



PLANT DETECTION FOR LEAVES DISEASE ANTICIPATION TECHNIQUE USING CONVOLUTIONAL NEURAL NETWORK (CNN)

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ABSTRACT: Tree health is critical for maintaining ecological balance and sustaining diverse ecosystems. Early detection of diseases affecting tree leaves can aid in timely intervention and mitigation efforts. This paper proposes a novel approach to tree disease prediction based on deep learning, specifically the VGG16 convolutional neural network architecture and focuses on analyzing high-resolution images of tree leaves to determine whether they are healthy or infected with a specific disease. The methodology entails gathering a large dataset of images of tree leaves from various species and disease types. To improve the model's robustness and generalization, data preprocessing techniques such as image resizing, normalization, and augmentation are used. For feature extraction, the pre-trained VGG16 model is used, and the top layers are tailored to the tree disease prediction task. To improve its performance, the proposed model goes through rigorous training and validation processes. To assess the model's effectiveness in disease classification, metrics such as accuracy, precision, recall, and F1 score are used. The study's goal is to develop a dependable and efficient tool for arborists, foresters, and environmentalists to quickly identify and treat tree diseases. The findings of this paper provide advance precision agriculture and environmental monitoring by providing a scalable and automated solution for early tree disease detection. Furthermore, the paper investigates potential applications in real-world scenarios, fostering sustainable practices for global ecosystem preservation. And also extend the framework to provide the fertilizer details based on predicted disease.

INDEX TERMS: Agriculture, Tree leaf-based disease prediction, Model selection, Deep learning, Fertilizer recommendation

1. INTRODUCTION

In agriculture and horticulture, the health and vitality of trees and plants is critical to crop yield, environmental balance, and food security. One of the most difficult challenges for growers and arborists is the early detection and management of tree and plant diseases. To address this issue, an innovative technology known as "Tree Leaves-Based Disease Prediction" was developed. This cutting-edge application uses machine learning and image analysis to examine the intricate details of tree leaves, potentially allowing for the rapid and accurate identification of diseases. This technology holds the promise of providing early warnings, precise diagnostics, and actionable recommendations for disease management by examining the visual cues presented by the leaves, such as discoloration, deformities, or lesions. This approach is a beacon of hope for farmers, foresters, and environmental stewards seeking to protect the health of our forests and crops, ultimately contributing to a more sustainable and resilient future for agriculture and ecosystems in this era of agricultural innovation. This article delves into the methodology, benefits, and potential of disease prediction based on tree leaves, shedding light on a transformative solution poised to redefine how protect our arboreal and agricultural landscapes. The basic flow chart of tree leaf-based disease prediction using convolutional neural network is shown in fig 1.

