obtained the best results in achieving detecting three variants of diseases that can be found in grape leaves separating from the healthy ones. Recommendations for this paper involves the use of other pre-trained networks and the use of either Fast RCNN or Faster RCNN to compare and determine which networks could possibly enhance the performance of the models.

ACKNOWLEDGMENT

The researchers would like to thank the Engineering Research and Development Technology (ERDT) of the Department of Science and Technology (DOST) of the Philippines and the De La Salle University (DLSU) Intelligent Systems Laboratory (ISL) for the support they provided.

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A Novel Classification Approach for Grape Leaf Disease Detection Based on Different Attention Deep Learning Techniques

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Abstract—Preventing and controlling grape diseases is essential for a good grape harvest. With the help of “single shot multi-box detectors”, “faster region based convolutional neural networks”, & “You only look once-X,” the study improved grape leaf disease detection accuracy with effective attention mechanisms, which includes convolutional block attention module, squeeze & excitation networks, & efficient channel attention. The various attention techniques helped to emphasize important features while reducing the impact of irrelevant ones, which ultimately improved the precision of the models and allowed for real-time performance. As a result of examining the optimal models from the three types, it was found that the Faster (R-CNN) model had a lower precision value, while You only look once-X and SSD with various attention techniques required the fewest parameters with the highest precision, with the best real-time performance. In addition to providing insights into grape diseases & symptoms in automated agricultural production, this study provided valuable insights into grape leaf disease detection.

Keywords—Grape leaves; faster region-based convolutional neural networks; you only look once (x); single shot detection attention techniques

I. INTRODUCTION

Preventing and controlling crop diseases is crucial for producing safe and healthy vegetables, minimizing losses, and reducing the use of pesticides in the production of crops [1]. Thus, early detection & prevention of diseases are crucial. Grape plants can be affected by various diseases, such as powdery mildew, brown blotch, and anthracnose, which can significantly impact the yield and quality of the fruit. Traditional methods of detecting grape diseases rely on the experience of the growers or the guidance of experts, which can be slow, inefficient, and lack real-time performance. Images of grape leaves are used to detect, identify, and provide guidance about diseases infected with grape leaves [2] because disease-infected grape leaves often have visible spots.

Grape leaf disease detection is crucial for several reasons. Firstly, it allows growers to monitor the health of their grapevines and take appropriate actions to prevent or

manage diseases effectively. Early detection enables timely interventions, minimizing potential damage and crop losses. Different grape leaf diseases require specific treatments, and accurate identification helps growers implement targeted control measures. This optimizes the use of pesticides, reduces environmental impact, and ensures effective disease management.

Grape leaf diseases can significantly impact the yield and quality of grapevine production. Some diseases cause defoliation, reducing the vine's ability to photosynthesize and produce energy, leading to decreased fruit quality, delayed ripening, and reduced yield. Early disease detection enables growers to protect the crop and implement measures to minimize yield losses. Early identification of grape leaf diseases is essential for preventing their spread within vineyards. Prompt isolation and treatment of infected vines help prevent diseases from affecting healthy plants. Additionally, preventive measures such as pruning, canopy management, and cultural practices can be implemented to reduce the likelihood of disease occurrence and spread. Economically, grapevines are valuable crops, and detecting diseases in grape leaves allows growers to make informed decisions on disease management, optimizing resource utilization, and reducing unnecessary costs. This helps preserve the economic viability of vineyards and sustain profitability in grape production.

Efficient disease detection and management practices also contribute to sustainable agriculture. Early identification minimizes the use of broad-spectrum pesticides, reducing their negative impact on the environment and non-target organisms. Targeted treatments based on accurate disease detection help reduce chemical inputs, promote ecological balance, and support sustainable cultivation practices for grapevines. In summary, grape leaf disease detection is vital for crop health monitoring, disease management, yield protection, disease prevention, economic considerations, and sustainable agriculture. Early detection allows for timely interventions, optimization of disease control measures, minimization of crop losses, and the long-term sustainability of grapevine production.

Due to the rapid development of artificial intelligence technologies, a wide variety of vision approaches are utilised in the processing of photos for various crop diseases [3][4][5]. Research into classifying agricultural diseases uses a wide range of approaches, including “genetic algorithms” [6], “support vector machines” [7], “K-means clustering” [8], “ensemble learning” [9], “Bayesian classification” [10], “radial basis functions” [11], & “filter segmentation” techniques [12]. Unfortunately, conventional approaches to crop disease classification and identification rely on labour-intensive, environment-dependent manual feature selection. In particular, the development of deep learning’s Convolutional Neural Network (CNN) has led to vast improvements in the field of autonomous detection and identification of agricultural diseases.

An object detection system that uses a convolutional neural network (CNN) has made great strides recently. Several applications make use of this technique, including recognition of faces [13], navigation [14], detection of road obstacles [15], detection of pedestrians, abnormal activity recognition[16], monitoring of physical activity[17][?], [18] detection of fruits, and detection of weeds [19]. Despite complex backdrops, crop leaf diseases can be detected using object detection algorithms due to CNN’s ability to extract high-dimensional properties from object images.

As a result, scientists in China and others have studied object detection algorithms to develop models for detecting crop diseases. For instance, Some authors have applied various models for object detection to the tomato disease dataset, including the Faster(R-CNN), and the Single Shot Multibox Detector. Faster (R-CNN) as well as VGG16, produced the best disease detection results. Dynamic identification of grape leaf illnesses was accomplished by using Faster (R-CNN) on time-series images of grape leaves. Using an enhanced Faster (R-CNN) model, the authors of [20] detected diseases in bitter gourd leaves with excellent results. Using an in-house dataset, The authors of [21] trained the SSD model to identify agricultural diseases with an overall accuracy of 83.90%. An enhanced model based on MobileNetv2 & YOLOv3 was proposed by the authors [22], which allowed for the early detection of grey speck disease in tomatoes. This refined model benefits from a number of desirable characteristics, including a low memory size, outstanding detection accuracy, and lightning-fast identification.

Previous studies have shown that using object detection technology to detect grape leaf diseases is feasible. Existing grape detector models, however, operate slowly and have low detection precision, which severely limits their application. This research included the attention methods of “convolutional block attention module,” “efficient channel attention,” & “squeeze & excitation attention” into the models of “Faster(R-CNN),” “SSD,” & “YOLO-X” to boost their accuracy and speed. The goal was to boost the feature extraction network’s efficiency and put more emphasis on health issues. Experiments were run on a plant village dataset of grape diseases, and the findings revealed that models based on diverse attention mechanisms, such as “Faster(R-CNN),” “SSD,” & “YOLO-X,” significantly improved detection accuracy and operation performance with only little parameter tweaks. The findings of this study can be used as a foundation for future work on grape disease control measures. The main objectives of the

paper are to enhance the accuracy and speed of grape leaf disease detection, improve the efficiency of feature extraction networks, validate the performance improvements on a grape disease dataset, and provide a foundation for future grape disease control measures.

However, the existing literature lacks research on incorporating attention mechanisms, such as the “convolutional block attention module,” “efficient channel attention,” and “squeeze & excitation attention,” into grape detector models like “Faster(R-CNN),” “SSD,” and “YOLO-X.” There is a gap in knowledge regarding the potential impact of attention mechanisms on improving detection accuracy and processing speed for grape leaf diseases. The main objectives of the paper are:

- Enhance the accuracy and speed of grape leaf disease detection: The purpose of this work is to enhance the efficiency of previously developed grape detection models by incorporating attention mechanisms such as “convolutional block attention module,” “efficient channel attention,” and “squeeze & excitation attention” into the models of “Faster(R-CNN),” “SSD,” and “YOLO-X.” The objective is to achieve higher detection accuracy and faster processing speeds, addressing the limitations of slow operation and low detection precision in existing models.
- Improve the efficiency of feature extraction networks: By integrating attention methods into the models, the paper aims to enhance the efficiency of the feature extraction networks. The attention mechanisms help to prioritize relevant features and emphasize health issues related to grape leaf diseases, leading to more effective and accurate detection.
- Validate the performance improvements on a grape disease dataset: The research conducts experiments using a dataset specifically focused on grape diseases. By evaluating the models based on diverse attention mechanisms, such as “Faster(R-CNN),” “SSD,” and “YOLO-X,” the paper aims to demonstrate significant improvements in detection accuracy and operation performance. The experiments involve minimal parameter tweaks, ensuring that the observed enhancements are primarily attributed to integrating attention mechanisms.
- Provide a foundation for future grape disease control measures: The findings of this study serve as a basis for future work on grape disease control measures. By demonstrating the effectiveness of attention mechanisms in improving detection accuracy and speed, the paper offers valuable insights and guidance for the development of advanced and efficient techniques for managing and controlling grape leaf diseases.

II. RELATED WORK

Detecting plant diseases in a timely manner is crucial for effectively managing plant losses. However, relying on manual diagnosis by humans is a time-consuming process that is prone to errors and can be costly. To address these challenges, researchers have been actively exploring automated

techniques for disease detection and classification in plants. The utilization of automated equipment and methods has emerged as a promising approach for monitoring crop fields. In this section, we will delve into the specifics of computer vision methods employed to identify and diagnose diseases in plant leaves.

The authors of [23] conducted a study focusing on detecting black rot in grape leaves using a YOLOv3-SPP-based deep learning method. The researchers employed a combination of super-resolution image enhancement and convolutional neural network techniques to identify the disease in grape leaves. The initial step involved upsampling the input image through bilinear interpolation. After enhancement, the processed inputs were fed into the YOLOv3-spatial pyramid pooling model, resulting in a remarkable detection accuracy of 95.79%. However, when tested in real field conditions, the precision of this method dropped to 86.69%. In a separate study, The authors of [24] proposed a deep learning approach specifically for accurately detecting black rot spots on grape leaves. They employed the DeepLab V3+ model, which incorporates feature maps from different levels and utilizes ResNet 101 as the backbone network. The test results demonstrated that the improved DeepLab V3+ model outperformed conventional methods.

The authors of [25], [26] developed a novel support vector machine & image processing-enabled technique for identifying and categorizing grape leaf disease. The authors of [27] employed a CNN-SVM-based approach to classifying five different species of grapevine leaves. They utilized the MobileNetv2 CNN model for leaf-type classification. Initially, features were extracted from the pre-trained MobileNet2 logits layer, and classification was performed using SVM with various kernels. The Chi-squares method was applied for feature selection, resulting in an impressive classification accuracy of 97.60%. The use of feature selection techniques significantly contributed to the improved accuracy of classification.

The authors of [28] focused on detecting grape black measles disease. They utilized the ResNet-50-based DeepLabV3 segmentation model in combination with fuzzy logic to determine the severity of the disease. The input image provided region of interest features and the percentage of infections. A fuzzy rule-based reference system was developed based on each feature, which was then used to grade the grape disease. The grading system allowed for the classification of healthy, mild, medium, and severe cases, specifically for measles disease.

III. MATERIALS AND METHODS

A. Image Acquisition

The plant-Village dataset provides 4,062 images of grape leaves displaying common symptoms. In this dataset, 1,180 images were found to be affected by Black Rot, 1,383 by Esca measles, 1,076 by Leaf spot, and 423 by healthy leaves, all with a resolution of 256 × 256 pixels. A leaf with black rot, a leaf with black measles, a leaf with blight, and a healthy leaf is displayed in Fig. 1.

The data set contains varying quantities of images for each category, indicating significant imbalances. Esca is the most

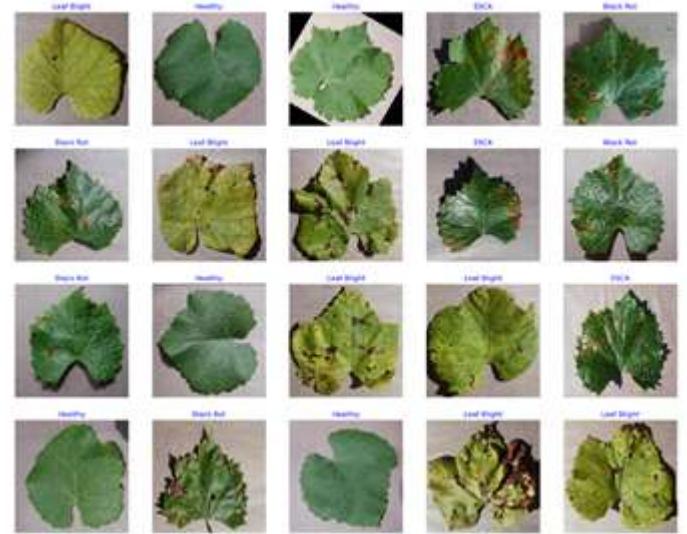


Fig. 1. Sample images from dataset.

TABLE I. LIST OF PARAMETERS USED FOR IMAGE ENHANCEMENT

Enhancement method	Parameters
gaussian filter	sigma-range(0.4,1.3)
mean filter	kernel-size-range(3,5)
median filter	kernel-size-range(2,5)
image acutance	alpha-range(0,0.2)
brightness	gamma(2.0)
contrast	alpha(1.0)

common classification, accounting for roughly 34% of the images, while Black Rot and Leaf Blight make up 29% and 26% respectively. There are also 1076 Healthy images and 10.4% Normal images in the collection.

B. Image Pre-processing and Augmentation

The size of the dataset must be increased by using data augmentation techniques in order to prepare grape leaves disease images for disease identification. Training the recognition model in this way ensures that it will be more resilient and can generalize more effectively. Using standard data augmentation methods, the experiment compared the effectiveness of the data augmentation method proposed in this study. The traditional methods included flipping the image horizontally and vertically, rotating the image, applying different types of filtering (Gaussian, mean, and median) with a probability of 0.2, enhancing image contrast, sharpening images with a probability of 0.3, and adjusting image brightness. According to Table I, the parameters used for each image enhancement method are listed. Table II provides more details about the dataset and can be accessed at <https://www.kaggle.com/datasets/rm1000/augmented-grape-disease-detection-dataset>.

C. Proposed Methodology for Grape Leaf Disease Detection

This study focuses on the detection of grape leaf diseases using three specific models: faster-rcnn, YOLOx, and SSD. The training process for these models to detect diseases in grape leaves is depicted in Fig. 2. The process begins with inputting

TABLE II. INFORMATION ABOUT THE DATASET

Class	No of images without augmentation	No of images with augmentation
Healthy	423	3000
Esca measles	1383	3000
Leaf spot	1076	3000
Black rot	1180	3000
Total	4062	12000

the selected grape leaf disease images. Next, classification features are extracted from the input images. Output is then derived from the findings of disease identification using the faster-rcnn, YOLOx, and SSD models.

A loss function is used throughout to quantify the degree to which the projected disease species deviates from the true disease species. This enables the models to learn and improve their detection accuracy over time. The optimization of the final output result is achieved through the utilization of the Adam optimizer, a widely used optimization algorithm in deep learning.

By following this approach, the study aims to leverage the capabilities of faster-rcnn, YOLO:x & SSD models to detect grape leaf diseases effectively. The training flow chart provides a systematic framework for the feature extraction and disease detection process, facilitating the accurate identification of different disease species in grape leaves.

D. Attention Mechanism Models

The study utilizes three attention mechanisms: “Squeeze & Excitation”, “efficient channel attention”, and “Convolutional Block Attention” spatial attention mechanism. We chose the SE attention mechanism because it is simple and adds only a few new parameters. With ECA attention, models become more accurate without significantly increasing model complexity. It is an enhanced version of the SE attention mechanism. Finally, the CBAM attention mechanism is useful because it connects the spatial domain and the channel domain, leading to more effective improvement in network performance.

1) *Squeeze & Excitation Attention*: In order to extract features, the SE channel attention mechanism employs the CNN channel. It requires re-calibrating features so that the model can pick up and remember relevant details from all of the available feature channels. Fig. 3 depicts the two steps involved in this mechanism: squeezing and excitement. After the feature image has been spatially compressed using the squeeze technique, the feature channel’s relative relevance can be determined using the excitation technique; a model is created based on the correlation between the channels. In doing so, the original feature images are excited into matching channels. The SE mechanism has few additional parameters and is computationally simple.

The “efficient channel attention” attention mechanism is utilized to enhance cross-channel interaction and reduce model complexity, while the Squeeze & Excitation attention mechanism is used to prioritize the most informative channel features for disease identification. For end-to-end training of the grape leaf disease detection model, the “Convolutional Block

Attention Module” attention mechanism is introduced to take into account the importance of pixels in different places. All three attention methods contribute significantly to improving the model’s efficiency and precision.

2) *ECA Attention Module*: It uses local cross channel interaction methods without reducing the magnitude of the dimensionality can be accomplished without using reduced-dimension SE. The functionality of the attention module is enhanced while its complexity is decreased thanks to this mechanism. In Fig. 4 we can observe the construction of the efficient channel attention mechanism.

3) *CBAM Attention Module*: The “CBAM Spatial Attention Module” is made up of 2 modules, first one is the “spatial attention module”, second one is the “channel attention module” and is designed to optimize input feature maps by inferring attention maps on both channel and spatial dimensions. These attention maps are then multiplied with the input feature map, resulting in self-adaptive feature optimization. The CBAM mechanism is effective in enhancing useful features while suppressing those that are not useful, making it a popular tool in practical applications. Fig. 5 illustrates the network structure of CBAM.

E. Detection Models for Disease Detection in Grape Leaves with Attention Mechanism

CNN-based object detection can be categorized into two main types. The first type uses a regional proposal to detect objects. This involves identifying candidate regions in the image, which are then divided to detect objects. This two-stage approach is exemplified by methods such as “R-CNN”, “Fast(R-CNN)”, & “Faster(R-CNN)”. The second type of object detection does not use a regional proposal and is referred to as one-stage object detection. An image is analyzed based on a CNN prediction of an object’s position & properties. There are a variety of algorithms available for this type of detection, such as SSDs and YOLOs.

The study used three models, namely the “Faster R-CNN model”, “YOLO-X model”, & “SSD model” for detecting grape leaves disease. The input of the selected grape leaf disease images, extraction of classification features, and use of the three disease detection models were involved in the process. The output was an analysis of the disease detection results. For optimizing the final output, an Adam optimizer was used to predict the difference between reality and the prediction of disease species.

Researchers found that the ” Faster(R-CNN)” model boosts high detection accuracy and can detect targets end-to-end. However, its running speed is relatively slow. On the other hand, the “YOLO-X” model runs quickly, but it doesn’t detect small objects. The “SSD” technique has faster running speed and higher detection accuracy than the “YOLO-X” model, but its training process heavily relies on prior experience, and its performance in detecting small targets is not as good as the “Faster(R-CNN)” model. The characteristics of these models are elaborated as follows:

1) *Grape Leaves Disease Detection using Faster (R-CNN) Model*: This model is comprised of three main components: the “Extraction of features”, the “Region Proposal Network”

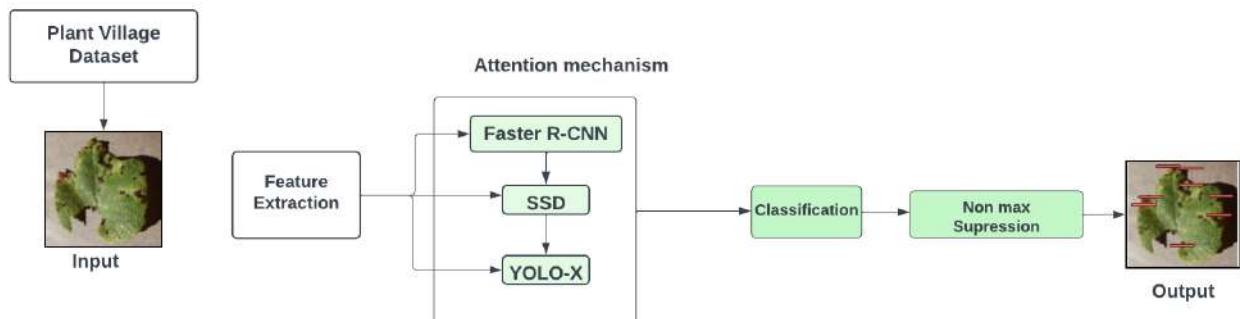


Fig. 2. Proposed attention model for grape disease detection.

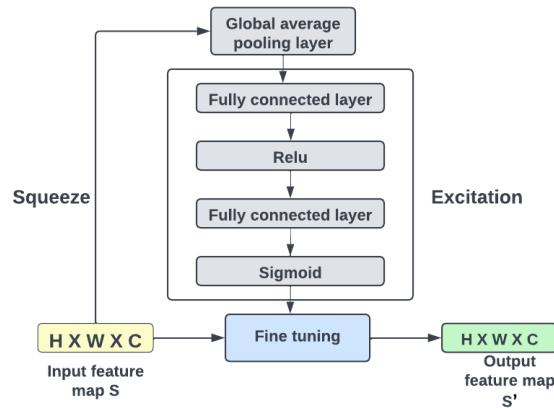


Fig. 3. SE attention mechanism.

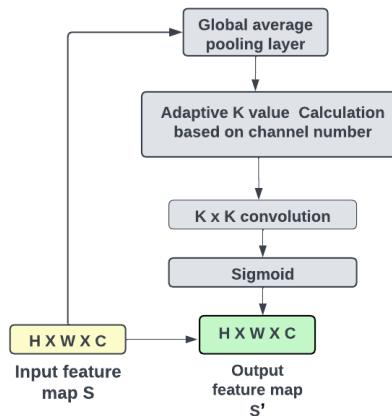


Fig. 4. ECA attention mechanism.

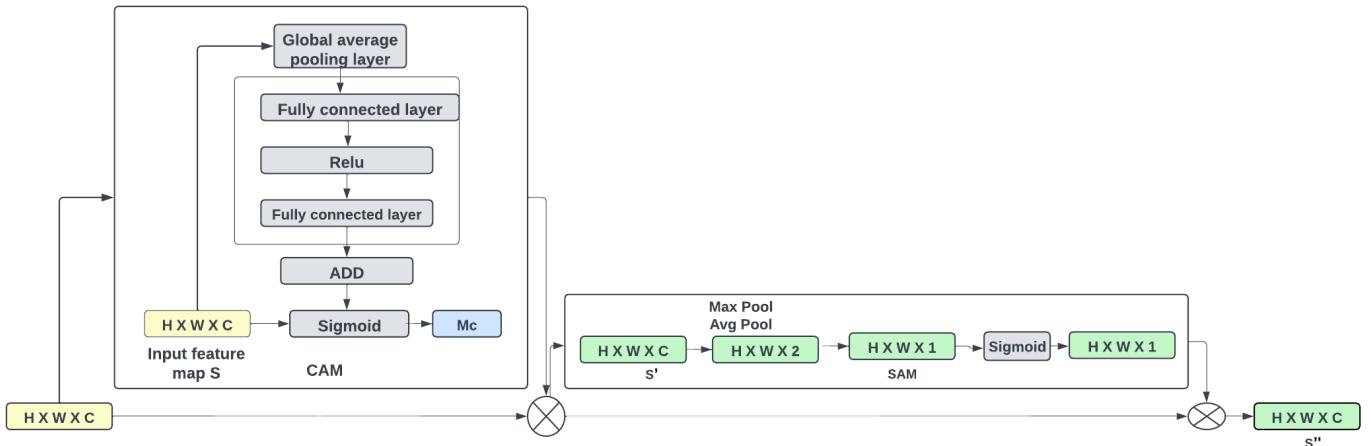


Fig. 5. CBAM attention mechanism.

, and the “Region with Convolutional Neural Network Features”. Fig. 6 depicts the Faster (R-CNN) model with attention techniques. A Faster (R-CNN) method is used to detect grape leaf diseases in four primary steps: generating candidate disease regions, extracting disease characteristics, categorizing the disease, and performing bounding box regression. The Faster (R-CNN) model utilizes convolutional neural networks for the extraction of features and then generates feature maps for corresponding images. However, the convolution kernel’s inherent locality means that only local information of disease images is retained, leading to information loss and reduced detection accuracy. To address this issue, the study introduced attention mechanisms, namely SE, ECA, and CBAM, without changing the feature extraction network’s structure or backbone features. As a result of forward propagation after the last identity block, these mechanisms were introduced to enhance the model.

2) *Grape Leaves Disease Detection using YOLO-X Model*:: The YOLO-X with Darknet53 network is a model with high operational speed and flexibility. It includes four primary components: the input end, Backbone network, Neck, and Prediction. Fig. 7 illustrates the YOLO-X model based on various attention mechanisms. In the YOLO-X model, the YOLO Head has been changed to a decoupled head in the prediction section, the anchor-based approach has been replaced with an anchor-free method, and the SimOTA method has been introduced for dynamic matching with positive samples. The model’s detection accuracy and speed have both been enhanced by these revisions, and the models’ parameter sizes have been significantly decreased. The YOLO-X model is known for its high detection speed and precision, but it has some limitations when applied directly for disease detection in different environments. For instance, its backbone lacks the ability to extract features and integrate high-quality contextual feature information, leading to a reduction in the model’s detection precision. Therefore, in this study, the Darknet53 network structure of the YOLO-X model remained unchanged, allowing pre-training weights to be directly loaded into model training. The YOLO-X model can selectively strengthen key features while suppressing irrelevant ones based on the branches of the backbone network, namely “Darknet53”, “convolutional block

attention module”, “efficient channel attention” and “squeeze & excitation attention mechanisms.

3) *Grape Leaves Disease Detection using SSD Model*:: Using a tiny convolution kernel and multi-dimensional feature prediction, the model combines the anchor mechanism of Faster (R-CNN) with the regression mechanism of “YOLO” for fast and accurate detection. Fig. 8 depicts the SSD model that includes attention mechanisms. The first component is an enhanced capability for disease detection based on the deep learning network model used to collect baseline disease features. The multi-scale feature detection network is the second part, and it uses cascaded-neural-networks to categorize features at various scales in order to learn about the disease’s category and location, as well as low-layer convolutional layer features to enhance detection precision and Non-Maximum suppression to generate the final detection results. Using a multi-dimensional prediction strategy, the SSD model is able to distinguish between small and large objects; the front-end deep-learning models are responsible for the former, while at the back-end multi-dimensional feature detection models handle them. Although the front-end network delivers precise coordinates and geometry, it has a limited range of perception and isn’t great at representing abstract concepts. Whereas the frontal network has a narrow receptive field and poor representational capacity for geometric data, the posterior network has a wide receptive field and excellent representational ability for semantic data. Because of this, the SSD model may overlook some diseases or incorrectly identify others. Six feature images of varying sizes were collected from the “SSD” model and supplied into the various attention modules in order to better represent critical feature information and identify disease object features. With this method, the SSD model is better able to recognize diseased items.

IV. RESULTS AND EXPERIMENTS

A. Evaluation Metrics

Results were evaluated based on standard measures for evaluating target detection. One class of targets will be evaluated using “Precision,” “Recall,” “Average Precision,” and

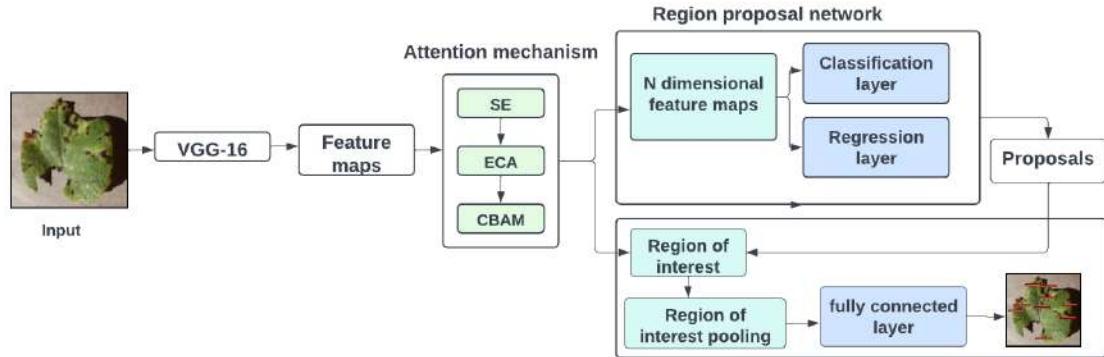


Fig. 6. Faster (R-CNN) model with attention techniques.

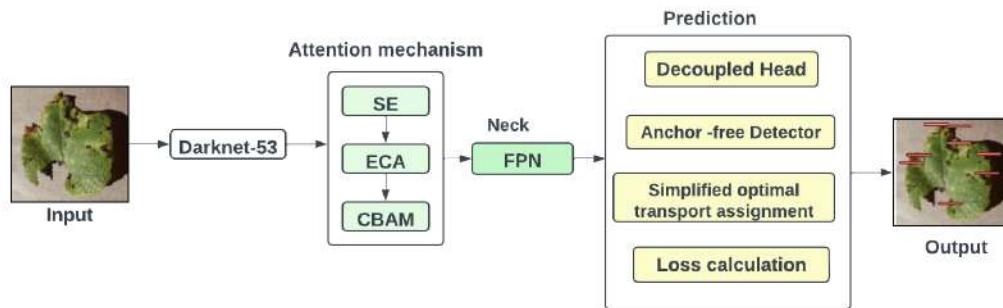


Fig. 7. YOLO-X model with attention mechanism.

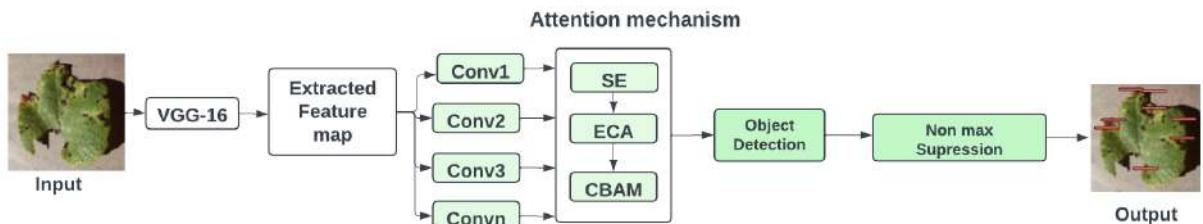


Fig. 8. SSD model with attention mechanism.

"Mean Average Precision," while all targets will be evaluated using "Mean Average Precision." However, in this study, we evaluated the grape leaf disease detection model's performance on a wider set of metrics, including the mean absolute percentage (mAP), the frame rate (FPS), the parameters, and the precision (P) and recall (R) values. The Eq. 1,2 and 3 were used to calculate P, R, and F1.

$$Precision = \frac{TruePositives}{TruePositives + FalsePositives} * 100 \quad (1)$$

$$Recall = \frac{(TruePositives)}{(TruePositives + FalseNegatives)} * 100 \quad (2)$$

$$F1score = \frac{(2 * Precision.Recall)}{(Precision + Recall)} \quad (3)$$

In Eq. 4, the variables P, TP, FP, R, FN, and F1 represent various metrics used to evaluate the performance of a model. P is the precision, which measures the percentage of correct positive predictions. The probability that grape disease leaves are accurately detected is denoted by true positives ('TP'), whereas the probability that they are mistakenly categorised as positive is denoted by false positives ('FP'). Recall, or the proportion of true positives that were correctly detected, is denoted by the letter R. The likelihood of mislabeling a positive sample as negative is known as the "False negatives" ('FN') rate. F1 is a measure of accuracy that is the harmonic mean of two other metrics, recall and precision.

$$\int_0^1 P R dR \quad (4)$$

TABLE III. COMPARISON ANALYSIS OF FASTER (R-CNN) MODELS WITH DIFFERENT ATTENTION TECHNIQUES FOR DETECTING GRAPE DISEASES

Model	Precision	Recall	F1-Score	mAP
Faster (R-CNN) model	75.06	74.42	74.74	79.12
Faster (R-CNN) with SE Attention	79.80	84.23	81.96	85.39
Faster (R-CNN) with ECA Attention	76.54	78.71	77.61	81.93
Faster (R-CNN) with CBAM Attention	75.75	75.89	75.82	79.65
Faster (R-CNN) with SE, ECA,CBAM Attention	84.52	86.32	80.79	84.31

A higher value for TP indicates a more accurate prediction & better performance of the model. A model's performance can be measured using mAP, which is a metric that averages the average precision of all diseases. Eq. 5 defines mAP as the average of all AP values. FPS stands for the number of pictures handled each second. The algorithm's ability to recognize items improves as the FPS increases.

$$mAP = \frac{1}{N} \sum_{m=1}^N AP \quad (5)$$

A computer with 16 GB of RAM is used for this research, which runs Windows 10. Model parameters and hardware configuration are considered in Pytorch 1.10.1.

B. Experiment Results and Analysis

The grape disease dataset was utilized to compare the Faster(R-CNN), YOLO-X, and SSD models with the classical versions based on different attention mechanisms. The models were all trained and detected with the same configuration information and training platform.

1) Faster (R-CNN) Result Analysis: The “Faster(R-CNN)” model can be combined with different attention mechanisms to create different versions. Also we have combined the three attention mechanisms i.e. Faster (R-CNN) with SE, ECA,CBAM Attention. To test their performance in detecting grape diseases, all these versions were used in the same experimental setup, and the results are presented in Table III and in Fig. 9. Table III presents a comparison between the Faster (R-CNN) model and four modified versions: “Faster (R-CNN) with SE Attention”, “Faster (R-CNN) with ECA Attention”, and “Faster (R-CNN) with CBAM Attention”. The results indicate that the Faster (R-CNN) with SE Attention model outperformed the original model with an increase in P, R, and F1 values by 4.74%, 9.81%, and 7.22% respectively, and an increase in mAP by 6.27%. Similarly, the Faster (R-CNN) with ECA Attention model showed improvements over the original model with an increase in P, R, and F1 values by 1.48%, 4.29%, and 2.87% respectively, and an increase in mAP by 2.81%. Finally, the “Faster (R-CNN) with CBAM Attention” model showed slight improvements over the original model with an increase in P, R, and F1 values by 0.69%, 1.47%, and 1.08% respectively, and an increase in mAP by 0.53%.

Based on the analysis above, it is evident that the performance of Faster (R-CNN) improved after the inclusion of attention mechanisms, despite a slight increase in parameters for “Faster (R-CNN) with SE Attention and Faster (R-CNN) with CBAM Attention”. Enhanced precision and accelerated

TABLE IV. COMPARISON ANALYSIS OF YOLO-X MODELS WITH DIFFERENT ATTENTION TECHNIQUES FOR DETECTING GRAPE DISEASES

Model	Precision	Recall	F1-Score	mAP
YOLO-X model	82.35	74.85	78.42	83.22
YOLO-X with SE Attention	82.46	82.21	82.33	84.02
YOLO-X with ECA Attention	87.77	86.07	86.91	88.66
YOLO-X with CBAM Attention	85.81	77.91	81.67	84.21
YOLO-X with SE, ECA,CBAM Attention	89.77	86.97	85.91	88.96

speed of detection are achieved through the attention mechanism for grape leaves images. Among the various models, “Faster (R-CNN) with SE, ECA, CBAM Attention” displayed the best detection effect when compared with “Faster (R-CNN) with SE Attention”. The “Faster (R-CNN) with SE Attention” model demonstrated a 3.26%, 5.52%, and 4.35% increase in P, R, and F1 values, respectively, with an increase of 3.46% in mAP. In comparison with ” Faster (R-CNN) with CBAM Attention”, ” Faster (R-CNN) with SE Attention” increased P, R, and F1 by respectively 4.05%, 8.34%, and 6.14%. When precision is considered, the ” Faster (R-CNN) with SE, ECA, and CBAM Attention” model shows optimal results. It focuses on channel features with the most significant information while suppressing un-important features, making it ideal for detecting grape diseases in the dataset.

2) YOLO-X Result Analysis: The YOLO-X model has been enhanced with different attention mechanisms: SE, ECA, and CBAM. To compare their performance, all the models (including the original YOLO-X model) were tested on the dataset under the same configuration. The results are shown in Table IV and in Fig. 10. Table IV shows that the “YOLO-X with SE Attention” model has improved performance compared to the YOLO-X model. Specifically, the precision, recall, and F1 values of the “YOLO-X with SE Attention” model increased by 0.11 %, 7.36 %, and 3.91 %, respectively, while the mAP increased by 0.8%. Similarly, the “YOLO-X with ECA Attention” model also outperformed the YOLO-X model, with increases of 5.42%, 11.22%, and 8.49% in precision, recall, and F1 values, respectively. The mAP also increased by 5.44% respectively. The “YOLO-X with CBAM Attention” model also showed improvements, with increases of 3.46%, 3.06%, and 3.25% in precision, recall, and F1 values, respectively, and a 0.99% increase in mAP. Based on the analysis above, it was found that the detection performance of the YOLO-X model was improved with the introduction of attention mechanisms, despite a slight increase in the parameters of the “YOLO-X with SE Attention” and “YOLO-X with ECA Attention” models. Models were able to identify disease objects more accurately due to the attention mechanisms that allowed them to extract more comprehensive and rich features.

Out of all the models, the “YOLO-X with SE, ECA,CBAM Attention” model had the best detection performance. Compared to the “YOLO-X with SE Attention” model, the “YOLO-X with ECA Attention” model had a 5.31%, 3.86%, and 4.58% increase in P, R, and F1 values, respectively, a 4.64% increase in mAP, a 4.8 increase in FPS value, and a 0.49 MB expansion in parameters. Compared to the “YOLO-X with CBAM Attention” model, the “YOLO-X with ECA Attention” model had a 1.96%, 8.16%, and 5.24% increase in P, R, and F1 values, respectively, a 4.45% increase in mAP, a 1.8 increase in FPS value, and a 0.66 MB expansion in parameters. Compared to other models YOLO-X with SE, ECA,CBAM Attention

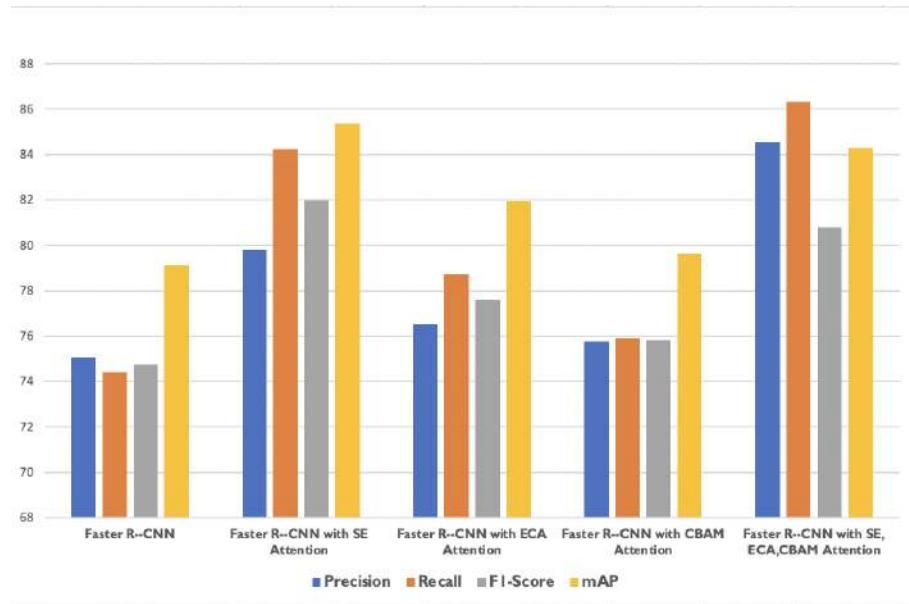


Fig. 9. Comparison analysis of Faster (R-CNN) models with different attention techniques.

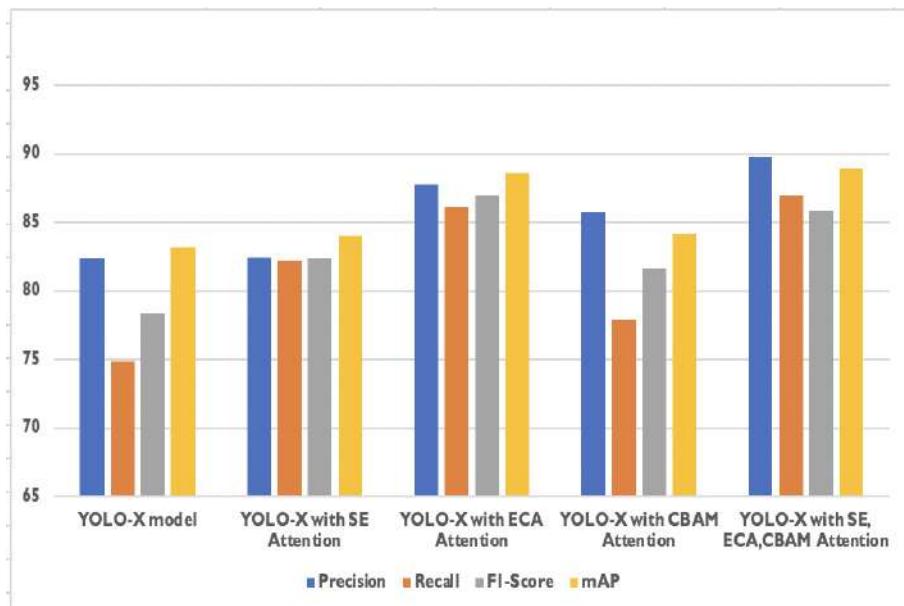


Fig. 10. Comparison analysis of YOLO-X models with different attention techniques.

models had outperformed than previous models. In conclusion, even though the “YOLO-X with SE, ECA,CBAM Attention” model had more parameters than the other three models, it achieved the best detection results with fast operation speed on the grape disease dataset, partially due to its ability to achieve cross-channel interaction.

3) SSD Result Analysis: Under the same experimental conditions, all the models were utilized to detect diseases on the plant village dataset, & the results of the experiment can be found in Table V and in Fig. 11.

Table V displays the results of various different models. The comparison is based on various metrics, including precision (P), recall (R), and F1 values, mean average precision (mAP).

Compared to the SSD model, the SSD with SE Attention model showed significant improvements in P, R, and F1 values by 2.72%, 15.23%, and 9.45%, respectively.

The SSD with ECA Attention model also showed improvements over the SSD model, but to a lesser degree. A relative increase of 1.35%, 8.77%, and 5.47% in P, R, and F1 values was experienced, while a relative increase of 6.67% was seen in mAP.

The SSD with CBAM Attention model showed the smallest improvements over the SSD model. There is an increase of 0.94 %, 3.61 %, and 2.48 % in P, R, and F1 values, respectively, as well as a 4.91% increase in mAP and a

TABLE V. COMPARISON ANALYSIS OF SSD MODELS WITH DIFFERENT ATTENTION TECHNIQUES FOR DETECTING GRAPE DISEASES

Model	Precision	Recall	F1-Score	mAP
SSD model	80.74	68.87	74.33	76.23
SSD with SE Attention	83.46	84.10	83.78	86.96
SSD with ECA Attention	82.09	77.64	79.80	82.90
SSD with CBAM Attention	81.68	72.48	76.81	81.14
SSD with SE, ECA,CBAM Attention	85.46	84.90	84.78	83.96

3.38 MB increase in the model parameters. "SSD with SE Attention", "SSD with ECA Attention", and "SSD with CBAM Attention" models were all enhanced by the incorporation of attention modules in the network architecture. However, the three models were able to effectively identify important information in feature images while filtering out irrelevant information based on feature importance. As a result, the detection performance of the three attention mechanisms with SSD was superior to that of the SSD model.

We have applied the different attention mechanism but, the "SSD with SE, ECA,CBAM Attention model" demonstrated the best detection performance with significantly faster real-time processing than the other three models. Compared to the "SSD with ECA Attention" model, the "SSD with SE Attention" model showed a 1.37%, 6.46%, and 3.98% improvement in P, R, & F1 values, respectively. Compared to the "SSD with CBAM Attention" model, the "SSD with SE Attention" model showed a 1.78%, 11.62%, and 6.97% improvement in P, R, and F1 values, respectively.

These experimental results demonstrate that the SE attention mechanism optimized feature images, resulting in significantly better detection performance and real-time processing compared to the other three models. Therefore, the "SSD with SE, ECA,CBAM Attention" model can be effectively applied in the detection of various grape diseases with superior comprehensive performance.

4) *Comparison Analysis* : After screening, the three optimal disease detection models were compared to present their disease detection performance. The analysis above showed that "Faster(R-CNN)", "YOLO-X", and "SSD" models when combined with multiple attention mechanisms were the optimal models of their respective detection methods. Fastest R-CNN models exhibited the lowest overall detection accuracy, the slowest operating speed, and the most parameters. The "SSD" models' rapid operation speed and great accuracy made them ideal for near-instantaneous disease diagnosis in vineyards. Strong robustness was demonstrated by the "YOLO-X" models, which achieved the maximum detection precision with the fewest parameters and performed well while identifying both small objects and items hidden by background clutter.