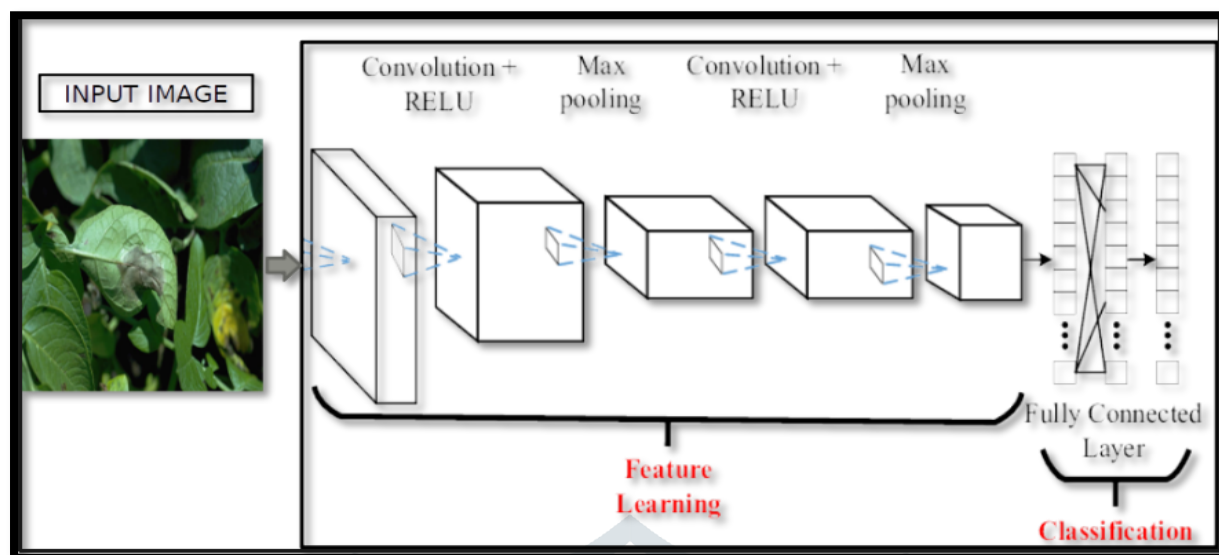


Fig 1: Tree leaf-based disease prediction

2. RELATED WORK

Jiangchuan Fan, et.al,...[1] Detection technology research has gotten a lot of attention. Plant phenomics research hopes to conduct high-throughput quantitative studies on specific genotypes of massive phenotypic parameters based on genome-wide sequencing. Furthermore, these phenotypic parameters include not only morphological data but also a large number of physiological and biochemical data, as well as deeper mechanistic data, allowing scientists to identify and predict heritable traits through controlled studies of phenotypes and genotypes. At the moment, the vast majority of the world's food is still grown in the field. As a result, research on plant phenotypic detection techniques and methods in the field environment is the focal point and hotspot for future breeding and plant yield research. Furthermore, improve the structural degree of big data in plant phenomics, strengthen the big data standard of plant phenomics, research on plant phenotype-environmental perception mechanism, strengthen the construction of large data of plant phenomics, develop visual data mining technology, and combine 5g technology to realize the wonderful presentation of the realtime visual mining results of the plant phenomics big data cloud. Accelerate the integration of multi-reformation big data in different ecological regions, reveal the laws of plant genetics and variation, and comprehensively improve agriculture's competitiveness and ability to innovate independently.

Shrikrishna Kolhar, et.al,...[2] examined various imaging techniques used in plant phenotyping and evaluated their applications, benefits, and limitations. Digital color imaging is useful for determining structural plant traits, whereas CFIM, thermal imaging, and hyperspectral imaging are useful for determining physiological plant traits. Plant roots are phenotyped using MRI and X-ray CT imaging. Imaging techniques outside the visible band are also used to quantify disease symptoms that visible RGB imaging cannot. A holistic and component phenotype is determined using 3-D imaging. Plant growth patterns, germination time, leaf emergence, and reproductive organ emergence can all be measured using time series images. This review compares color-based segmentation, threshold-based segmentation, and learning-based segmentation methods and applications. Despite being widely used for plant phenotyping, color index-based methods suffer from shadow and high light variations. Threshold-based segmentation methods work well in changing light conditions but require more computation time because the threshold must be adjusted in several steps. Learning-based approaches have high accuracy but are complex because accurate segmentation requires several training steps. This paper also examines recent machine vision methods for plant phenotyping, which range from simple image processing algorithms to complex deep neural networks.

Dr. V. Anantha Natarajan, et.al,...[3] examined the effectiveness of deep learning architectures for pest and disease detection in cultivated land. Collected a comprehensive dataset of 1090 real-time tomato leaf images infected by early blight, leaf curl, septoria leafspot, and bacterial spot, images were taken by camera devices with 12MP, 48MP resolution, different illumination conditions (lighting), all stages of tomato disease (early, medium, and final) and fed into the proposed system. A deep detector-based automated disease detection system is proposed: Farmers can detect early blight, leaf curl, septoria leafspot, and bacterial spot diseases in tomato plants using faster R-CNN with ResNet. In addition, trained and tested the proposed system end-to-end with our tomato disease dataset specified in this work, which contains 1090 comprehensive images of tomato disease's early, medium, and final stages.

Jingyao Zhang, et.al,...[4] created a novel method for identifying cucumber leaf diseases using a small sample size and a deep convolutional neural network. The lesion images were obtained using a two-stage segmentation method with strong discrimination ability to extract disease spots from cucumber leaves with minimal human intervention. The high-quality training samples were generated using the rotation, translation, and AR-GAN operations. With the addition of convolutional layers, the proposed DICNN demonstrated powerful feature extraction and fast convergence. The experimental results demonstrated that the proposed method could effectively identify cucumber leaf diseases. The study investigated a feasible method for field agricultural IoTs to timely implement the identification of plant leaf diseases, which is of great practical importance. The future work will concentrate on identifying more types of cucumber leaf diseases as well as expanding our approaches to disease recognition in more plants.

Shuiqin Zhou, et.al,...[5] created an automated procedure to aid plant salinity tolerance studies via image stitching, automatic segmentation, and trait extraction. According to the findings of this study, the green channel in RGB color space and the value channel in HSV color space were effective in removing image background while effectively preserving salt damages. Furthermore, the RGB-

based vegetation index ExG could automatically segment single plants of soybean from images. The developed procedure was able to identify the distinct image features associated with symptoms of salt damage in soybean leaves. The findings demonstrated that the phenotypic traits of five soybean genotypes exposed to salt stress can effectively differentiate their salt tolerance. This procedure allows for the automatic analysis of stitched images taken from the top view. The procedure can be adapted to analyze other plant species recorded by a high-throughput phenotyping platform after size and color calibration. This method allowed us to generate biologically relevant outputs at both the image and pot levels on the same day, as well as analyze the growth procedure and salinity tolerance variation.

Zhenbo Li et.al.,...[6] provide a comprehensive review of plant phenotyping solutions based on computer vision, summarize the benefits and limitations of imaging technologies and analysis methods from two perspectives: plant organ and whole plant, and then provide some typical algorithm principles and processing frameworks. discovered that image-based plant phenotyping methods have a lot of potential for automatically measuring and quantifying phenotypes. Deep learning, in particular, greatly simplifies the process of extracting phenotypic features and improves plant phenotyping applications. Plant phenotyping is a complex and difficult task that necessitates not only the use of hardware systems (imaging equipment and phenotyping platforms) to collect raw data, but also the creation of a multi-domain, multi-level, multi-scale plant phenotypic database. In addition, to extract information from massive omics data, a trait identification technology system and bioinformatics technology must be developed. This review focuses solely on extracting phenotypes from images. Source phenotyping and genetic analysis remain difficult tasks. must collaborate to solve these issues and move the process forward. Furthermore, will collaborate with other disciplines to integrate expertise in various fields and provide technically sound solutions with biological or agronomic significance.

Vemishetti Sravan, et.al.,...[7] The plant village database was used to collect the data for this study. The dataset includes three crops (potato, pepper, and tomato) representing 15 different disease classes as well as healthy classes. The ResNet50 model is used in this study to solve the crop disease classification problem. The Resnet50 model's final three layers are replaced with new layers. The entire workflow was completed by fine-tuning the ResNet50 model with hyper parameters such as learning rate, mini-batch size, and epoch count. The fine tuning ResNet50 method has a classification accuracy of 99.26%. These diseases spread primarily through three plant components before spreading to all parts of the plant, including plant tissues, leaves, stems, roots, seeds, and leafs, among others. As a result, early detection and classification of crop diseases is critical to preventing the spread of diseases that affect the entire crop. Continuous monitoring necessitates more time and money for disease detection. These techniques can solve the problem by implementing automatic classification, saving time and money.