V. CONCLUSION

After initial screening, three top disease detection models were selected and their performance was compared. The results of the foregoing investigation demonstrated that the "Faster(R-CNN)", "YOLO-X," and "SSD" models, when enhanced with numerous attention mechanisms, provided the most accurate detection results. Overall, "Faster (R-CNN)" models exhibited the lowest detection precision, the slowest operating speed, and the most parameters of the three types of models. Due to its excellent accuracy and quick processing speed, the

"SSD" model was found to be ideal for monitoring field grapes in real time. The "YOLO-X" models demonstrated the highest detection accuracy with the fewest parameters, and they performed well while recognising both small objects and items that were partially obscured.

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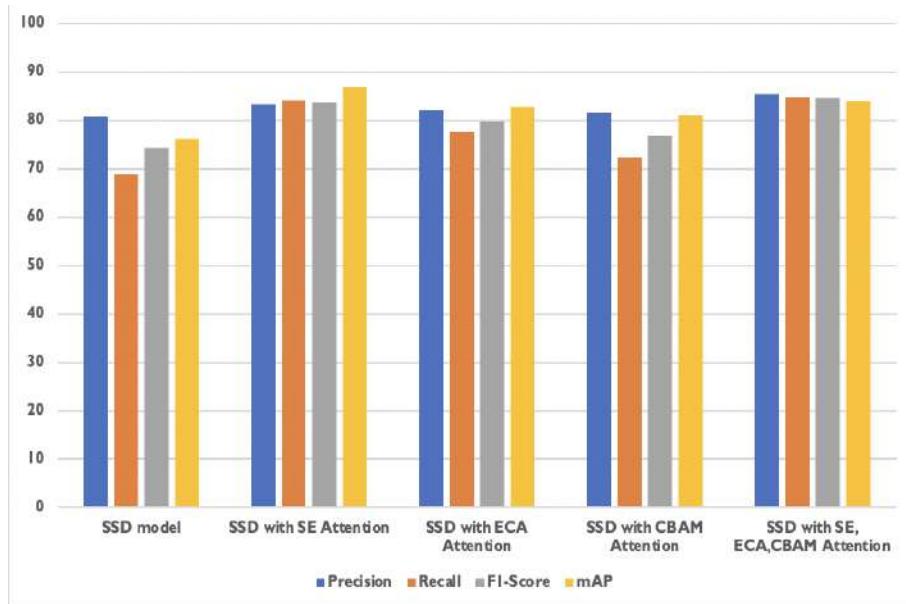


Fig. 11. Comparison analysis of SSD models with different attention techniques.

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A Deep-Learning-Based Real-Time Detector for Grape Leaf Diseases Using Improved Convolutional Neural Networks

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Edited by:

Ping Ma,
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Nankai University, China

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Specialty section:

This article was submitted to
Bioinformatics and Computational
Biology,

a section of the journal
Frontiers in Plant Science

Received: 24 January 2020

Accepted: 12 May 2020

Published: 03 June 2020

Citation:

Xie X, Ma Y, Liu B, He J, Li S and
Wang H (2020) A
Deep-Learning-Based Real-Time
Detector for Grape Leaf Diseases
Using Improved Convolutional Neural
Networks. *Front. Plant Sci.* 11:751.
doi: 10.3389/fpls.2020.00751

Black rot, Black measles, Leaf blight and Mites of grape are four common grape leaf diseases that seriously affect grape yield. However, the existing research lacks a real-time detecting method for grape leaf diseases, which cannot guarantee the healthy growth of grape plants. In this article, a real-time detector for grape leaf diseases based on improved deep convolutional neural networks is proposed. This article first expands the grape leaf disease images through digital image processing technology, constructing the grape leaf disease dataset (GLDD). Based on GLDD and the Faster R-CNN detection algorithm, a deep-learning-based Faster DR-IACNN model with higher feature extraction capability is presented for detecting grape leaf diseases by introducing the Inception-v1 module, Inception-ResNet-v2 module and SE-blocks. The experimental results show that the detection model Faster DR-IACNN achieves a precision of 81.1% mAP on GLDD, and the detection speed reaches 15.01 FPS. This research indicates that the real-time detector Faster DR-IACNN based on deep learning provides a feasible solution for the diagnosis of grape leaf diseases and provides guidance for the detection of other plant diseases.

Keywords: grape leaf diseases, object detection, deep learning, convolutional neural networks, feature fusion

INTRODUCTION

China is a modern agricultural country with more than 2000 years of history in grape planting. At present, China has the largest grape export in the world. At the same time, grape juice, raisins, wine, and other grape products also have great commercial value. However, severe diseases take a great toll on yield and quality during the growing process of grapes, especially in rainy areas and periods. Thus, timely and effective detection of grape leaf diseases is a vital means to ensure the healthy growth of grapes.

Traditionally, the diagnosis of plant leaf diseases relies on trained experts performing visual inspection (Dutot et al., 2013), which usually leads to high cost and a large risk of error. With the rapid development of artificial intelligence, machine learning methods have been applied to plant disease detection to make it more intelligent. Researchers began to apply machine learning

algorithms to plant disease diagnosis, such as support vector machines (SVM) and K-means clustering (Es-saady et al., 2016; Mwebaze and Owomugisha, 2016; Padol and Yadav, 2016; Qin et al., 2016; Islam et al., 2017; Dickinson et al., 2018; Tian et al., 2019). However, because of the complex image preprocessing and feature extraction, these methods still have low detection efficiency. In recent years, the convolutional neural network (CNN) has been developed as an end-to-end deep learning approach, they take full advantage of image big data and discover the discriminative features directly from original images, avoiding complicated image preprocessing and reducing the memory footprint. Inspired by the breakthroughs of CNNs in pattern recognition, using CNNs to identify early plant leaf diseases has become a new focus of smart agriculture. In (Fuentes et al., 2017; Liu et al., 2017; Lu Y. et al., 2017; Ramcharan et al., 2017; Boulent et al., 2019; Bresilla et al., 2019; Polder et al., 2019; Saleem et al., 2019; Zhu et al., 2019), CNNs were mainly used to diagnose crop diseases. Nevertheless, many difficulties remain in realizing the real-time detection of grape leaf diseases due to the following characteristics of grape leaf diseased spots. Multiple small and dense diseased spots may occur on the same leaf, which are usually of various shapes. Moreover, environmental factors and shielding of other leaves also affect the detection of grape leaf diseases.

To overcome these problems, this article proposes a deep-learning-based detector based on improved CNNs to monitor grape leaf diseases in real-time. The main contributions of this article are summarized as follows:

- A grape leaf disease dataset (GLDD) is established. The GLDD provides a necessary guarantee for the generalization ability of the model. First, to improve the practicability of the model, images of diseased grape leaves with simple backgrounds in the laboratory and complex backgrounds in the grapyery are collected. Furthermore, to prevent the CNN overfitting problem, the dataset is expanded via digital image processing technology to form the GLDD for providing sufficient training disease images.
- A real-time detection model for grape leaf diseases, Faster DR-IACNN, is proposed. By introducing the Inception modules and SE-block, the backbone network ResNet is modified to obtain a novel pre-network, named INSE-ResNet. Through upsampling and downsampling, the double-RPN structure is designed and achieves stronger feature extraction ability of small diseased spots. The proposed Faster DR-IACNN model improves the extraction ability of multiscale diseased spots and the detection speed of ResNet, reducing the depth and increasing the width of the neural network.
- The deep CNN is first applied to real-time detection of grape leaf diseases. The proposed end-to-end real-time detector based on deep learning can automatically extract the features of grape leaf diseases and detect the four common diseases of grape leaves efficiently. At the same time, this method can also detect a variety of diseases in the leaves at one time.

The experimental results show that the mean Average Precision of Faster DR-IACNN is 81.1%, which is 2.3% higher than that of Faster R-CNN, and the detection speed reaches 15.01 FPS. The experiments indicate the deep-learning-based detector exhibits higher detection precision and can satisfy the actual demand for real-time detection in graperies.

The rest of the article is organized as follows: section “Related Work” introduces and summarizes the related work. The GLDD is introduced in section “Generating Grape Leaf Disease Dataset.” In section “Detection Model of Grape Leaf Diseases” describes the detection model of grape leaf disease in detail. In section “Experimental Evaluation,” an evaluation of the experimental performance and analyses of the experimental results are presented. Finally, section “Conclusion” summarizes this article.

RELATED WORK

With the development of artificial intelligence, deep learning has made breakthroughs in computer vision. It has been widely utilized to identify plant diseases and is a satisfying alternative for the classification of plant diseases. In Wang et al. (2012), proposed a grape disease recognition method based on principal component analysis and backpropagation networks. The dataset of grape diseases includes grape downy mildew and grape powdery mildew, and the prediction accuracy was up to 94.29%. In Sannakki et al. (2013), came up with a method to diagnose two types of grape diseases. Using thresholding and anisotropic diffusion to preprocess images and K-means clustering to segment disease spots, the method achieved high training accuracies when using hue features. In Mohanty et al. (2016), trained two deep learning models (AlexNet and GoogLeNet) to identify 14 crop species and 26 diseases. By examining two types of training mechanisms, three dataset types and five types of training-testing set distributions, they achieved an accuracy of 99.35%. In Lu J. et al. (2017), proposed an in-field wheat disease diagnosis system that has since been implemented in a mobile app to help agricultural disease diagnosis. By implementing two different frameworks VGG-FCN-VF16 and VGG-FCN-S, they obtained mean recognition accuracies of 97.95 and 95.12%, respectively, on WDD2017, demonstrating further improvement over the accuracies of 93.27 and 73.00% obtained using traditional CNN frameworks. In Yu et al. (2019), reported several deep CNN models for weed detection in bermudagrass turfgrasses and demonstrated that VGGNet achieved a high score at the detection of three common diseases in turfgrasses, while DetectNet could better detect disease in annual bluegrass. Based on these results, they proposed a DCNN-based recognition system for weed control. In Ferentinos (2018), applied five basic CNN architectures to an open database of 87,848 images including 25 plant species of 58 distinct classes, with the best performance reaching a recognition accuracy of 99.53%. Though deep CNNs have made great achievements in plant disease classification, real-time detection of diseases during the growth of the plant is more essential in order to control the diseases effectively at an early time.

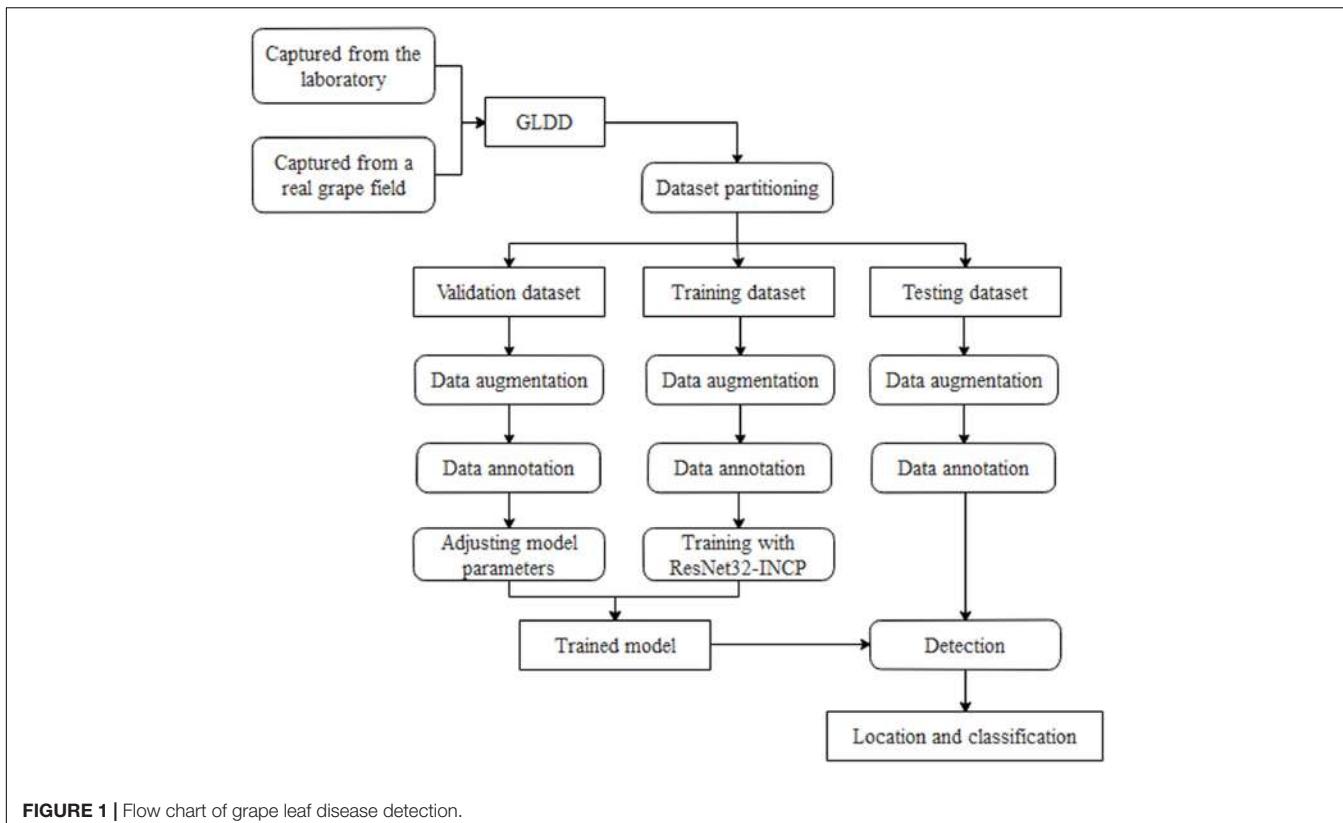


FIGURE 1 | Flow chart of grape leaf disease detection.

Many researchers have begun to study how to detect plant leaf disease precisely through deep learning methods. In Rançon et al. (2018), provided a recognition and detection method based on grape leaf Esca symptoms during summer. In experiments, they compared SIFT encoding with pretrained deep learning feature extractors and implemented the MobileNet network on the ImageNet database to get a classification accuracy of 91%. Then, they combined the classification network with a one-stage detection network (RetinaNet) to obtain the best Esca AP of 70%. In Jiang et al. (2019), presented a new network architecture named INAR-SSD based on VGGNet and Inception construction. They applied the architecture to the apple leaf disease in the detection and reached 78.8% mAP. In Fuentes et al. (2018), designed a Refinement Filter Bank framework for tomato plant diseases and pests to solve the problem of false positives and class unbalance based on deep convolution neural networks. The system consists of three units—a primary diagnosis unit, a secondary diagnosis unit, and an integration unit—and the mAP was 13% greater than the best result based on Faster R-CNN. It is more efficient to detect plant leaf disease and easier to obtain higher accuracy when using a novel deep learning approach based on CNNs. According to these studies, CNNs have made a great contribution to the identification and detection of plant diseases. Unfortunately, there are no suitable CNN models for the real-time detection of grape leaf diseases, which would have high practical value in grape planting. Thus, a real-time detector based on Faster R-CNN for grape leaf diseases is proposed in this article.

GENERATING GRAPE LEAF DISEASE DATASET

Details of grape leaf disease detection are shown in **Figure 1**. First, the original grape leaf disease images are acquired from the laboratory and a real grapy. Then, the original grape leaf disease images are expanded by data argumentation operations and further refined by expert annotation. Finally, the dataset is divided into three parts: the training set is used to train the Faster DR-IACNN model, the validation set is used to adjust the parameters and evaluate the model, and the testing set is used for verifying the generalization of the model.

Grape Leaf Disease Images Collection

Since there are few available datasets of grape leaf diseases for disease detection, many human and material resources have made significant contributions to collecting and building GLDD. Grape plants suffer from diseases in different seasons, temperatures, and humidity. For instance, Black rot causes severe damage to the grape industry in continuous hot and humid weather, but it rarely occurs in dry summer. Grape Leaf blight is extremely serious in September when the tree is weak, the temperature is low, and rain is frequent. Considering the above situations, the disease images in the GLDD were collected under various climate conditions to make the GLDD widely used. Apart from capturing images manually, the other disease images in the dataset were

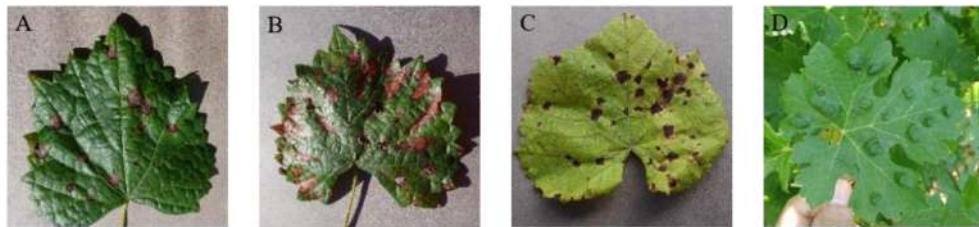


FIGURE 2 | Four common types of grape leaf diseases. **(A)** Black rot. **(B)** Black measles. **(C)** Leaf blight. **(D)** Mites of grape.

collected from Wei Jiani Chateau, Yinchuan, the Ningxia Hui Autonomous Region, China.

A total of 4,449 original images of grape leaf diseases were obtained, they contain four disease categories: Black rot (a fungal disease caused by an ascomycetous fungus), Black measles (also named Esca, caused by a complex of fungi such as *Phaeoacremonium*), Leaf blight (a common grape leaf disease caused by a fungus), and Mites of grape (caused by parasitic infestation of rust ticks). There are two reasons for choosing these four types of grape leaf diseases: first, some of the diseased spots cannot be distinguished visually, but it is easy for CNNs to extract features. Moreover, the occurrence of these diseases causes great losses to the grape industry.

Figure 2 shows typical images of four types of grape leaf diseases in GLDD. It can be intuitively observed that the four diseased spots on the grape leaves have similarity and diversity: the disease effects caused by the same disease with similar natural conditions are basically the same, while the characteristics of diseased spots caused by different diseases are usually various. Leaf infected by Black rot appears reddish-brown and have nearly round small spots that expand into the large gray spots with brown edges in the later period. The diseased spots of Black

measles resemble tiger stripes, which are reddish-brown bands of necrosis. The characteristic lesions of Leaf blight are irregular, with dark red to brown spots appearing at first, followed by black spots. Mites of grape are caused by parasitic rust ticks and feature bubble-like uplift on the leaf surface. These observations are helpful for the real-time diagnosis and detection of various grape leaf diseases using deep CNNs.

The collected dataset has three following features: first, multiple diseased spots of different diseases may simultaneously appear on the same leaf. Second, many images contain complicated backgrounds of interfering spot detection, which guarantees the high generalization of Faster DR-IACNN. Finally, all images in the dataset are manually annotated by reliable experts.

Image Augmentation

Due to the insufficient disease images, neural networks excessively obtain the information of the training set, leading to the overfitting problem in the training process of CNNs. Hence, data augmentation technology is used to simulate real-life interference, which plays an important role in the model training stage. As more images are generated via data augmentation, the

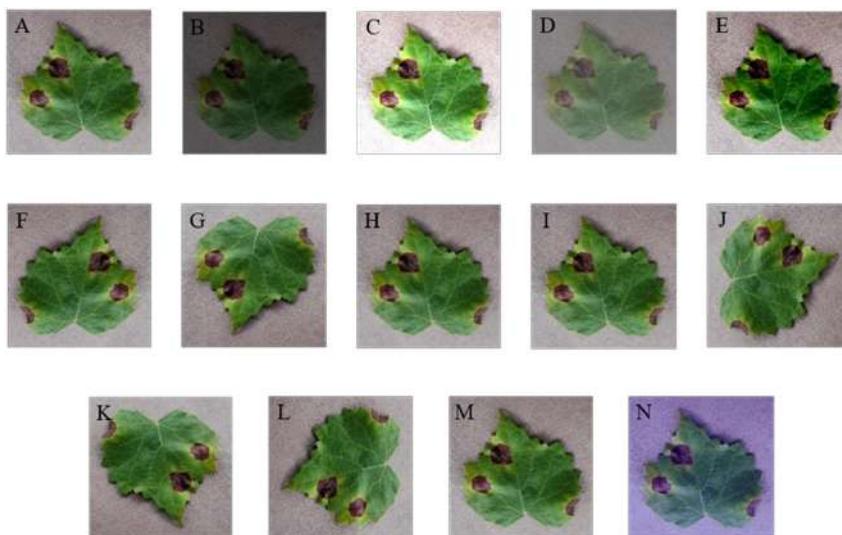
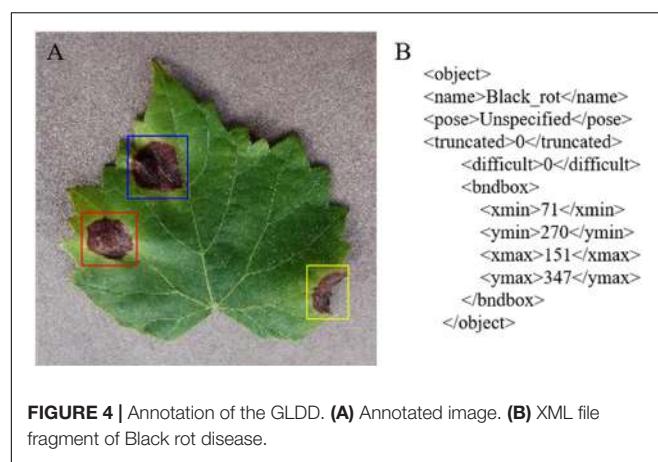


FIGURE 3 | Data augmentation of grape leaf disease images. **(A)** Original image; **(B)** low brightness; **(C)** high brightness; **(D)** low contrast; **(E)** high contrast; **(F)** vertical flip; **(G)** horizontal flip; **(H)** low sharpness; **(I)** high sharpness; **(J)** 90° rotate; **(K)** 180° rotate; **(L)** 270° rotate; **(M)** Gaussian noise; **(N)** PCA jittering.



model can learn as many different patterns as possible during the training, avoiding the overfitting problem and achieving better detection performance in practice.