Seyed Vahid Mirnezami, et.al.,...[8] demonstrated that fully automated image-processing approaches for trichome counting do not outperform methods that incorporate some user input. Given the difficulty of automated trichome counting, advocate for the use of machine learning algorithms (particularly object-detection and crowd-sourcing algorithms) as promising techniques for future work, as these algorithms can outperform image processing methods in cluttered images. Images of sufficient quality and with varying trichome density, on the other hand, will be required. created a simplified image processing method for automated and semi-automated trichome counting. demonstrate this process using 30 leaves from ten different genotypes of soybean (*Glycine max*) with varying trichome abundance. To facilitate trichome counting, investigated various heuristic image-processing methods such as thresholding and graph-based algorithms. The semiautomated manually annotated trichome intersection curve method outperformed the two automated and two semi-automated methods for trichome counting tested, with an accuracy of close to 90% compared to the manually counted data.

Cody S. Bekkering,et.al.,...[9] developed An integrated phenotyping approach that accounts for many aspects of plant growth can unravel the effects of genetics, environmental factors, and management practices on the physiology of wheat and ultimately translate this to enhancing its performance and productivity in the field. Rapid, comprehensive evaluation of wheat at varying stages in the breeding pipeline—from wild species to landraces to elite breeding lines—will be instrumental in increasing wheat yields to accommodate the increase in the demand for wheat that comes with a rapidly growing world population. Moreover, the increasing accessibility of these tools, particularly for shoot and seed phenotyping, has resulted in lower learning curves and imaging requirements so that a wider range of breeders can rise to meet this global need without being required to reinvent their breeding pipelines. Research trajectories for shoot, root, and seed phenotyping in wheat, and in crops in general, are discussed in the above sections. Looking forward, several developments will continue to improve the throughput, accuracy, and accessibility of the phenotyping outlined here. From the biological sciences, advances in next-generation sequencing, genetic, and functional genomic analyses collectively improve our ability to leverage phenotypic observations to explore the idiosyncrasies of the wheat genome and to develop new cultivars

Muhammad Hammad Saleem, et.al.,...[10] analyzed a comprehensive comparative analysis has been performed between various state-of-the-art deep learning architectures divided into three categories namely well-known, modified, and cascaded versions. Moreover, the performance of the best-obtained models was further improved by using various deep learning optimization algorithms. It was found that the Xception, Improved GoogLeNet and cascaded version of AlexNet with GoogLeNet models obtained the highest validation accuracy and F1-score in their respective category. When these three DL models were trained by using various deep learning optimizers, the Xception model trained by the Adam optimizer achieved the highest F1-score of 0.9978 which suggests that this combination of the CNN model and the optimization algorithm is the most suitable way to classify the plant disease

3. BACKGROUND OF THE WORK

In existing approach computer vision techniques introduced that are essential for the diagnosis of leaf diseases without human intervention. The automatic detection and classification of leaf diseases are necessary as it not only save the leaves and plants from being infected but is also helpful in order to increase agricultural yields. This existing method contains five stages such as pre-processing, segmentation, feature extraction and reduction, fusion, and classification. Initially, noise in the images was removed and opted watershed algorithm for infected regions detection. The computer vision techniques based on some important steps such as pre-processing of raw images, disease segmentation using image processing techniques such as K-Means, saliency methods, and many more, features extraction (i.e. color, shape, and texture), reduction of redundant features, and finally classification using machine

learning classifiers. K-mean clustering used to segment the leaf parts based on manual annotation. It divides tainted images into several clusters. A solitary cluster is a group of image elements comparable together but separates from the values of other clusters. Initially, input images by the K-means methodology are segmented, and then these segmented pictures are accepted via a NN classifier in the second phase. The techniques that followed these steps, improve the accuracy when the smaller dataset is available. In the next step, shape, color and texture features are extracted from the infected regions and serially fused. At the end multi class SVM classifier is employed for final classification. The SVM is a monitored knowledge-based algorithm used for sorting, regression, clustering, and detection. SVM is essentially a binary linear classifier that separates two groups with the maximum hyperplane margin. A hyperplane with the longest distance to the closest data points, thus called a maximum margin hyperplane, provides a good separation; the more significant the margin lowers the generalization error. The feature set may occur in a finite-dimensional space, but it is not linearly separable in that space.