In this section, several digital image processing technologies are applied to data augmentation operations. Considering the effects of weather factors on the image intensity, interference of brightness, contrast, and sharpness are implemented. The variety in the relative shooting position of camera and diseased leaf is simulated via rotation (including 90, 180, and 270°) and symmetry (including vertical and horizontal symmetry). Gaussian noise is used to imitate the influence of equipment factors. Moreover, PCA jittering is used to expand the original dataset as well to simulate the real acquisition environment and increase the diversity and quantity of the grape leaf diseases training images. Thus, the GLDD is formed via expanding the original dataset by 14 times. **Figure 3** presents a grape leaf disease image example generated through image augmentation technology.

Image Annotation

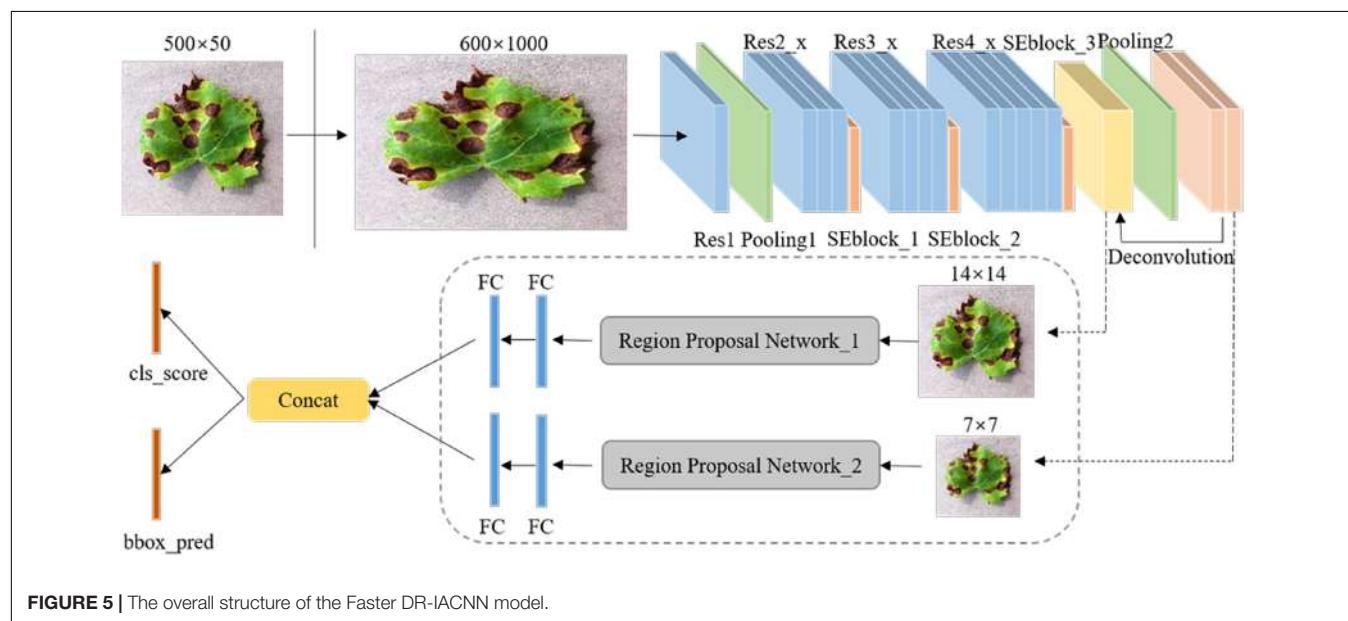
Image annotation is a crucial step in building the dataset; it is used to mark out the location and category of diseased spots in infected leaves. In this section, a tool has been developed to annotate images through rectangular bounding boxes. Using the annotation tool and the knowledge of experienced agriculture experts, areas of diseased spots in the image can be accurately labeled. When the annotation is complete, an XML file is generated for each image, which includes the types of diseased spots and their locations.

Take an image of Black rot as an example. The annotated image in **Figure 4A** shows the infected areas surrounded by red, blue, and yellow boxes. **Figure 4B** is a fragment of the generated XML file, in which the disease name of Black rot is described and the location of diseased spots is determined by upper left and lower right coordinates of the red box.

Due to the limitation of manual annotation and the annotation tool, inevitable random errors will occur in image annotation process. In order to reduce the influence of the errors on subsequent experiments, the image labels have been checked repeatedly. Moreover, the probability of such errors is too small to affect a large number of datasets, which can be ignored.

DETECTION MODEL OF GRAPE LEAF DISEASES

Figure 5 shows the overall framework of the Faster DR-IACNN model for detecting four typical grape leaf diseases. The DR-IA means double-RPN with Inception module and Attention structure, which contains all the characteristics of our model. The proposed Faster DR-IACNN consists of three parts: (1) a pre-network for extracting disease image features. The pre-network, namely, INSE-ResNet, includes residual structure, inception



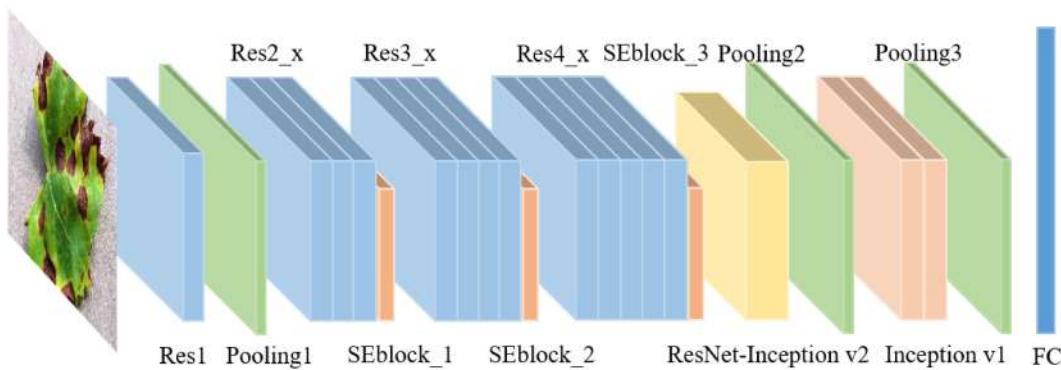


FIGURE 6 | Structure of INSE-ResNet.

modules and SE-block. The backbone ResNet is designed for extracting images' feature information, while the inception modules and SE-block aim to widen the receptive field and obtain multiscale features. (2) A Region Proposal Network (RPN) for locating objects. After the processing of pre-network, feature maps are sent to the RPN. In this part, the diseased spots are located and predicted by bounding boxes. (3) Fully connected layers for classification and regression. In this part, categories and scores are calculated through fully connected layers. All the information is fused in the concatenation layer. Finally, the class scores and prediction boxes are output.

Multiscale Feature Extraction of

Diseased Spots

Backbone Networks for Extracting Features

Due to the specialty of Black rot and Leaf blight with small and dense diseased spots, a variety of backbone networks, such as AlexNet, VGGNet, and ResNet, were experimented with and analyzed, and ResNet has been found to be the most suitable backbone network. According to the characteristics of grape leaf diseased spots, ResNet34 has a high recognition accuracy for the GLDD. Therefore, ResNet34 was selected as the pre-network of the detection model. ResNet with residual learning enables the network structure to be further deepened without the disappearance of the gradient (He et al., 2016), which solves the degradation problem of deep CNNs and fits for the small diseased spots. In addition, it is easy to optimize and achieve high accuracy in classification.

Table 1 lists the detailed parameters of the adjusted ResNet34, named INSE-ResNet, and **Figure 6** shows the structure of INSE-ResNet. The first several layers of CNNs usually learn low-level features such as color and edges (Zeiler and Fergus, 2013), and the deeper layers extract complete and discriminative features. Thus, Res1 to Res3 of ResNet34 are completely retained. Meanwhile, the article applies Squeeze-and-Excitation Blocks in the tail of ResNet blocks. The Res_4f layer is removed, and the Res_4e layer is replaced with Inception-ResNet-v2 module to enhance the multiscale feature extraction ability of the pre-network. To fix the input size of the following-up network, the feature map is adjusted to the size of 14×14 through the RoI pooling layer.

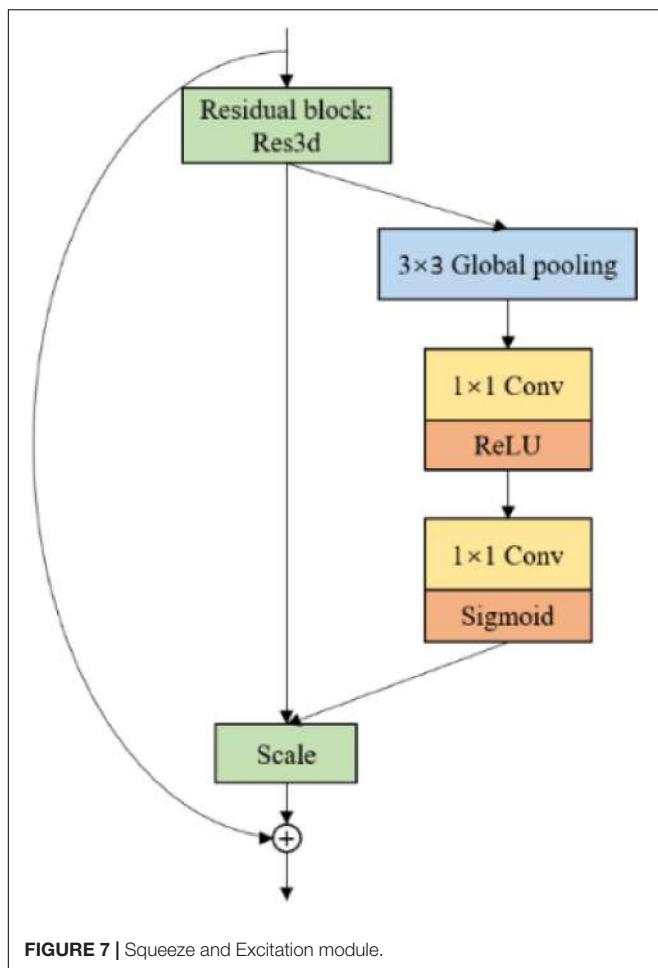
TABLE 1 | The related parameters of INSE-ResNet model.

Output size	Name	Related parameters (kernel size, output size, stride)
112×112	Res1	Convolution, 7×7 , 64, stride 2
56×56	Pool1	3×3 max-pooling, stride 2
	Res2_x	$\left[\begin{array}{l} \text{Conv } 3 \times 3 \text{ 64} \\ \text{Conv } 3 \times 3 \text{ 64} \end{array} \right] \times 3$
	SEblock_1	FC, [16, 256]
28×28	Res3_x	$\left[\begin{array}{l} \text{Conv } 3 \times 3 \text{ 128} \\ \text{Conv } 3 \times 3 \text{ 128} \end{array} \right] \times 4$
	SEblock_2	FC, [32, 512]
14×14	Res4_x	$\left[\begin{array}{l} \text{Conv } 3 \times 3 \text{ 256} \\ \text{Conv } 3 \times 3 \text{ 256} \end{array} \right] \times 5$
	SEblock_3	FC, [64, 1024]
	Inception-ResNet-v2	As in Figure 8A
7×7	Pool2	3×3 max-pooling, stride 2
	Inception_5a	As in Figure 8B
	Inception_5b	As in Figure 8B
1×1	Pool3	7×7 average-pooling, stride 1
	Softmax	5

In the subsequent network, the Res5 layer is replaced with two Inception-v1 modules. The final output is the concatenation of the category and location losses.

High Semantic Feature Extraction Modules for Diseased Spots

Considering GLDD includes numerous complex background images, the network needs to focus on diseased spots, instead of the background. Thus, the article introduces Squeeze-and-Excitation Blocks (Hu et al., 2018). The SE-blocks learn the feature weights via the loss, such that the available feature map with diseased spots has a large weight, and the invalid or tiny feature map has a lightweight. **Figure 7** shows the SE block structure, which stacks 3×3 average pooling layers and 1×1 convolution layers.



The characteristics of grape leaf diseased spots are various. Black rot spots and Leaf blight spots are small and dense, while Black measles spots are similar to stripes. Thus, a single scale convolution kernel is inefficient to perceive multiscale diseased spots. To extract features of multiscale diseased spots

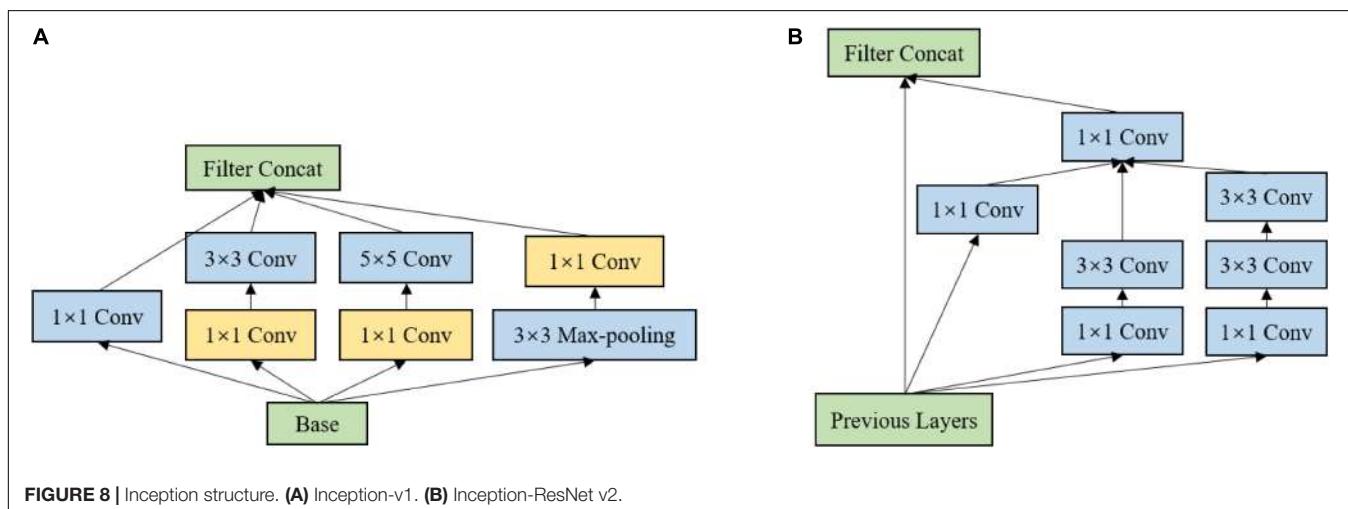
of GLDD, Inception modules are introduced. **Figure 8A** shows the Inception-v1 (Szegedy et al., 2014) structure, which stacks 1×1 convolution layers, 3×3 convolution layers, 5×5 convolution layers, and 3×3 max-pooling layers, enhancing both the width of the network and adaptability of scales. **Figure 8B** shows the Inception-ResNet-v2 (Szegedy et al., 2016) structure, which applies the idea of residual learning to the inception network and makes it a speed boost. In the Inception modules, 1×1 convolution layers are inserted before or after the parallel convolution layers to reduce the thickness of feature maps and the number of weights. Inception modules can increase the depth and width of the network while reducing the number of parameters. Considering the advantages of the two inception models, the above two inception modules are brought into the backbone to improve the multiscale feature extraction capability.

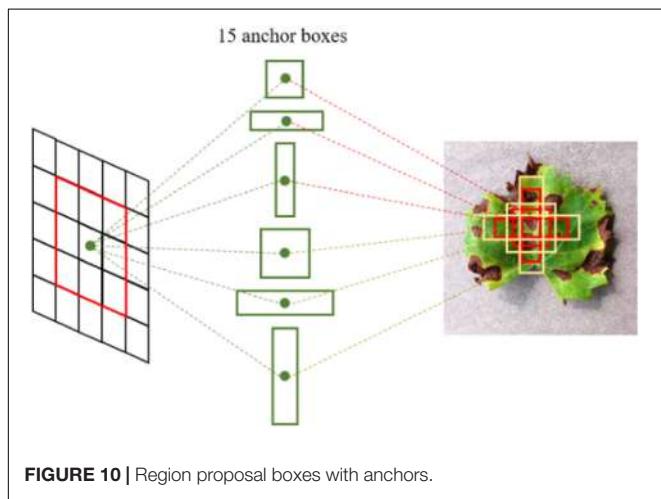
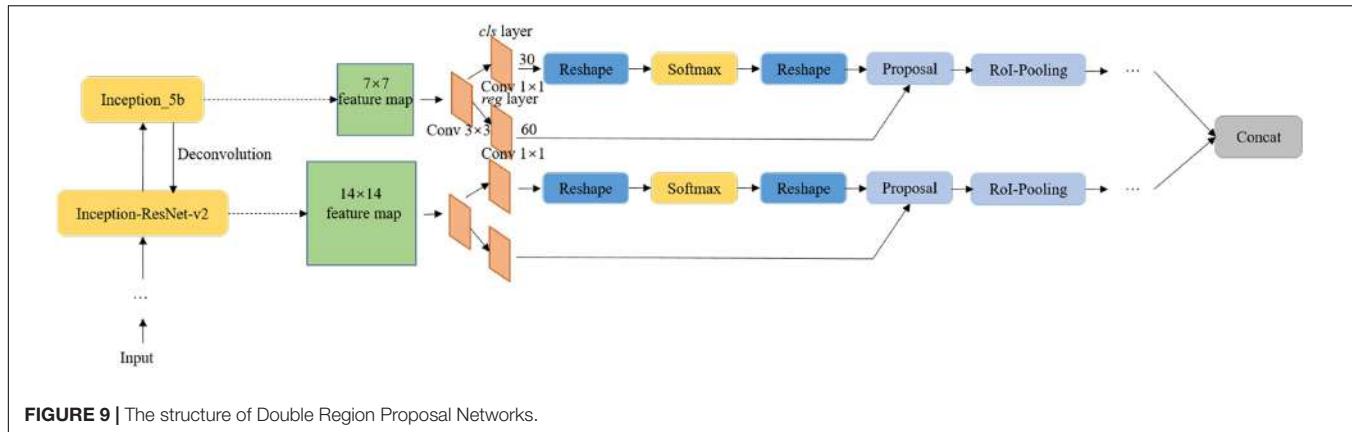
Locating and Predicting Diseased Spots

Locating Multiscale Diseased Spots

Region Proposal Networks are the crucial part of the detection model Faster DR-IACNN. Take Inception_5b as an example: through the pre-network, a shared feature map sizing $7 \times 7 \times 256$ is obtained. Then, the feature map is reshaped to $7 \times 7 \times 512$ using 3×3 convolution kernels. To obtain categories and regression results, the 1×1 convolution process is implemented in the *classification* layer and *regression* layer, obtaining feature maps of size $7 \times 7 \times 30$ and $7 \times 7 \times 60$, respectively. Finally, with the arranged anchors, the candidate boxes are gained.

Inspired by Feature Pyramid Networks (Lin et al., 2017), a double-RPN structure is proposed for locating the irregular and multiscale diseased spots, as shown in **Figure 9**. Through a deconvolution process, the high semantic information of Inception_5b is integrated with the high resolution of Inception_ResNet-v2. Thus, the proposed detection model can predict diseased spots separately in each feature layer. Furthermore, the bottom-up feature extraction and top-down upsampling method enhance the ability of the model to detect small diseased spots.





Guaranteeing the Translation Invariance

Due to the multiple-convolution process, the scale of feature maps is changed. It is essential to guarantee translation invariance between the feature maps and original images. To accurately locate the diseased spots on the original images, anchor boxes (Ren et al., 2018) are employed in the grape leaf diseased spot detection. As shown in Figure 10, multiple region proposals are predicted when the sliding window slides at each location. The anchor boxes' sizes are related to scale and ratio. The default in Faster DR-IACNN is set as 5 scales and 3 ratios. That is, it generates 15 anchor boxes in the original images due to mapping. The region proposal process guarantees the essential properties of multiscale detection ability and translation invariance.

EXPERIMENTAL EVALUATION

This section describes the experimental setup. First, the details of the experimental platform and the dataset are introduced, and then the experimental results are analyzed and discussed.

TABLE 2 | Hardware and software environment.

Configuration item	Value
CPU	Intel(R) Xeon(R) CPU E5-2650 v4
GPU	NVIDIA Tesla P100 PCI-E GPU 16 GB
Memory	128 GB
Hard disk	2 TB
Operating system	Ubuntu 16.04.2 LTS (64-bit)

TABLE 3 | Grape leaf disease dataset.

Disease	Training/validation/testing image	Total quantity
Black rot	9,912 / 3,304 / 3,304	16,520
Black measles	11,617 / 3,872 / 3,873	19,362
Leaf blight	9,038 / 3,013 / 3,013	15,064
Mites of grape	6,804 / 2,268 / 2,268	11,340
Total	37,371 / 12,457 / 12,458	62,286

Experimental Setup

The experiments were performed on a 16.04.2-Ubuntu server with an Intel(R) Xeon(R) CPU E5-2650 v4 @ 2.20 GHz × 48. It is accelerated by an NVIDIA Tesla P100 PCI-E GPU, which has 3,584 CUDA cores and 16 GB of memory. The core frequency is up to 1328 MHz, and the single-precision floating-point performance is 9.3 TFLOPS. The proposed Faster DR-IACNN model was implemented on Caffe, a deep learning framework. Table 2 presents the configuration parameters.

Dataset

In the experiment, 60% of the dataset was used for training, and the other 40% was used for validation and testing. The ratio size of the training dataset and validation dataset and testing dataset is 3:1:1. Through digit image processing technology, the number of original grape leaf disease images was expanded to 62,286. The partition of GLDD is reported in Table 3.

Experimental Results and Analyses

Accuracy Comparison With Various Detection Models

To compare the performance of various detection algorithms, a typical one-stage algorithm SSD and two-stage classical detection

TABLE 4 | Detection results of various CNN models.

Method	SSD		R-FCN		Faster R-CNN				Faster DR-IACNN
	Feature extractor	VGG 16	ResNet 50	ZF	VGG 16	ResNet 50	ResNet 34	ResNet 18	INSE-ResNet (our work)
Classes									
Input	512	500	500	500	500	500	500	500	500
Iterations	120 k	200 k	200 k	200 k	200 k	200 k	200 k	280 k	280 k
Black rot	74.7	79.0	63.5	64.5	64.4	69.3	65.8	73.7	76.7
Black measles	81.6	82.5	75.4	79.9	79.0	81.4	75.0	85.3	88.0
Leaf blight	72.0	68.2	59.2	60.0	60.8	64.4	64.4	71.1	73.7
Mites of grape	77.9	69.4	69.3	70.4	70.2	70.8	73.6	84.0	86.2
mAP (%)	76.6	74.8	66.9	68.7	68.6	71.5	69.7	78.5	81.1

The meaning of the “bold” is the best experimental results.

TABLE 5 | Precision and speed of various models.

Method	R-FCN				Faster R-CNN				Faster DR-IACNN
	Backbone	ResNet 50	ZF	VGG 16	GoogLeNet	ResNet 50	ResNet 34	ResNet 18	INSE-ResNet (our work)
mAP (%)	74.8	66.9	67.5	64.3	68.6	71.5	69.7		81.1
Speed (FPS)	15.75	16.08	15.85	18.65	7.11	10.33	13.94		15.01

The meaning of the “bold” is the best experimental results.

algorithms Faster R-CNN and R-FCN have been selected to detect grape leaf diseases on GLDD under the condition of using different backbone networks. The experimental results are reported in **Table 4**.

The mean Average Precision (mAP) is the standard index in the evaluation of the object detection algorithm, which is used in this section. In the two-stage algorithm, with the same input size of 500×500 , the proposed model Faster DR-IACNN achieves a high accuracy of 81.1% mAP, and the detection performance in all categories is better than those of other detection models based on Faster R-CNN. The overall accuracy is 9.6% higher than that of the model with the backbone network ResNet34. Meanwhile, the Faster DR-IACNN model has higher detection accuracy than all of the other detection models.

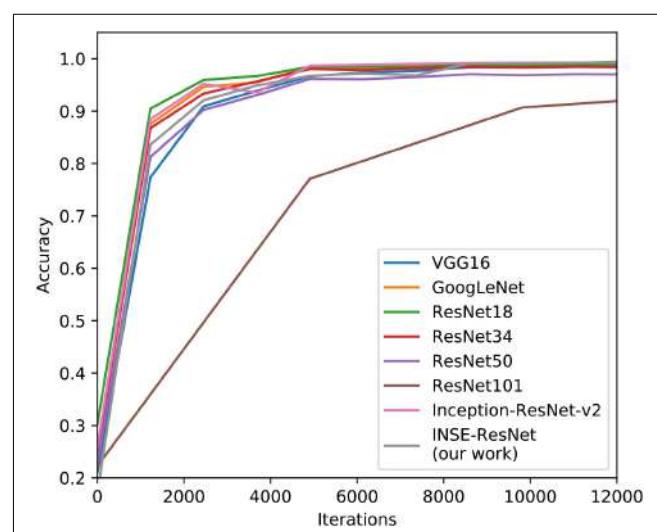
To determine whether the deeper neural network can improve the detection performance of the model, ResNet50, ResNet34, and ResNet18 have been verified with 200 k iterations. The results show that ResNet50 has the worst effect, and ResNet18 did not obtain satisfactory improvement, either. The reasons for unsatisfying results are that the feature of diseased spots disappear with increasing CNN depth, while superficial layers cannot extract features accurately. Therefore, ResNet34 is the most suitable network for our dataset, with an improvement of 2.9 and 1.8% relative to ResNet50 and ResNet18, respectively.

In this experiment, Black rot and Leaf blight are relatively difficult to detect because they are similar in shape and have small diseased spots. Our proposed model, Faster DR-IACNN, shows significant improvement in the above two types of diseased spots, with 3 and 2.6% improvement compared with Faster R-CNN. Additionally, all the models have the highest detection accuracy for Black measles; the reason is that Black measles lesions are

large, shaped like strips, and greatly differ from other categories, which can be easily distinguished by all the detection models.

Detection Accuracy and Speed

The detection speed is another important index to evaluate the object detection algorithm, which plays a vital role in real-time detection. Usually, FPS (frames per second) is utilized to evaluate detection speed. The larger the FPS is, the faster the detection speed will be. In this part, the detection speed of two-stage algorithms Faster R-CNN and R-FCN with the proposed models are evaluated. The experimental results are reported in **Table 5**.

**FIGURE 11 |** Accuracy curve of pre-networks models.

In Faster R-CNN, the model with GoogLeNet as the backbone network has the fastest detection speed, up to 18.65 FPS. The reason is that the Inception module expends the network and reduces the parameters while deepening the network, which improves the efficiency of feature extraction. Considering the detection efficiency, the Inception module and ResNet structure have been combined to propose the Faster DR-IACNN model, which further improved the accuracy on GLDD to reach 81.1% mAP with a detection speed of 15.01 FPS, reaching the highest accuracy compared with the traditional Faster R-CNN method with a high speed that meets the actual demands in grapy. Compared with the average detection speed reached 13.66 FPS of Faster R-CNN model, which was described as a real-time detection model, the proposed Faster DR-IACNN has higher detection speed of 15.01 FPS and meets the requirements of real-time detection.

The Selection and Comparison of Pre-networks

The detection algorithm Faster R-CNN consists of three parts, the feature extraction network, RPN, classification and regression, among which feature extraction network (as known as a pre-network) plays an important role in the implementation of detection. In this section, several general CNNs such as GoogLeNet, VGG16, and ResNet series are trained and validated. The recognition performance of INSE-ResNet is compared with these traditional networks on GLDD. In the training process, the stochastic gradient descent (SGD) algorithm and weight attenuation strategy are adopted to minimize the loss function. In the SGD algorithm, the training image is selected randomly to update the model parameters, the batch size is set to 32, the base learning rate is 0.01, and the learning rate is attenuated three times in 10 epochs of training, which is 0.1 times of the previous learning rate such that the obtained results avoid inability to converge. To make the algorithm converge to the optimal speed, the momentum is set to 0.9.

As shown in **Figure 11**, the X-axis represents the iterations of training, and the Y-axis represents the corresponding training accuracy. The test accuracy of each identification network in the experiments is reported in **Table 6**. As shown in **Figure 11**, the recognition results of ResNet networks and Inception networks are satisfying, which inspired us to make good use of their

TABLE 6 | The recognition accuracy of pre-network models.

Pre-network model	Input size	Recognition accuracy (%)
VGG16	224 × 224	98.48
GoogLeNet	224 × 224	98.91
ResNet18	224 × 224	98.92
ResNet34	224 × 224	98.40
ResNet50	224 × 224	97.01
ResNet101	224 × 224	88.61
Inception-ResNet-v2	224 × 224	99.28
INSE-ResNet (our work)	224 × 224	99.47

The meaning of the “bold” is the best experimental results.

TABLE 7 | Detection precision with and without data augmentation.

Method	Without data augmentation	With data augmentation
Black rot	69.1	76.7
Black measles	81.4	88.0
Leaf blight	66.7	73.7
Mites of grape	80.1	86.2
mAP (%)	74.3	81.1

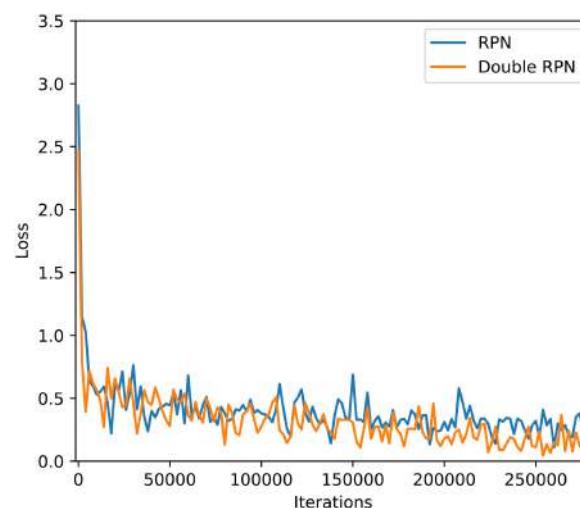


FIGURE 12 | Influence of double-RPN.

strengths to build INSE-ResNet. Therefore, considering the subsequent model establishment, the INSE-ResNet structure is proposed based on ResNet34 combined with the Inception-v1 module, Inception-ResNet-v2 module and SE-block, which achieves a better performance in term of recognition accuracy.

Effect of Data Augmentation on the Detection Accuracy

To avoid overfitting, various methods are used in this article. First, the grape diseased leaves were collected in multiple environments and areas. Most diseased grape leaf images with complex background were captured in the Wei Jiani Chateau, while the other images with simpler backgrounds were collected in the laboratory, which guarantees the generalization of the proposed model and reduces the occurrence of overfitting.

TABLE 8 | Detection precision with and without double-RPN.

Methods	INSE-ResNet in Faster R-CNN	Faster DR-IACNN
Diseases		
Black rot	73.7	76.7
Black measles	85.3	88.0
Leaf blight	71.1	73.7
Mites of grape	84.0	86.2
mAP (%)	78.5	81.1

TABLE 9 | Evaluation of different anchor scales.

Anchor base size	Number of anchors (scales)	Aspect ratios	mAP (%)
3 scales, 3 ratios	{128 ² , 256 ² , 512 ² }	{2 : 1, 1 : 1, 1 : 2}	75.2
5 scales, 3 ratios	{32 ² , 64 ² , 128 ² , 256 ² , 512 ² }	{2 : 1, 1 : 1, 1 : 2}	81.1
6 scales, 3 ratios	{16 ² , 32 ² , 64 ² , 128 ² , 256 ² , 512 ² }	{2 : 1, 1 : 1, 1 : 2}	77.8
8 scales, 3 ratios	{32 ² , 48 ² , 64 ² , 96 ² , 128 ² , 192 ² , 256 ² , 512 ² }	{2 : 1, 1 : 1, 1 : 2}	78.4

The meaning of the “bold” is the best experimental results.

Moreover, due to the difficult work involved in collecting diseased grape leaves, the dataset is still insufficient. Thus, data augmentation is a satisfactory approach to solve the insufficient training image problem.

As reported in **Table 7**, the accuracy without data augmentation is lower, which reaches 74.3% mAP, and the loss is high during the training process. In contrast, the proposed model with data augmentation realizes 81.1% mAP, which corresponds to a detection precision improvement of 6.8% relative to the dataset without data augmentation.

Effect of Double-RPN on the Detection Accuracy

Compared with the original RPN structure, the proposed double-RPN in Faster DR-IACNN has greatly improved the detection effect on GLDD. Double-RPN performs well at small diseased spots detection by making full use of high layers’ semantic information and low layers’ location information.

This article evaluated the performance of Faster DR-IACNN on GLDD through two sets of experiments, which tested the model with original RPN and double-RPN. As shown in **Figure 12**, for the Faster R-CNN, the loss is relatively large and fluctuates in a large range during the training, while for the Faster DR-IACNN model, the loss function changes steadily and presents a significant downward trend. As reported in **Table 8**, the detection accuracy of Faster DR-IACNN for four grape leaf diseases has also improved simultaneously, and the mAP of the GLDD reaches 81.1%, increasing 2.6% compared with single RPN in Faster R-CNN.

Effect of the Anchor Scales on the Detection Accuracy

Translation invariance is a challenge of deep CNNs. Traditionally, there are two mainstream solutions to this problem: first, sampling the feature map layer in scale or aspect ratio, and second, using a filter (also considered as a sliding window) to sample in scale or aspect ratio. Faster R-CNN samples the center of convolution kernel in terms of scale and aspect ratio, which uses 3 scales and 3 aspect ratios to produce 9 anchor boxes. On the feature map, RPN proposes a sliding window, whose size is 3 × 3, and takes the center of 3 × 3 sliding windows as the center of the anchor boxes.

In this article, due to the characteristic of small and dense diseased spots, the aspect ratios are set as 0.5, 1, and 2; the base size is set as 16; and the number of anchor boxes is adjusted among 3, 5, 6, and 8 for comparison. The experimental results are reported in **Table 9**. The results show that when the number of anchor boxes is 5 and scales are 2, 4, 8, 16, and 32—that is,

the sizes of the anchor boxes are 32 × 32, 64 × 64, 128 × 128, 256 × 256, and 512 × 512—and 90 k anchor boxes are generated in each image, the highest precision of 81.1% mAP is obtained in the Faster DR-IACNN, which is 5.9% mAP higher than the original 3 anchor boxes. Especially, the detection result of small diseased spots Leaf blight is increased by 9.4% mAP.

Detection Results of the Grape Leaves

The detection results of four common diseases of grape leaves are shown in **Figure 13**. **Figures 13A–D** show the detection results of single disease of Black rot, Black measles, Leaf blight and Mites of grape, respectively, while **Figure 13E** shows infected leave with Black rot and Black measles simultaneously, which has been detected precisely by the detector at one time. The results show that the detection model can detect not only multiple diseased spots of the same disease in one leaf but also multiple spots of different diseases on one leaf at one time, demonstrating the strong generalization and robustness of the model. As seen in **Figure 13**, most scores of detection boxes are greater than 0.99, and most diseased spots on leaves are detected, demonstrating the high detection precision and accurate location of the Faster DR-IACNN model.

CONCLUSION

This article proposed a deep-learning-based detector, Faster DR-IACNN, for detecting grape leaf diseases. The proposed method can automatically extract the features of diseased spots and detect four common grape leaf diseases with high accuracy and a satisfactory detection speed. To improve the generalization of the model and ensure a sufficient GLDD, 4,449 original images with both simple and complex backgrounds were collected in the laboratory and real vineyards, and a total of 62,286 diseased leaf images were generated for training via data augmentation technology. The proposed Faster DR-IACNN detector improved the detection performance of multiscale diseased spots and small diseased spots by introducing the Inception-v1 module, Inception-ResNet-v2 module and SE-blocks.

The new deep-learning-based detection method was implemented in the Caffe framework on the GPU platform. The detection performance of Faster DR-IACNN reached 81.1% mAP, and the speed was 15.01 FPS. The results demonstrate that the proposed Faster DR-IACNN method can detect four common grape leaf diseases efficiently and accurately, and it provides a feasible solution for the real-time detection of grape leaf diseases.

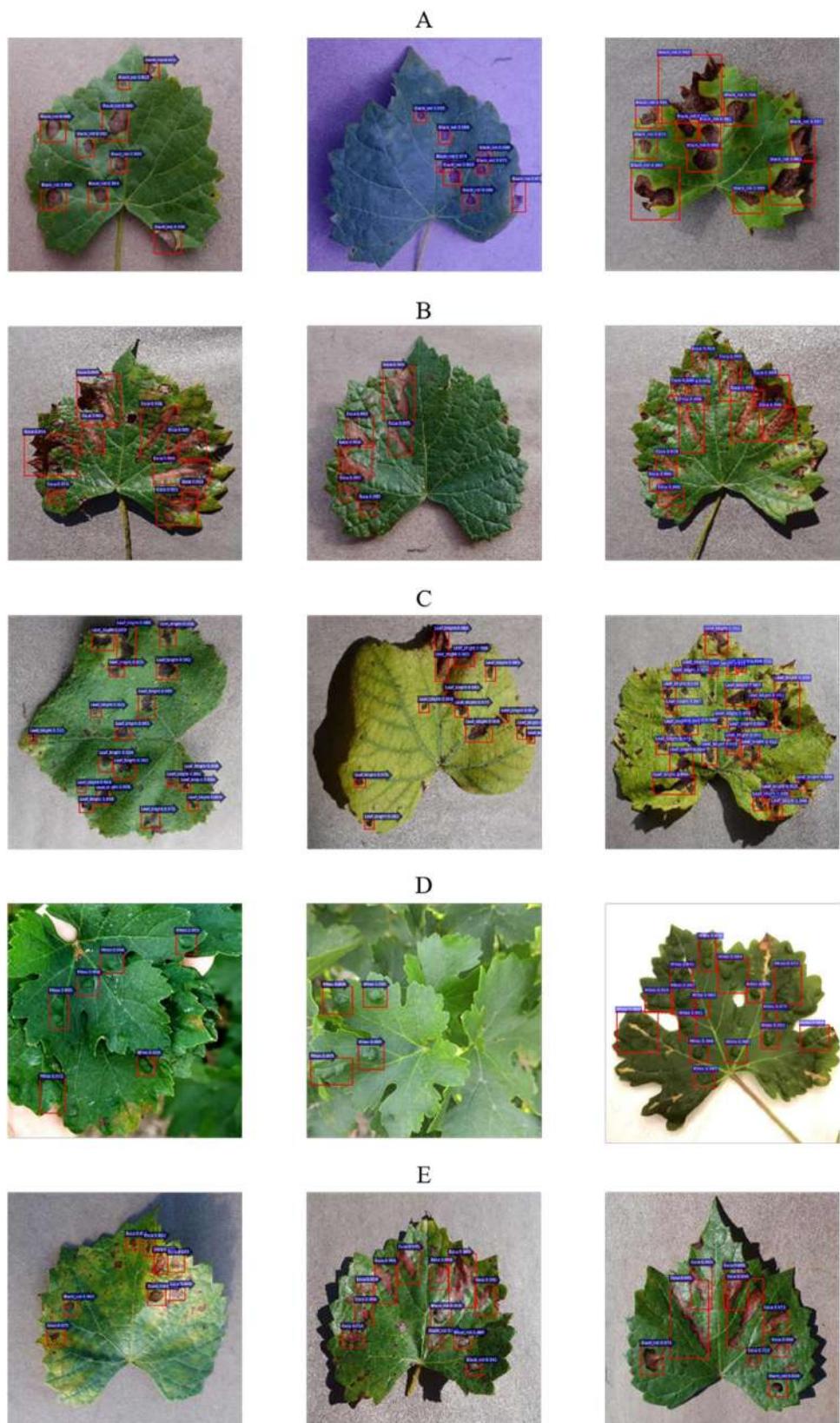


FIGURE 13 | Grape leaf diseased spots detection results. **(A)** Multiple Black rot spots in one leaf. **(B)** Multiple Black measles spots in one leaf. **(C)** Multiple Leaf blight spots in one leaf. **(D)** Multiple Mites of grape spots in one leaf. **(E)** Diversified diseased spots in one leaf.

DATA AVAILABILITY STATEMENT

The datasets generated for this study are available on request to the corresponding author.

AUTHOR CONTRIBUTIONS

XX and YM contributed significantly to conducting the experiment, implementing and validating the method, writing the original draft, and revisions. BL contributed significantly to proposing the idea, providing the research project, acquiring funding, preparing, and revising the manuscript. JH, SL, and HW helped perform the analysis and provided constructive discussions.

FUNDING

We are grateful for the reviewers' hard work and constructive comments, which allowed us to improve the quality of this

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Conflict of Interest: HW was employed by the company West Electronic Business Co., Ltd.

The remaining authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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Black Rot Disease Detection in Grape Plant (*Vitis vinifera*) Using Colour Based Segmentation & Machine Learning

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Abstract—Black Rot is a fungal disease which affects the yield as well as the wine quality and can also cause complete crop loss. It can be identified as brown/tan coloured circular spots/lesions distributed unevenly on the leaf of the plant. A proper detection of the disease is required which can be further helpful in taking active measures like Spraying of Fungicides, Pruning, etc. can be done on time. The PlantVillage Dataset is used, which contains images of grape plant leaves affected from Black Rot Disease as well as the pictures of healthy leaves. HSV and L*a*b* colour models are used for the segmentation purposes. The healthy part and the diseased part of the leaves are separated using colour-based techniques and the features are stored for each leaf. The color of diseased part is very much different from the healthy part of the leaves which makes it easier to detect the disease on the basis of color. The machine learning is done using the Support Vector Machine Classifier and the results are analysed on different Kernels of SVM. The highest accuracy achieved is 94.1%.

Keywords—Disease Detection, Pattern Recognition, SVM, HSV, Colour Based Detection, Grape Plant, Image Processing, L*a*b*, K-means Clustering, PlantVillage Dataset, Supervised Learning, Machine Learning.

I. INTRODUCTION

There are many pathogens which can cause disease in the plants, one of them is fungus. The most common fungal disease among grape plants is Black Rot disease caused by a fungus named as *Guignardiabidwellii*. Black Rot Disease was observed in the Grape Plants which were growing in the places with high humid conditions. The pathogens release some toxic compounds on the leaves of the plant which results in necrotic (causing the effected tissue's death) spots which appeared to be brownish-tan coloured. These spots can be seen on all green regions of the leaf. This disease can also become an epidemic sometimes resulting in yield loss from 5 % to 80 % [1]. Some protocols have been developed to eradicate this disease which are cost effective and also secure the productivity. One of them includes the cutting of affected vines of the plant to save the healthy leaves [2]. Most of the methods which can be used as a preventive or control

measurefor the diseases, require the early detection of the disease so that the planning can be done and some strategy can be developed which can further help in preventing the yield and the further loses like economic loss and the yield quality loss.

This paper discusses about a model which can be used for early detection of Black Rot disease in Grape Vines. It uses a colour-based segmentation and detection of the disease. The two-colour models i.e. HSV and L*a*b* are used to segment the affected areas from the pictures of diseased leaves. The system is developed using machine learning algorithms which collects the features of the disease and get trained by that data. The trained feature vectors are then compared with the feature vectors to be tested. The accuracy is computed on the basis of those comparisons. Support Vector Machine (SVM) is used to classify the diseased and non-diseased (healthy) leaves. This data can be used for further analysis and can be used to automate the early disease detection procedure using robotics, etc.

II. RELATED WORK

There are many methods used by researchers to segment and detect the disease from the plant leaves. The color comprehensive features are used by Juncheng&Keming which included the Excess Red Index and H component of HSV image and b* components of L*a*ab* model. A CCF map is used to segment and detect the disease [3]. Esmael and Brian used HSV model in combination with morphological operations to compute the perimeter and area of the contour of the region of interest for detecting the crop [4]. The color models namely HIS, CIELAB, &YCbCr are used by Piyush and Anand, followed by the Otsu Method to detect the disease spots in Monocot & Dicot family plants [5]. Color Co-occurrence Method was used by R.Pydipati with statistical methods. The accuracy found to be 95% [6]. Massimo and Muhammad designed a novel model used to segment the leaves using Active Contour methods with accuracy of 96.7% [7]. Sparse Representation is used by Shanwen to extract the features for lesions present on Cucumber Leaves. The accuracy obtained was 91.25% [8]. Hernandez analyzed the optimal color space for the segmentation purpose of the

disease and computed the percentage of green cover perimeter for the feature vector [9]. Color and size features are used by Hrishikesh followed by the computation of the connected components [10]. LBP & ULBP are used by Chandan in collaboration with color histogram and color models to create a novel model which worked on the basis of color & texture properties [11]. Shanwen used Super-pixel Clustering method in combination with Expectation Maximization Algorithm to segment disease from the leaves [12]. Namita and Malay achieved 99% accuracy by implementing L*a*b* model with Adaptive Thresholding Method for detecting Powdery Mildew in Cherry Leaves [13]. Rillian and Diogo achieved 98% accuracy with SIFT, DSIFT, SURF & PHOW. Local Descriptor models are implemented to detect Soybean Disease [14]. Viraj and Arun used texture features-Local Homogeneity, Contrast, Cluster Shade, Energy and Cluster Prominence with HIS Model to achieve an accuracy of 97.6% [15]. Marian & Gabriel used digital color analysis using HIS model and by estimating the Euclidean distances between the colors of different leaves which has Magnesium and Potassium deficiency [16]. Local Binary Pattern with one class Classifier (SVM) is used to achieve 95% accuracy with 46 different plant conditions [17]. Zahid suggested many feature extraction techniques such as SURF, SIFT & HOG to detect diseases in citrus plants such as oranges, lemons, grapefruits [18]. Konstantinos suggested Deep learning models such as AlexNet, GoogLeNet, VGG to detect plant disease and achieved 99.53% of accuracy [19].