4. TRANSFER LEARNING BASED DISEASE PREDICTION

In this paper we proposed a system designed for predicting tree diseases based on images of tree leaves, employing the VGG16 convolutional neural network (CNN) architecture. The primary objectives include the development of a diverse dataset of tree leaf images, preprocessing techniques such as resizing and augmentation to enhance model performance, and the customization of the VGG16 model for disease prediction. In this module we can resize the image and remove the noise in image using Median filtering algorithm. The goal of the filter is to filter out noise that has corrupted image. It is based on a statistical approach. Typical filters are designed for a desired frequency response. Filtering is a nonlinear operation often used in image processing to reduce "salt and pepper" noise. A median filter is more effective than convolution when the goal is to simultaneously reduce noise and preserve edges. In image preprocessing using the median filtering algorithm, the initial step involves importing essential libraries, such as OpenCV and NumPy, to facilitate image manipulation. The target image is then loaded, and optionally, converted to grayscale to simplify subsequent processing steps.

INPUT: Image X of size M X N, filter size n

OUTPUT: Image Y of the same size as X

Initialize histogram H

for i=1 to M do

for j= 1 to N do

for k= -n/2 to n/2 do

Remove $X_{i+k, j-n/2-1}$ from H

Add $X_{i+k, j+n/2}$ to H

end for

$Y_{ij} \leftarrow \text{median}(H)$

end for

end for

The methodology involves utilizing the pre-trained VGG16 model for feature extraction and adapting its fully connected layers for the specific task of tree disease classification. Building upon the proposed system for tree disease prediction using the VGG16 architecture, the study emphasizes the significance of early detection in mitigating the impact of diseases on tree populations and ecosystems. The system's capacity to analyze diverse leaf images from various tree species and identify potential diseases contributes to a comprehensive approach to environmental monitoring. The system undergoes thorough training and validation processes on the prepared dataset, and its performance is evaluated using key metrics like accuracy, precision, recall, and F1 score. The anticipated outcomes include a well-trained model capable of accurately classifying tree leaves as either healthy or affected by specific diseases. The significance of the proposed system lies in its potential to enable early detection of tree diseases, thereby facilitating timely intervention and contributing to sustainable forestry and environmental conservation. Ultimately, the study aims to provide a valuable tool for professionals in arboriculture and forestry, leveraging advanced technology to address the challenges associated with maintaining the health of global ecosystems. Fig 2 shows the proposed work for tree leaf-based disease prediction using VGG16 model.