III. DATASET & METHODOLOGY

The images used in the study are accessed from a web-based repository and has monochrome background. The images are mainly of the Grape Vine Leaves.

A. Image Database

The images that are used for analysis are taken from the PlantVillage Grape Plant Dataset (Black Rot Disease) [20]. The database contained the images of leaves of grape plant which are commonly single leaves and the background was monochrome hence, it was easier to segment the leaf areas with no complex background. 400 images were used in total. Each image in the dataset was of 256x256 resolution. The healthy leaves have no spots and has flawless texture, on the other hand, diseased leaves are affected with brown spots or lesions as shown in Fig 1.

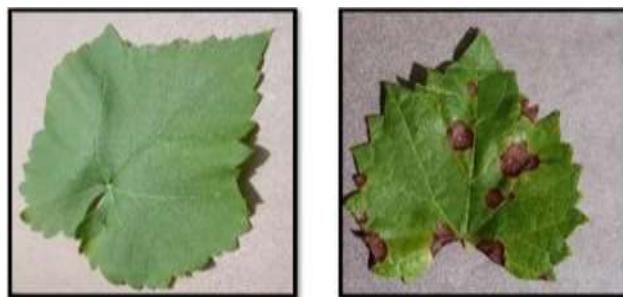


Figure 1 Healthy Leaf (left) and Diseased Leaf (right)

B. Methodology

The methodology explained below uses 2 colour models HSV model and L*a*b* model, Fig 2:

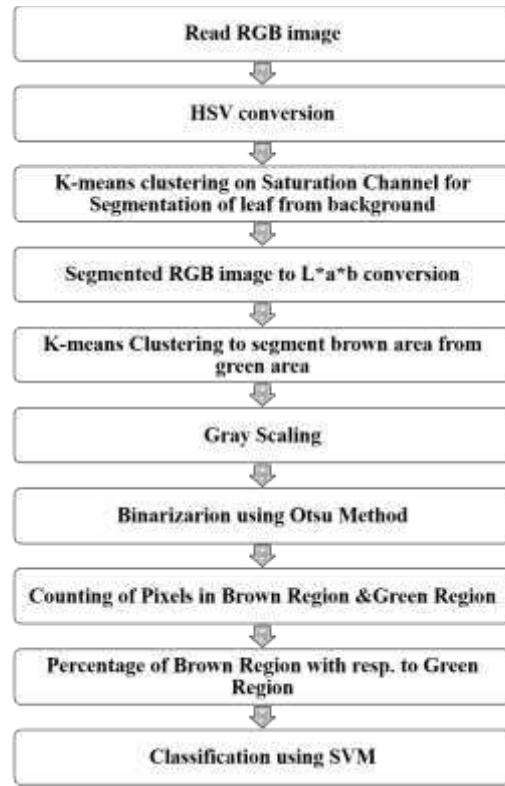


Figure 2 Proposed Methodology

It involves the image to be converted into HSV format. The leaf part is segmented from the image. Then, the diseased part is extracted using L*a*b* model in combination with K-means Adaptive Clustering. Gray-Scaling is applied on the extracted healthy and diseased images and binarization is done using Otsu's Global Threshold method. The pixel count is computed on the basis of white pixels in both cases (healthy as well as diseased). The classification is applied using supervised machine learning algorithm, Support Vector Machine with its different Kernels.

IV. FEATURES EXTRACTION USING COLOR MODELS HSV & L*A*B*

The RGB image in the dataset is loaded into the system and converted into HSV image. This is done to extract the saturation channel from the image. It signifies the amount of colour in the pixel. The Hue, Saturation and Intensity values are computed using the formulae 1-9 [21]. R, G & B signifies the values for Red, Green and Blue channel values respectively for the pixel. H, S & V are the Hue, Saturation and Intensity/Value images:

$$R' = \frac{R}{255} \dots (1), \quad G' = \frac{G}{255} \dots (2), \quad B' = \frac{B}{255} \dots (3)$$

$$D_{max} = \max(R', G', B') \dots (4)$$

$$D_{min} = \min(R', G', B') \dots (5)$$

$$L = D_{max} - D_{min} \dots (6)$$

Hue calculation:

$$H = \begin{cases} 0 & , L = 0 \\ 60 \times \left(\frac{G' - B'}{L} \text{ mod } 6 \right), D_{max} = R' \\ 60 \times \left(\frac{B' - R'}{L} + 2 \right), D_{max} = G' \\ 60 \times \left(\frac{R' - G'}{L} + 4 \right), D_{max} = B' \end{cases} \dots (7)$$

Saturation calculation:

$$S = \begin{cases} 0, & D_{max} = 0 \\ \frac{L}{K_{max}}, & D_{max} \neq 0 \end{cases} \dots (8)$$

Value calculation:

$$V = D_{max} \dots (9)$$

The k-means adaptive clustering is applied on the saturation channel to cluster the pixels and label them [22]. The pixel clusters which contained the only the leaf part and not the background, are accepted and used for further analysis. The segmented image is then converted into L*a*b* image and the K-means Adaptive Clustering is applied on a & b components. The significance of the K-means Clustering Algorithm is that it doesn't need the predefined K-value (no. of clusters). It starts with taking the K-value =2 and goes up to the K-value=10 until all the pixels are clustered correctly.

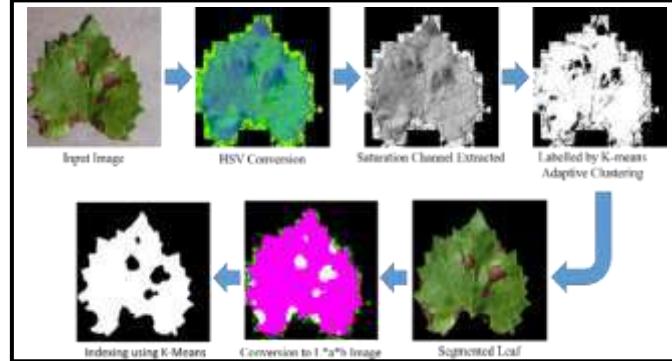


Figure 3 Feature Extraction a). Input Image, b). Image after conversion to HSV Model, c). Extracted Saturation Channel, d). Labelled Clusters by Adaptive K-Means Clustering, e). Segmented Leaf, f). Conversion to L*a*b* Model, g). Segmented Unaffected Part

The K-means clustering extracted the green part cluster and the diseased part cluster separately, as shown in Fig 3. Gray scaling is applied on the green cluster as well as the diseased cluster. The Gray scaled images are then binarized using Otsu Binariization using Global Threshold method. The Global Thresholding is used because there is no complex background in the image. Also, due to presence of monochromic and non-complex background the task of

segmentation proves to be easier. Thresholding provides a Binary Image for each cluster image, as shown in Fig 4.

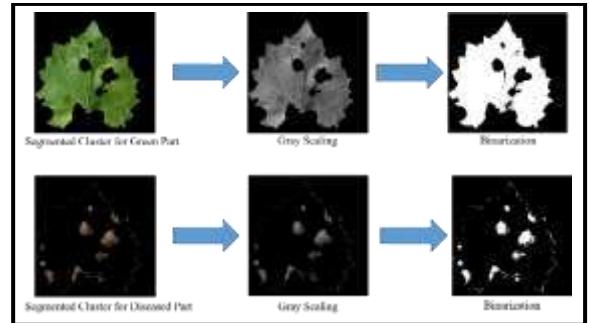


Figure 4 a). Segmented Green/unaffected area, b). Gray Scaling, c). Binarization using Otsu Global Thresholding, d). Segmented Brown/affected Area, e). Gray Scaling of affected area, f). Binarization of affected area using Otsu Global Thresholding Method

The white pixels in each cluster (healthy/green cluster and diseased/brown cluster) are counted. The formula used for obtaining colour percentage ratio is as shown in eq. (10). The brown area/diseasedarea percentages w.r.t. green area is used as features. The classification using SVM is done with its 3 Kernels.

$$\text{ColorPercentageRatio} = \frac{\text{Brown (Diseased) Pixels}}{\text{Green (Healthy) Pixels}} \dots (10)$$

The percentage of brown region pixels are computed with respect to Green Region pixels for each image.

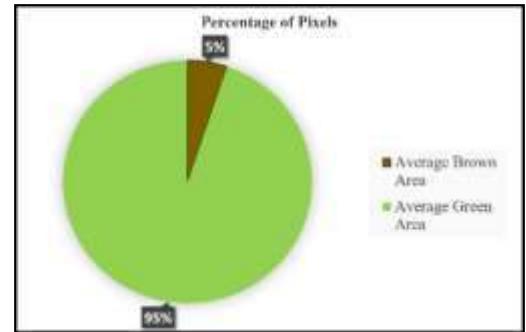


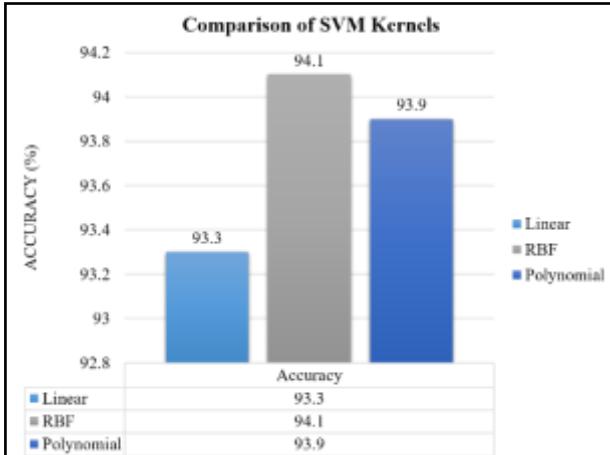
Figure 5 Brown (Diseased) area percentage with resp. to Green (Healthy) area percentage

The whole dataset has been observed and it has been found that the average percentage of brown pixels over green pixels is came out to be 5% as shown in Fig 5.

V. RESULTS

The image dataset contained 400 images, out of which, 250 images are used for training purpose and 150 images are used for testing purpose. The feature vectors made are then processed for classification phase. Support Vector machine is used for classification. The data is analyzed on SVM's 3 Kernels- Lineal, RBF and Polynomial Kernel [23]. The below mentioned graph shows the comparison between the accuracies provided by each of the kernel for classification:

TABLE I COMPARISON OF ACCURACY OF EACH KERNEL



The accuracy is computed with kernels came out to be 93.3% with Linear Kernel, 94.1% with RBF Kernel and 93.9% with Polynomial Kernel. The highest accuracy found is 94.1% as shown in Table I.

VI. CONCLUSION

The above mentioned 2 color models- HSV model and L*a*b* model can be used to segment the leaf from the background and diseased part from the leaf. The diseases in plants can be segmented/separated with the use of color-based image processing techniques. The color percentage ratio is proven to be a successful method in detecting the disease if the affected area has different color to the non-affected area. The system performs best with SVM's RBF Kernel.

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Plant Leaf Detection and Disease Recognition using Deep Learning

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Abstract

The latest improvements in computer vision formulated through deep learning have paved the method for how to detect and diagnose diseases in plants by using a camera to capture images as basis for recognizing several types of plant diseases. This study provides an efficient solution for detecting multiple diseases in several plant varieties. The system was designed to detect and recognize several plant varieties specifically apple, corn, grapes, potato, sugarcane, and tomato. The system can also detect several diseases of plants.

Comprised of 35,000 images of healthy plant leaves and infected with the diseases, the researchers were able to train deep learning models to detect and recognize plant diseases and the absence these of diseases. The trained model has achieved an accuracy rate of 96.5% and the system was able to register up to 100% accuracy in detecting and recognizing the plant variety and the type of diseases the plant was infected.

Keywords: plant disease recognition, deep learning, computer vision, convolutional neural network

Introduction

Early plant disease detection plays a significant role in efficient crop yield. Plant diseases like black measles, black rot, bacterial spot, etc. affect the growth, crop quality of plants and economic impacts in the agriculture industry. To avoid the impact of these diseases, expensive approaches and the use of pesticides are some solutions the farmers usually implement. The use of chemical means damages the plant and the surrounding environment. In addition, this kind of approach intensifies the cost of production and major monetary loss to farmers. Early discovery of diseases as they occur is the most important period for efficient disease management. Manual disease detection through human experts to identify and recognize plant diseases is a usual practice in agriculture [1]. With the improvements in technology, automatic detection of plant diseases from raw images is possible through computer vision and artificial intelligence researches [2]. In this study, the researchers were able to investigate plant diseases and pest's infestation that affects the leaves of the plants.

Image processing techniques are now commonly employed in agriculture and it is applied for the detection and recognition of weeds [3], fruit-grading [4], identifying and calculating disease infestations of plants [5], and plant genomics [6]. Currently, the introduction of deep learning methods turns out

to be popular [7].

Deep learning is the advanced methods of machine learning that uses neural networks that works like the human brain [8]. Traditional methods involve the use of semantic features as the classification method [9]. LeChun et al. describes deep learning as a neural network learning process and one feature of deep learning is that it can automatically obtain features through image patterns [10].

A convolutional neural network (CNN) is a deep learning model that is widely used in image processing. The work of Lee et al. [11] presents a hybrid model to obtain characteristics of leaves using CNN and classify the extracted features of leaves. The study of Ferentinos, K.P. uses simple and infected plant leaf images to detect plant diseases using pre-trained CNN model [12]. Durmus et al work on the detection of diseases of the tomato leaves using AlexNet and SqueezeNet pre-trained CNN architectures [13]. While Atabay et al. [14] contributed a new CNN architecture to do disease classification and identification.

The methodology in the study involves three key stages: acquisition of data, pre-processing of data and image classification. The study utilized dataset from Plant village dataset [15] that contains plant varieties of apple, corn, grapes, potato, sugarcane, and tomato. There are 11 types of plant diseases identified in the study including healthy images of identified plants. Image pre-processing involves re-sized images and enhancement before supplying it for the classification model.

Convolutional Neural Network

Deep learning is a subsection of Artificial Intelligence and machine learning that uses artificial neural networks (ANN). Training the deep learning models divides the feature extraction and extracts its features for classification. There are several applications of deep learning which include computer vision, image classification, restoration, speech, video analysis, etc.

A convolutional neural network with nominal process can simply detect and categorize. It is efficient in evaluating graphical images and extracts the essential features through its multi-layered structure. As shown in Fig. 1, the CNN involves four layers, that is: input image, convolutional layer and pooling layer, fully connected layers, and output.

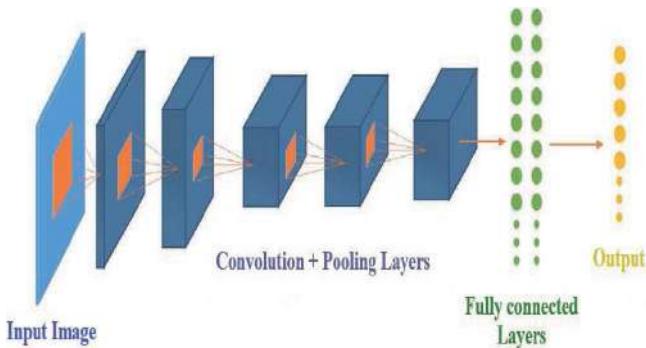


Fig 1. Illustration of Convolutional Neural Network Architecture

A. Convolutional Layer

Convolutional layers store the output of the kernels from the previous layer which consists of weights and biases to be learned. The generated kernels that represent the data without an error is the point of the optimization function. In this layer, a sequence of mathematical processes is done to extract the feature map of the input image [16]. Fig. 2 exhibits the operation of the convolution layer for a 5x5 image input and a result is a 3x3 filter that reduced to a smaller size [17]. Also, the figure shows the shifting of filter starting from the upper left corner of the input image. The values for each step are then multiplied by the values of the filter and the added values are the result. A new matrix with the reduced size is formed from the input image.

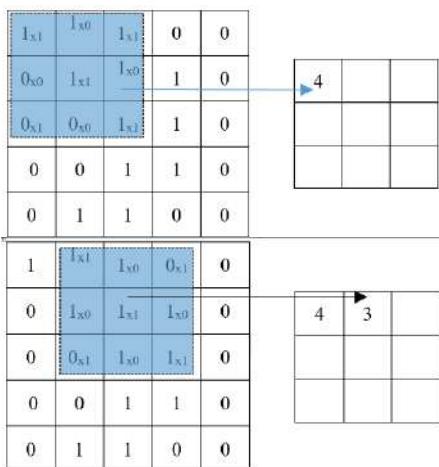


Fig. 2 5x5 input and 3x3 filter operation of convolution layer.

B. Pooling Layer

This layer reduces overfitting and lowers the neuron size for the downsampling layer. Fig. 3 illustrates an example of the pooling operation. This layer reduces the feature map size, reduce parameter numbers, training-time, computation rate and controls overfitting [20]. Overfitting is defined by a model by achieving 100% on the training dataset and 50% on test data. ReLU and max pooling were utilized to lower feature map dimensions [21].

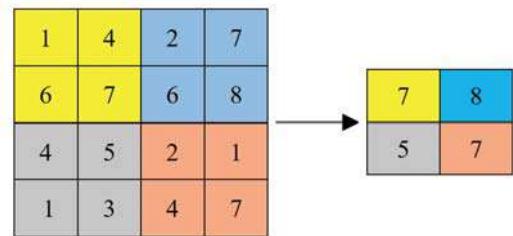


Fig. 3. Pooling operation

C. Activation Layer

Utilizes a non-linear ReLU (Rectified Linear Unit) activation layer in every convolution layer. The application of dropout layers to prevent overfitting is also applied in this layer.

D. Fully Connected Layer

This layer is used to analyze the class probabilities and the output is the input of the classifier. Softmax classifier is the well-known input classifier and recognition and classification of sugarcane diseases are applied in this layer.

Methodology

A block diagram presented in Fig. 4 shows the Input Dataset, Image Acquisition, Image pre-processing and Classification.

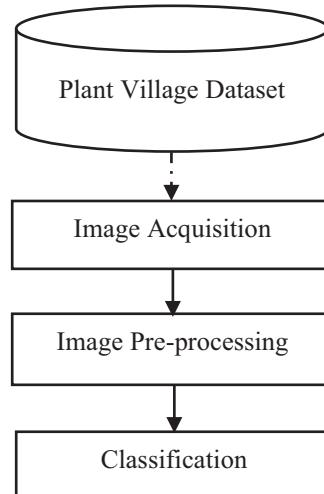


Fig. 4 Plant leaf detection and disease recognition methodology

A. Image Acquisition

Image dataset used for training the model was acquired in the Plant Village repository [15]. A python script was used to download images of the plant diseases from the repository. The acquired dataset consists of approximately 35,000 images with 32 different classes plant varieties and diseases.

B. Image Pre-processing

Pre-processed images are reduced image size and image crop to a given input. It processes and enhances the image to its needed color scale. The study uses colored and resized images to 96x96 resolution for processing.

C. Classification

Classification uses a fully connected layers and for feature extraction it uses convolutional and pooling layers. The classification process classifies the plant leaf if it is infected

with the disease or not, identifies the type of plant disease and recognize the plant variety.

Experimental Settings

The dataset consists of approximately 35,000 images containing 9 different types of tomato leaf diseases, 4 different types of grape leaf diseases, 4 different types of corn leaf diseases, 4 different types of apple leaf diseases, and 6 different types of sugarcane diseases. A neural network application program interface (API) written in Python was applied for the CNN model application. All the image dataset was used for training and testing uses 1,000 images that was taken from the field. Data augmentation techniques were integrated into the application to enhance the image dataset by rotating the images to 25 degrees, flipping and shifting of images horizontally and vertically. Adam optimizer is incorporated using a categorical cross-entropy. The model trained 75 epochs using a batch size of 32. All the experimentations were performed on Dell Inspiron 14-3476 i5 processor and memory size of 16GB.

Results and Analysis

A 96.5% accuracy rate was achieved using 75 epochs during the training of the model. The model also achieved a maximum accuracy rate of 100% when testing random images of plant varieties and diseases. The visualization of plots of train and test accuracy is described in fig 5. shows the model is effective in detecting and recognizing plant diseases.

Fig. 6 shows of detection and recognition of a corn plant with 100% accuracy and it shows an accuracy rate of 100% recognition of healthy plant leaf on the left image and 99.56% affected with gray leaf spot disease on the right image. Fig. 7 shows the result of 99.77% and 99.58% accuracy of detecting and recognizing a tomato plant and it shows a 99.62% accuracy rate that it is infected with a late blight disease on the left image and 75.36% infected of early blight disease on the right image. Fig. 8 shows a 100% result of detection and recognition of a grape plant and shows a 100% rate that the leaf is infected with a late blight disease on the left image and 95.09% infected with a black rot disease on the right image. Fig. 9 shows the result of the detection and recognition of an apple plant with 100% accuracy and shows a 100% result that the leaf is infected with a black rot disease on the left image and a 99.99% that it is a healthy leaf on the right image.

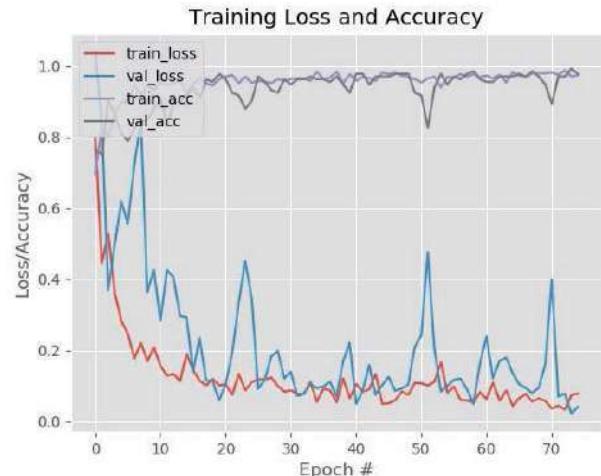


Fig. 5 Accuracy and loss against epochs

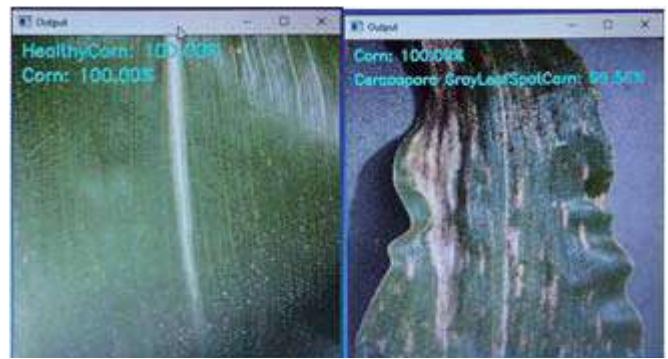


Fig. 6 Result of detection and recognition of a corn plant with 100% accuracy and shows a healthy plant leaf on the left image and diseased infected plant on the right image.

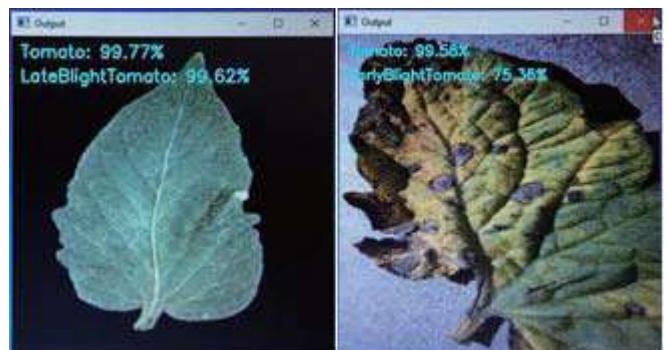


Fig. 7 Result of detection and recognition of a tomato plant with 99% accuracy and shows a leaf infected with a late blight disease on the left image and early blight disease on the right image.



Fig. 8 Result of detection and recognition of a grape plant with 100% accuracy and shows a leaf infected with a late blight disease on the left image and black rot disease on the right image.



Fig. 9 Result of detection and recognition of an apple plant with 100% accuracy and shows a leaf infected with a black rot disease on the left image and a healthy leaf on the right image.

Conclusion

The people around the world rely on the agricultural sector as one of the most important sectors where crops are the basic need for food. Early recognition and detection of these diseases are crucial to the agricultural industry. This paper has achieved its goal to detect and recognize 32 different plant varieties and plant diseases using convolutional neural network. The trained model can be used to test real-time images to detect and recognize plant diseases. For the future work, additional plant varieties and different types of plant diseases may be included in the existing dataset to increase the trained models. Other CNN architectures may also use different learning rates and optimizers for experimenting the performance and accuracy of the model. With the achieved accuracy of 96.5%, the proposed model can assist farmers to detect and recognize plant diseases.

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Detection and Classification of Diseases of Grape Plant Using Opposite Colour Local Binary Pattern Feature and Machine Learning for Automated Decision Support System.

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Abstract—Plant diseases cause major economic and production losses as well as curtailment in both quantity and quality of agricultural production. Now a day's, for supervising large field of crops there is been increased demand for plant leaf disease detection system. The critical issue here is to monitor the health of the plants and detection of the respective diseases. Studies show that most of the plant disease can be diagnosed from the properties of the leaf. Thus leaf based disease analysis for plants is an exciting new domain.

The technique proposed for identification of plant disease through the leaf texture analysis and pattern recognition. In this work we focus on Grapes plant leaf disease detection system. The system takes a single leaf of a plant as an input and segmentation is performed after background removal. The segmented leaf image is then analyzed through high pass filter to detect the diseased part of the leaf. The segmented leaf texture is retrieved using unique fractal based texture feature. Fractal based features are locally invariant in nature and therefore provides a good texture model. The texture of every independent disease will be different. The extracted texture pattern is then classified using multiclass SVM. The work classifies focus on major diseases commonly observed in Grapes plant which are downy mildew & black rot. The proposed approach avails advice of agricultural experts easily to farmers with the accuracy of 96.6%.

Keywords- Plant disease; Decision Support System (DSS); HSV (Hue Saturation Value); Support Vector Machine (SVM), Texture analysis, OC-LBP.

I. INTRODUCTION

India is an agriculture dependent country where agriculture contributes to broadest economic sector as well as plays an

important role in socio-economic growth of India. India ranks as one of the largest agriculture country of fruits and vegetables. Modern agriculture is now aiming at producing the maximum amount of yield with the minimum expenditure of resources, energy and time to meet the needs of an enormous and growing population.

Agriculture products such as fruits, milk, rice, sugar cane, vegetables, etc. need proper quality control in order to gain more valuable products [1]. Management of fruits and vegetables crops always requires close monitoring as it affects the production and post-harvest life significantly [2].

Plant diseases are major cause of quality reduction of agricultural products. There are several diseases that affect plants with the potential to cause devastating ecological, social and economic losses. Therefore, in order to have a proper yield, diagnosing diseases is the utmost important. Technology plays a pivotal role in ameliorating in the field of agriculture. Image processing tools helps to monitor the health of the plant. Normally almost all kinds of diseases need sophisticated analysis, image processing technique deals with such kind of scrutiny [3].

This paper focuses on Grapes plant diseases detection and classification using image processing techniques. Grapes plant is one of largely produced crops in India. Improving the productivity of grapes can significantly reduce the food deficiency and can contribute towards improvement in health care. Grapes are crops that are susceptible to many diseases such as Downy mildew, powdery mildew, black rot, anthracnose, etc. These diseases are caused by fungi which attack on grape leaves as well as berries. Powdery mildew is mostly observed on grape leaves and appears as a whitish-grey powdery coating on leaf surface whereas downy mildew shows yellow infected surface over leaves. Automatic detection of

plant diseases is a forthcoming research area as it proves helpful in monitoring large fields, and automatically detects the plant diseases based on the symptoms that are visible on the plant leaves. Therefore the objective of this paper is to develop image processing technique that can accurately analyse the disease of the grape plants based on images of the leaves, since leaf is a good indicator of the plant health and offer a solution to major national issue of increasing agriculture productivity.

Decision Support Systems (DSS) for agriculture is based on the technology that can be useful for farmers and help to increase the agricultural productivity. The efficiency of decision making in agriculture sector can be improved by reducing the technological gap between research and farmers using Decision Support System (DSS). But, the current Decision Support Systems (DSS) are call center based which require that the farmers should orally give inputs regarding the health of crops which is not effective. This can be made friendlier for the farmers by integrating image processing with DSS.

In this paper, we propose a novel framework that focuses on the disease detection for plants. The farmers can capture the images of plant leaves using any mobile camera having resolution greater than 2 mega pixels. The farmer needs to just capture the image of the plant leaf through the mobile camera and send the image to a central system through mobile internet. After acquiring images, through the proposed work, normal and abnormal leaves are classified based upon the extracted features from leaf images. The extracted features, class and the percentage area of abnormality will be given as input to the DSS. The proposed algorithm will automatically recognize the plant based on the color, texture and shape of the leaf. The purpose of the proposed project and research work is to provide inputs for the DSS, developed for providing advice to the farmers as when they require over mobile internet.

The rest of the paper is organized as follows: Section II describes the literature survey. The proposed approach is illustrated in section III. The pre-processing steps used in the algorithm are introduced in section IV. Section V describes the details regarding classification. The experimentation and results are projected in section VI and finally section VII concludes the paper.

II. LITERATURE SURVEY

Extensive research has been conducted to explore various methods for automatic detection of plant diseases. The disease can manifest in different parts of the plant such as roots, stem, fruit or leaves. As stated before, this work concentrates particularly on leaves.

P. Revathi, M. Hemalatha [3] worked on classification of diseases in cotton leaves. Authors have considered six types of diseases in the cotton plant for classification. Based on advanced computational techniques the significance of this work design is to reduce the time, cost and complexity. To identify the affected region of a leaf the author has used Enhanced Particle Swarm Optimization (EPSO) for feature selection. For calculating the edge, color, texture variance for feature analysis of the diseased part Skew divergence technique

is made used. The results obtained using Skew divergence and EPSO technique is 98%.

To detect the diseases automatically and to give the accurate and fast solutions to the farmers, A. Camargo, J.S. Smith [4] addressed the problem of developing image processing algorithms that recognizes abnormalities in the crops. Maize plant images are used in the given paper as the data. The author has considered various diseases like Brown stripe downy mildew, Stem borer etc. for classification. The accuracy of the classification has been rated up to 95%. In this paper we are processing leaf images based on texture, shape and colour and get back to the farmers with solution with the help of SMS. Two Algorithms are used at the processing side first for extracting HSI values color transformation is used. And for second Momentum back propagation Neural Network is used.

Using SVM, Zambre R. [5] have precisely classified cotton leaf diseases. Segmentation technique used in the proposed system involves enhancements of the images first, and then extraction features such as texture, shape, color and boundary etc., Color and Texture feature extraction techniques are used to recognize the diseases. The various diseases recognized on the cotton leaf plants are classified as Bacterial blight, Leaf curl, Grey mildew, Verticillium wilt, Alternaria Macro Spora, Fusarium wilt and Alternaria Leaf Spot. Efficiently cotton leaf diseases were analysed and classified using SVM accuracy.

In [6], brown spot and the leaf blast diseases of rice plant are classified. S. Phadikar used Bayes' formula and Support Vector Machine (SVM) for classification. Mathematically Bayes' formula is given as,

$$p(\omega_i/x) = p(\omega_i)p(x/\omega_i) \quad (1)$$

$$r_j(x) = -\sum L_{ij}p(\omega_i)p(x/\omega_i) \quad (2)$$

In the first stage, based on the number of peaks in the histogram, diseased and the uninfected leaves are classified. The success rate is 92% for uninfected leaf, 96.4% for leaf with brown spot and 84% for leaf with blast, where wrong classification may occur due to shadow effect and color distortion of aging leaves.

In the next level the efficiency of Bayes' classifier and SVM are computed and compared. The success rate is 79.5% for Bayes' classifier and 68.1% SVM classifier; therefore Bayes' classifier is proved to be time efficient as compared to SVM.

To improve agricultural product yields, Arti N. Rathod [7] proposed various methods to identify leaf disease detection using image processing. For leaf disease detection this paper provides the survey of different techniques. In order to increase the recognition rate of final classification process various neural networks & hybrid algorithms can be developed in the future work.

Revathi [8] proposed a novel approach of identification of Cotton crop diseases from RGB images has been exposed in this paper. The author has Proposed Enhanced PSO feature selection method which adopts user features like variances, texture, color and edge to extract the features and Skew divergence method. Using Back propagation neural network (BPN), Fuzzy and SVM classifiers the obtained features are extracted with the help of and Genetic algorithm (GA) feature

selection and Edge CYMK color feature. Cross validation of three classification models were assessed to test this hypothesis. Six types of diseases such as, Root rot, Leaf Blight, Micro Nuriert, Verticillium Wilt, Bacterial Blight, Fusarium wilt have been accurately classified to evaluate its efficiency. The Results of accuracy is as shown in table 1.

TABLE I. ACCURACY OF DIFFERENT METHODS

Sr. No.	Methods	SVM	BPN	Fuzzy
1	Edge features extraction method	68	70	78
2	CYMK features extraction method with edge	73	77	78
3	GA features extraction method with edge	81	81	82
4	GA features extraction method with SVM	83	83	85
5	CYMK features extraction method with SVM	83	83	85
6	Edge features extraction method	91	93	94
7	Color feature extraction with SVM	91	93	94

Sabine D. Bauer [9] proposed approach based on high-resolution multispectral stereo images, they have described three methods of automatic classification of leaf diseases. Images of sugar beet leaves are captured by 2 cameras i.e. multispectral and RGB in a laboratory with proper settings of lights. The leaves infected with the rust fungus Uroources betae or Cercospora beticola were considered. The classification rates achieved in experiments are 86% for Uroources betae and 91% for Cercospora beticola.

Vinita Tajane [10] analyzed CBIR technique accurately detecting the diseases in medicinal plants. Edge histogram and color histogram are the approaches used for identifying leaves based on its features. For edge histogram canny edge detection method is used. To check the intensity of each color pixels in the given sample image color Histogram separates the layers to plot the blue, green and red layer histogram which also tests for abnormalities in the leaf. This paper compares testing sample with the diseased sample, then follow few steps and shows which type of disease the leaf is suffering from.

Radha Kokare and Yogesh Dandawate [11] proposed an image processing based approach used for automated plant iseases classification based on leaf image processing. It is concerned with the discrimination between diseased and healthy soybean leaves using SVM classifier. The algorithm is tested over the database of 120 images taken directly from different farms using different mobile cameras. The SIFT algorithm enables to correctly recognize the plant species based on the leaf shape. The SVM classifier can significantly support in recognizing normal and affected soybean leaves with an average accuracy as high as 93.79%. This system will provide help to the farmer with minimal efforts. The farmer only needs

to capture the image of the plant leaf using mobile camera and send it to the DSS, without any additional inputs.

III. PROPOSED TECHNIQUE

The proposed approach consists of four main steps: image acquisition of grape leaves, extraction of grape leaves from background, statistical analysis and disease classification. Figure 1 shows the block diagram of the overall system. In the proposed approach, the first step is image acquisition in which the images of grape leaves are captured using mobile camera having resolution of 2,5,8,13 mega pixels. A total of 450 images are included in the database which comprises of healthy, diseased and pest-infected images. The image format is jpg. Figure 2 shows sample images from our database.

In the second step, a set of pre-processing steps are applied to the input image so that the image becomes suitable for further processing. Image resizing is one of the important steps so as to maintain the uniformity in terms of size of the images without loss. The next step in pre-processing is background subtraction i.e. segmentation of the region of interest from the image. The third step is to extract the features from the infected part of the leaf based on properties such as color, correlation, homogeneity, contrast and energy.

In the last step, statistical analysis of the features is done and final classification is done using Support Vector Machine (SVM) which classifies the plant leaves in one of the two classes as healthy or diseased.

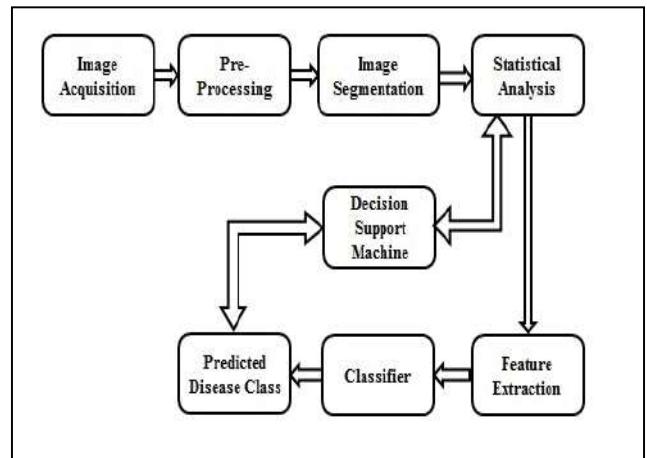


Fig. 1. General Block diagram for Disease Detection System

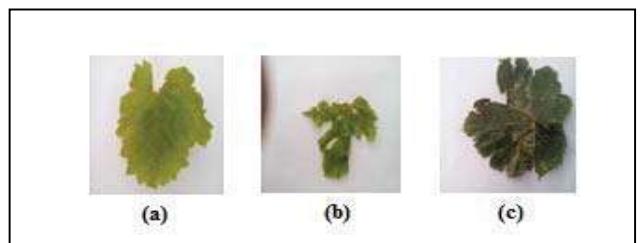


Fig. 2. Sample images from database. (a) Healthy leaf. (b) & (c) Diseased leaf.

IV. PRE-PROCESSING

A set of pre-processing steps are applied to the input image so that it becomes suitable for further processing. The first pre-processing step applied to the input image is image resizing. The original images are of larger size which takes more time for processing. Thus, all images are resized into a smaller size of 256 X 256 to avoid time consumption.

A. Color Transformation

The next step in pre-processing is color transformation. The input RGB images are converted into Hue Saturation Value (HSV) color space. HSV is more close to human perception. Hue component is usually taken into consideration for further analysis as it is the dominant color perceived by an observer. Figure 3 shows the results of RGB to HSV color transformation of the leaves from the database. In the next step, multi thresholding using Otsu algorithm [12] is applied on the HSV images.

Multilevel thresholding segment the images into number of distinct regions which corresponds to one background and several objects by selecting the threshold value based on the largest inter-class variance between the foreground and background [13].

B. Background Subtraction

The initial goal in the pre-processing step is to divide the input image into two classes as soil (i.e. background) and leaf. Background subtraction techniques are applied to the HSV images to remove the unwanted background from the image and to extract the desired part of the image.

In color based background subtraction, the intensity values of R, G and B components are used to remove the unwanted background. Since the green colored pixels contribute to the healthy part of the leaf, these pixels are preserved and the other pixels are made black. The pixels having G component greater than R and B components are preserved and the rest pixels are made black.

In order to get more accurate background subtraction, color based background subtraction is used. In this technique, the connected components in the image are found out. The largest connected component (i.e. the leaf) is preserved and the other unwanted components are removed. Figure 3 shows the results of background subtraction.

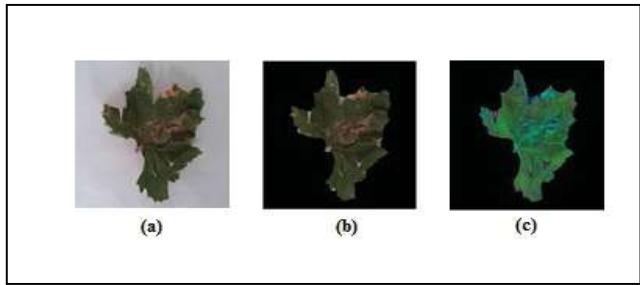


Fig. 3. (a) Original Image (b) Background subtraction results

C. Analysis of Texture using Opposite Color LBP

Local Binary Pattern (LBP) is an efficient and uniform feature for analyzing local texture structures. Texture formation is defined on local patterns instead of explaining it on pixel level. The different simple primitives are used by LBP to describe complex structures in an image. LBP consider texture primitives as well as placement rule property of structure analysis [14].

The method of opposite color LBP feature extraction is adapted by Jain and Healey [15]. Here, opposite color represents the opposite pairs of color perceived by human eyes. In opposite color LBP, LBP operator is applied to each color component also additionally each pair of color component is used to form opposite color patterns [14].

Consider a texture T as a joint distribution [14] of the gray levels $P + 1$ image pixels normalized as:

$$T \approx t(s(g_0 - g_c), \dots, s(g_{P-1} - g_c)) \quad (3)$$

Where, g_c is the center pixel value, g_p ($p = 0, \dots, P - 1$) represents gray values of P equally spaced pixels on a circle of radius: R ($R > 0$)

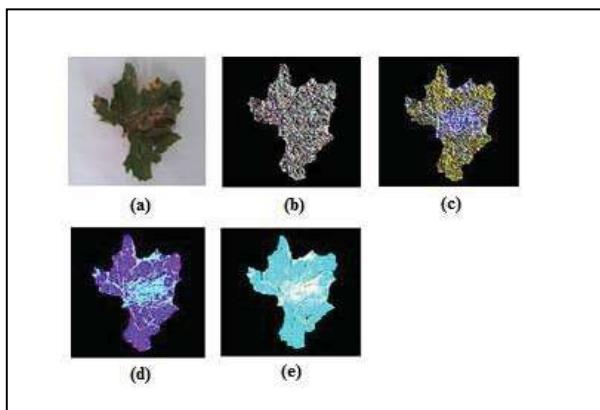


Fig. 4. Results of texture analysis. (a) Original images (b), (c), (d), (e) Results of texture analysis

$$\text{And } s(x) = \begin{cases} 1 & x \geq 0 \\ 0 & x < 0 \end{cases} \quad (4)$$

The local image texture around $R(x_c, y_c)$ is characterized as given below:

$$\begin{aligned} LBP_{P,R}(x_c, y_c) &= \sum_{p=0}^{P-1} s(g_p - g_c) 2^p \end{aligned} \quad (5)$$

Thus, the texture can be approximately represented as:

$$T = t(LBP_{P,R}(x_c, y_c)) \quad (6)$$

Figure 4 shows the result of texture analysis using OC-LBP on leaf images.

V. FEATURE GENERATION AND CLASSIFICATION

After segmentation of leaf image, features are extracted from the image and classified as healthy or diseased image. For classification, the information in the image is generally processed as image statistics such as first order statistics (mean, standard deviation), second order statistics (variants, moments), etc. Edge, texture, shape, color, etc. are some of the others features used for classification. Broken edges, patches in leaf image, roughness or smoothness of leaf texture, etc. can be used for leaf disease detection and identification.

Classification comprises of training and testing processes, where features extracted from training leaves are compared with those extracted from testing leaves. The image is then classified based on the matched features. Image acquisition, segmentation and feature extraction comes under the training process. A simple training and testing process is shown in figure 5.

Support Vector Machine (SVM) is one of the popular techniques used for classification. It was first introduced by Vapnik and coworkers [16]. SVM is a model consisting of learning algorithms which analyses image features used for classification. It uses the principle of structural risk minimization (SRM) which maximizes the margin of class separation for better generalization performance of SVM. The standard SVM classifier classifies the input data into only two distinct classes [16]. Necessity of multi class classifications based on image features has given rise to multi class support classifiers. In one-against-all approach of multi class SVM, each binary classifier is trained to discriminate between its own class data vectors and data vectors of the remaining classes. In the testing process, margins from the separating hyperplane are calculated for classifying the data vectors. The SVM corresponding to the maximum margin is the resultant output [3]. Consider a dataset with N training samples: $\{x_1, y_1\}, \dots, \{x_N, y_N\}$ which is to be classified into M classes. Here, $x_i \in R^m$ is the m-dimensional vector and $y_i \in \{1, 2, \dots, M\}$ represents the corresponding class label [1]. Mathematically, i th SVM performs the following equation [17] that yields the i th decision function

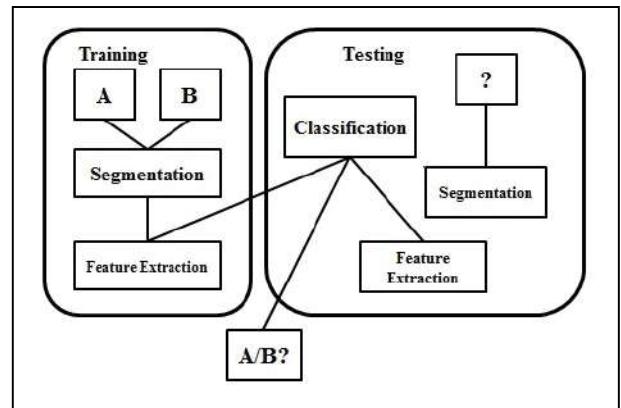


Fig. 5. Classification Process

$$\begin{aligned} f_i(x) &= \omega_i^T \phi(x) + b_i \\ \text{Minimize: } L(\omega, \xi_j^i) &= \frac{1}{2} \|\omega_i\|^2 + C \sum_{l=1}^N \xi_j^l \\ \text{Subject to: } \tilde{y}_j (\omega_i^T \phi(x_j) + b_i) &\geq 1 - \xi_j^i, \xi_j^i \geq 0 \end{aligned} \quad (7)$$

Where, $\tilde{y}_j = 1$ if $y_j = i$ and $\tilde{y}_j = -1$ otherwise. At the classification stage, sample x is classified as in class i^* whose f_{i^*} gives the maximum value [14]:

$$i^* = \arg \max_{i=1,\dots,M} f_i(x) = \arg \max_{i=1,\dots,M} (\omega_i^T \phi(x) + b_i) \quad (8)$$

VI. EXPERIMENTATION AND RESULTS

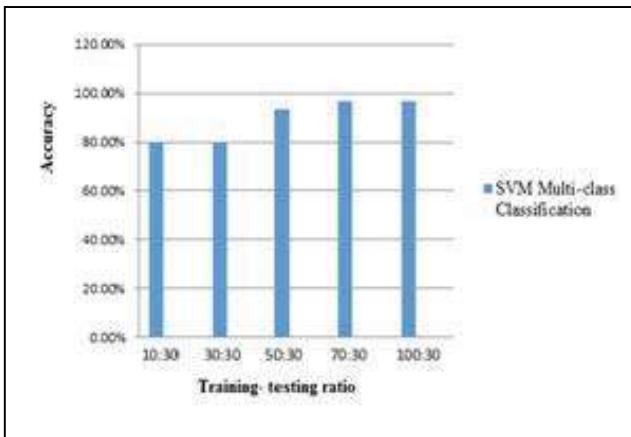
The proposed algorithm is tested over the database of 450 images of Grape leaves. The database consists of images of 160 healthy leaves and 290 diseased leaves. The database is generated by capturing the images directly from the farm using different mobile cameras with different resolutions. The size of original images depends on the resolution of the mobile camera. The algorithm is applied on the RGB images with jpg format.

In the pre-processing step, the input image is first converted into HSV color space and also analyzed texture using Opposite Colour Linear Binary Pattern so that it becomes suitable for segmentation and classification.

For experimentation purpose, the database is divided into two sets: the training set and the testing set. Different training testing ratios are taken into consideration to find out the accuracy of classifier.

Figure 6 shows the graphical representation of the accuracy obtained by multiclass SVM classifier. The classification results show that multiclass SVM classifier yields an average accuracy of 89.3%.

However the classification accuracy improves as the training-testing ratio is increased. With the highest training-testing ratio of 100:30, the accuracy obtained is about 96.66%.

**Fig. 6.** Results of classification accuracy

Thus, threshold based detection yields accurate classification of Grape leaves into two classes as healthy and diseased. The diseased leaves can be further classified based on type of diseases using multi class classifiers and by extracting the diseased clusters for further feature extraction.

VII. CONCLUSION

In this paper, applications of Multiclass SVM are formulated for classification of diseases which are observed in Grapes plants to make Decision Support Systems (DSS) automated and easily available for farmers. The system performs segmentation of a single leaf as input and analyses it through high pass filter to detect the diseased part of the leaf. The segmented leaf texture is retrieved using fractal based texture feature which are locally invariant in nature and therefore provides a good texture module. The extracted texture pattern is then classified to train Multiclass SVM classifiers into healthy or diseased classes respectively.

In this paper major disease commonly observed in Grapes plant such as Downy Mildew, Powdery Mildew, Black rot, etc. are taken into consideration to carry out the experiment. Experimental results shows that integration of image processing techniques with DSS using multiclass SVM gives accuracy up to 96.66% for grape plant disease classification. The accuracy of the system can be further improved by improving the training ratio. The purpose of this work is to provide an automated Decision Support System (DSS) to perform classification between healthy and diseased leaf efficiently as well easily available for Farmers.

ACKNOWLEDGMENT

We would like to thank Vishwakarma Institute of Information Technology for all great support.

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Grape Leaf Disease Identification using Machine Learning Techniques

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Abstract—Having diseases is quite natural in crops due to changing climatic and environmental conditions. Diseases affect the growth and produce of the crops and often difficult to control. To ensure good quality and high production, it is necessary to have accurate disease diagnosis and control actions to prevent them in time. Grape which is widely grown crop in India and it may be affected by different types of diseases on leaf, stem and fruit. Leaf diseases which are the early symptoms caused due to fungi, bacteria and virus. So, there is a need to have an automatic system that can be used to detect the type of diseases and to take appropriate actions. We have proposed an automatic system for detecting the diseases in the grape vines using image processing and machine learning technique. The system segments the leaf (Region of Interest) from the background image using grab cut segmentation method. From the segmented leaf part the diseased region is further segmented based on two different methods such as global thresholding and using semi-supervised technique. The features are extracted from the segmented diseased part and it has been classified as healthy, rot, esca, and leaf blight using different machine learning techniques such as Support Vector Machine (SVM), adaboost and Random Forest tree. Using SVM we have obtained a better testing accuracy of 93%.

Index Terms—Grape Leaves, Disease Identification, Machine learning, SVM

I. INTRODUCTION

Indian Economy is highly dependent on agricultural productivity of the country. Grape is very commercial fruit of India. It can easily be grown in all tropical, sub-tropical and temperate climatic regions. India has got different types of climate and soil in different parts of the country. This makes grapevines a major vegetative propagated crop with high socio-economic importance. The grape plant will cause poor yield and growth when affected by diseases. The diseases are due to the viral, bacteria and fungi infections which are caused by insects, rust and nematodes etc., These diseases are judged by the farmers through their experience or with the help of experts through naked eye observation which is not accurate and time consuming process. Early detection of disease is then very much needed in the agriculture and horticulture field to increase the yield of the crops. We have proposed a system that can detect and identify diseases in the leaves of the grape plants.

II. LITERATURE SURVEY

Web enabled disease detection system have been proposed in [8]. The system proposed a segmentation method which has used mean based strategy for computing threshold and textual features were extracted and classification was done by SVM. The survey proposed by Vijai et al. in [12], discusses about different disease classification techniques used for plant leaf disease and used genetic algorithm for image segmentation. An integrated approach of particle swarm optimization and SVM for plant leaf disease detection and classification was proposed in [10]. Disease detection system for pomegranate leaves was proposed in [5] which used colour-based segmentation and features like color, morphology and texture for classifying the leaves. Agrawal et al. proposed a leaf detection and climatic parametric monitoring of plants using IOT in [1]. Neural Network based classification was proposed in [9] for detecting plant leaf diseases based on the texture features extracted using GLCM matrix. Mokhtar et al. proposed SVM based classification by extracting the texture based features in [6]. SVM classifier with different kernel functions including Cauchy kernel, Invmult Kernel and Laplacian Kernel were employed to evaluate the ability of the approach to detect and identify the infected tomato leaf. Leaf detection system for pomegranate leaves was proposed in [13] which uses K-means for segmentation and statistical features for classification using SVM. Sabrol et al. have proposed a system for leaf disease classification using decision tree by extracting different features after segmenting the leaf using ostu thresholding [4]. A system for two type of disease classification such as Downy mildew and Powdery mildew in grape leaves was proposed in [11] using Back propagation Neural Network. A fast system was proposed for disease detection and classification using Neural Network after extracting the texture features using gray level co-occurrence methodology in [2]. A smartphone based system was developed by Mwebaze et al. in [7] using machine learning technique to detect the state of the disease of the plant and also the severity levels of each diseases. Machine learning based techniques such as decision tree, Navie Bayes theorem, Neural Network, K-Means and Random forest algorithms were proposed for leaf disease classification in [3] using the features such as size, shape, dryness, wilting. Most of the work in the

literature uses K-means segmentation for segmenting the leaf and extract low level features of the image to classify the plant leaf diseases. We have proposed a system which uses global features to classify the plant diseases and segmented the region of interest using graph cut method. We have also compared the results obtained using different machine learning techniques.

III. PROPOSED METHODOLOGY

We have proposed an automated disease detection and classification system for grape leaves using traditional image processing and machine learning techniques. The proposed system first segments the ROI from the background using grab cut algorithm and classify the segmented leaves as healthy, black-rot, esca and leaf blight. Figure. 1 depicts different types of disease in grape leaves.

These diseases are caused due to fungi infection on the leaves. Each disease has different characteristics where black rot appears to be circular in shape and has dark margins, esca appears as dark red stripes and leaf blight appears to be solid reddish-purple spots. The proposed system consists of five different process such as image preprocessing, image segmentation, feature extraction, disease detection and identification. The overall flow of the proposed system is depicted in the Figure. 2

A. Image Preprocessing

The images are acquired from the web and are from different sources and sizes. The images also contain noise due to bad lighting condition, weather occlusion etc. To reduce the computational complexity the images are scaled down to a standard width and height. This scaled image are then processed to filter the noise using Gaussian filter. The Gaussian blur is a low pass filter that reduces the high frequency components, we have used 5*5 kernel size to filter the noise

B. Image Segmentation

From the preprocessed image, the leaf part of the image is segmented from the background image Grabcut segmentation algorithm. This algorithm labels a pixel as foreground or background using Gaussian Mixture Model (GMM) and also takes initial rectangle which is a rough segmentation between background and foreground. We have used a rectangle of dimension (10, 10, w-30 and h-20) as the bounding box where w and h are width and height of the image. The results of the Grab-cut method is depicted in Figure. 3.

From extracted foreground i.e. the leaf part, the diseased parts are extracted. The disease part contains lesions, coloured spots and some yellowish part of the leaf. For extracting diseased region from the leaves we have proposed two different methods.

1) *Diseased Part Identification- Global Thresholding:* In this method, the RGB image is converted into grey scale image and then global thresholding is applied to convert the image into a binary image. On the thresholded image, connected

component labelling is applied to find the contours. The contour with the largest area is then identified and morphological operations such as dilation and erosion is applied. The original image is converted to an HSV image and in the h channel, thresholding is applied. Binary AND operator is then applied to contour detected image and the HSV image. The resultant image was again thresholded using binary invert thresholding. The output of this method is shown in Figure.4

2) *Diseased Part Identification - Semisupervised Learning:* The diseased part of the leaves generally appears in blue color in BGR image. To segment the diseased part blue color pixels are filtered out by converting the RGB image into BGR image. To filter blue color pixels we have used the training image to find the lower and upper boundary of blue color pixels. The pixels which lies within lower and upper boundary is then filtered as blue pixels from the input image. In the filtered image thresholding is applied and finally the diseased areas are identified. The output of this method is depicted in Figure.5

3) *Feature Extraction:* Image features provide rich information about the content of the image. These features represent certain distinctive characteristics that can be used for differentiating among the categories of input patterns. In this work, we have used texture and colour features of the images for classification.

The texture of an image is usually expressed by contrast, uniformity, entropy etc. A statistical method of examining the texture of image is Gray-level Co-occurrence matrix (GLCM). GLCM extracts second order statistical texture features from the training images. GLCM is an (N x N) matrix where N is the number of grey levels in the image. Before extracting GLCM features, wavelet decomposition of an image is done. The Discrete Wavelet Transform decomposes an image into different sub-band images such as LL (low-low), LH (low-high), HL (high-low), and HH (high-high). LL image is used for texture analysis as it contains the highest quantity of information. In a GLCM matrix M, if i represents a row and j represents a column, the element M(i, j) represents the count of a pair of two pixels having i and j as their intensities that are separated by a distance d and lies along a direction specified by an angle theta. The algorithm takes d and theta values as input by the user. In this system, we have extracted six texture features namely, energy (randomness of intensity distribution), homogeneity (closeness of distribution of GLCM element to the diagonal of GLCM), contrast (amount of local variations), dissimilarity, correlation (image linearity) and angular second moment in combination with different values of d and theta. The values of d and theta are chosen as (1, 2, 3) and (0, 45, 90, 135) respectively. So the total number of features are (6 x 3 x 4) = 72 texture features for an image.

After segmentation of disease affected portion of the leaf, colour features were examined to find whether the given input leaf is healthy or not. If the input leaf image is healthy leaf then the segmented image will not have any region and it contains only black pixels. For healthy leaves image colour feature vector contains only 0s whereas for non-healthy leaves feature vector contains some color information.



Fig. 1. Different types of disease in Grape Leaves

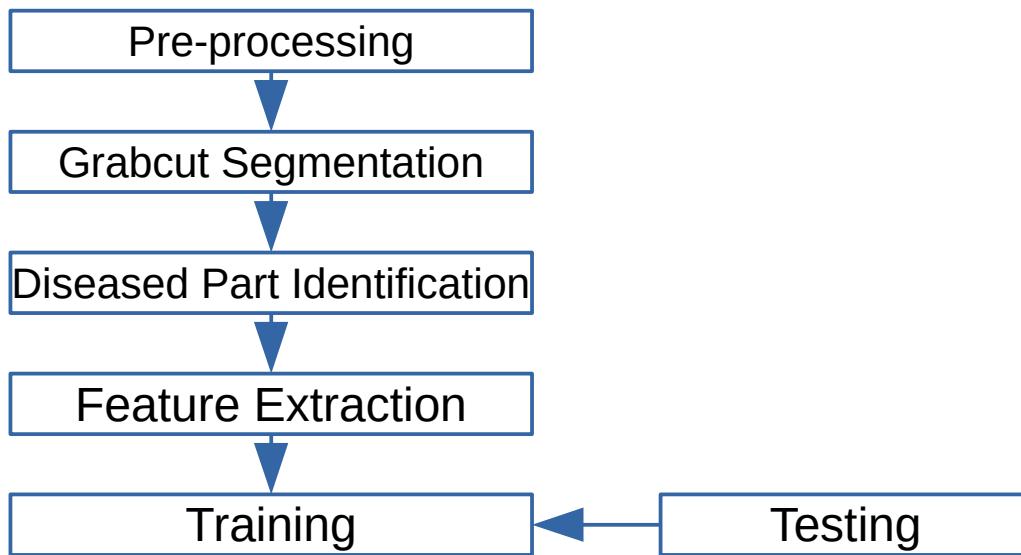


Fig. 2. Architecture of the Proposed System

4) Classification using Different Classifiers: The extracted feature vectors are then used to train different classifiers and the results were analysed.

Support Vector Machine: Given a labelled training data, SVM outputs an optimal separating hyperplane. This hyperplane categorizes new data point into classes. In order to improve the accuracy of SVM, some parameters of the SVM classifier needs to be tuned. One of the parameters is kernel which defines whether separation should be linear or non-linear. Another parameter is regularization which defines the extent to which misclassification of a training sample needs to be avoided. Linear kernel and regularization parameter with value 1000 is used in this system. A larger value of regularization chooses small margin of hyperplane if it ensures minimum misclassification of training examples.

Random Forest: Random Forest is an ensemble learning method and also a supervised learning algorithm. It builds a forest of decision trees. Many trees fit into a random forest classifier. The extracted feature vector is passed as input vector to each tree of the forest and a decision rule is obtained. In other words, the trees vote for a class. The class having the majority votes by the trees is chosen by the forest.

AdaBoost: AdaBoost is used to boost the performance of a machine learning algorithm. It is used with weak learners. Weak models are trained using weighted training data where each instance is weighted. After training the model, the misclassification rate is calculated. This error rate is modified further and used to update the weights of training instances. The purpose of weight updating is to give more weight to misclassified instances. This process continues until there is no



Fig. 3. Result of applying Grabcut segmentation algorithm for a sample image

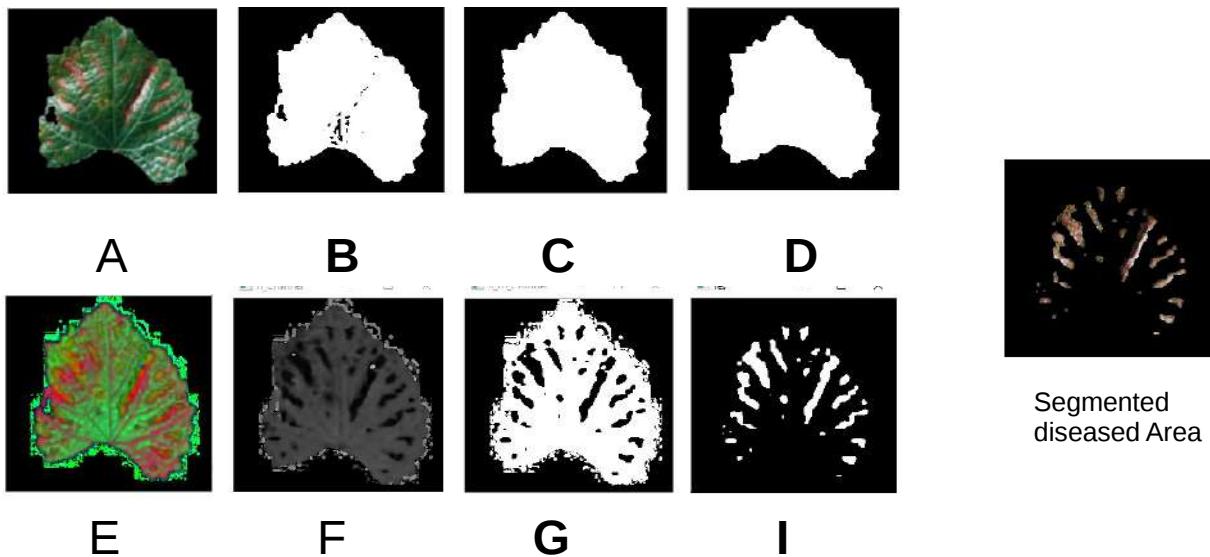


Fig. 4. Disease Part Identification using Global Thresholding. A. Input Image B. Thresholded Image C. Dilation D. Erosion E.HSV Image F. h channel Image G. Thresholded Image F. Binary AND Between D and G

scope for improvement. In this way, the AdaBoost algorithm improves the learning of weak learners.

C. Result And Discussion

We have evaluated the proposed system using 5675 grape leaves which have been downloaded from the plant village website and also from web. We have used 80% of the images for training and others for testing.

The global thresholding method used for segmenting leaf disease part was found to be more suitable for training the model as it segments the precise diseased part of the leaves which leads to improved classification results. Training

accuracy obtained using different machine learning techniques are summarized in Table. I.

From the results it is evident that good training accuracy is achieved when the features are extracted from the diseased part of the images using global thresholding and trained using SVM classifier with tuned parameters since SVM performs good when the data is highly non-linear. The overall accuracy obtained is 93.035% for 1135 test images.

D. Conclusion

In this paper, we propose an automatic leaf recognition system that identify diseases in grape leaves using machine

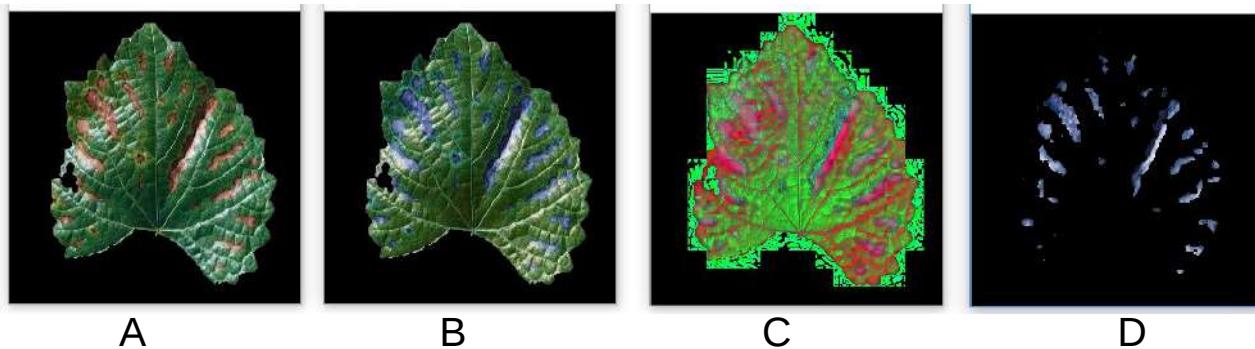


Fig. 5. Disease Part Identification- Semisupervised learning. A. Input Image B. BGR Image C. HSV Image D. Filtered Blue pixels

TABLE I
TRAINING ACCURACY OBTAINED USING PROPOSED METHODS

Classifier	Global Thresholding	Semisupervised Method
SVM	91%	86.57%
Adaboost (Decision Tree)	83%	76%
Random Forest Tree	74.79%	74%

TABLE II
CLASSIFICATION RESULTS FOR TEST IMAGES USING SVM

Class	No. Of Images	Healthy	Black Rot	Esca	Leaf Blight	Accuracy
Healthy	423	407	16	-	-	96.2%
Black Rot	230	-	208	14	8	90.4%
Esca	262	-	24	236	2	90.08 %
Leaf Blight	220	-	9	1	210	95.45 %
Average						93.035 %

learning technique. The proposed system first segments the leaf part from the background using grab cut segmentation technique. From the segmented leaves diseased region are identified using two different methods. The first method uses global thresholding technique whereas the second method using semisupervised learning technique. From the identified diseased part texture and color features are extracted and trained using different classifiers and the results are compared. We have used SVM, random forest and Adaboost algorithms for classification. We have achieved a better result of 93.035% as testing accuracy by using global thresholding and SVM.

ACKNOWLEDGMENT

The authors would like to thank the management of Vellore Institute of Technology, Vellore, India and SSN College of Engineering, Chennai India for funding the respective research labs where the research work is being carried out.

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