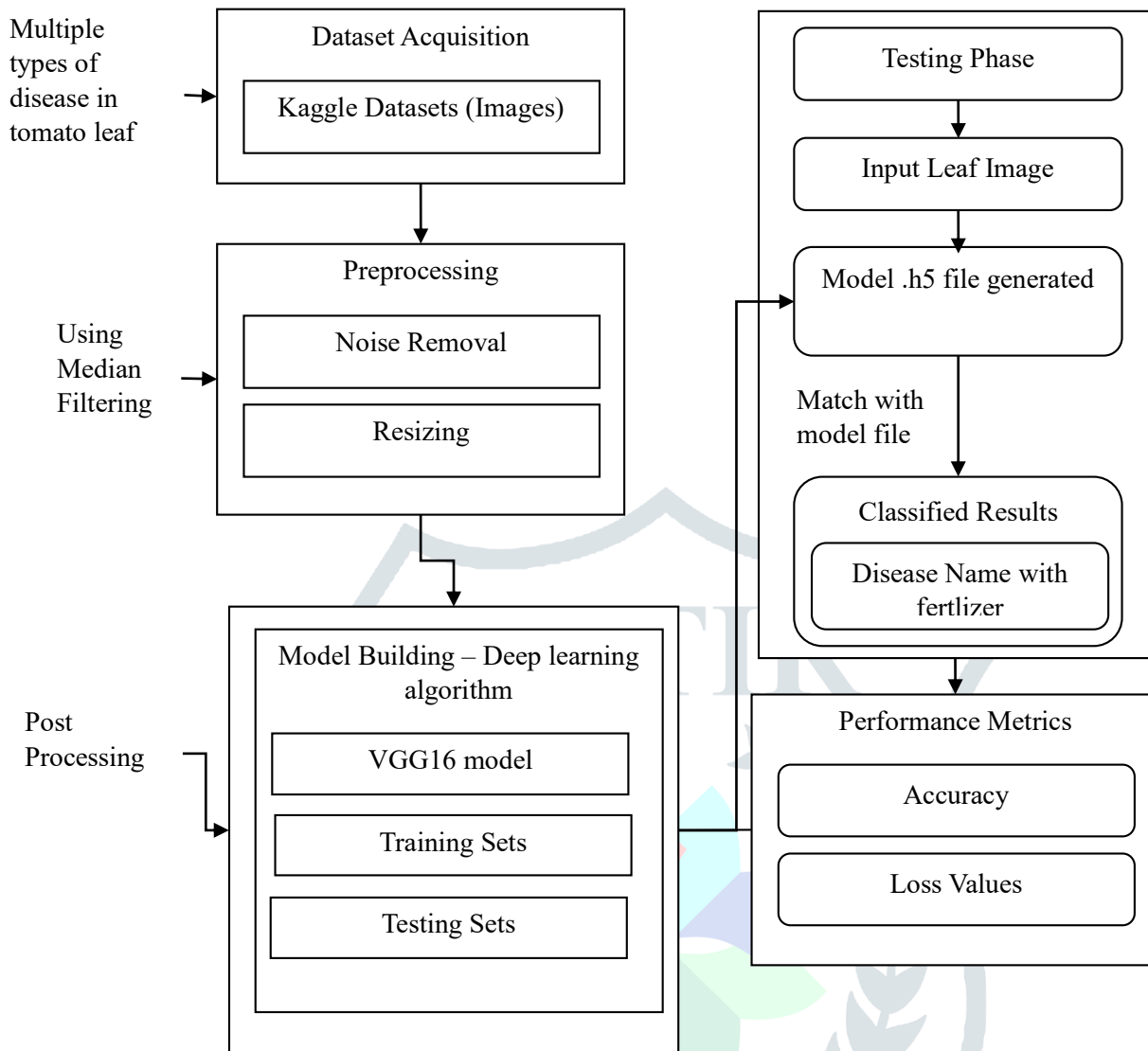


Fig 2: Proposed work

The VGG16 model is a convolutional neural network (CNN) architecture that has gained popularity in computer vision tasks, including image classification. It was developed by the Visual Geometry Group (VGG) at the University of Oxford and was a part of the ImageNet Large Scale Visual Recognition Challenge in 2014. The "16" in its name refers to the number of weight layers it has.

Key characteristics and components of the VGG16 model include:

- **Convolutional Layers:** VGG16 consists of 13 convolutional layers, which are used to extract features from input images. These layers are followed by max-pooling layers that downsample the feature maps to capture hierarchical information.
- **Fully Connected Layers:** After the convolutional layers, VGG16 has three fully connected layers, followed by an output layer for classification. These fully connected layers are responsible for making the final decisions about the input image's class.
- **Receptive Fields:** VGG16 uses relatively small 3x3 convolutional filters in its layers. This architecture results in very small receptive fields for each neuron, allowing it to capture fine-grained details in the images.
- **Stacking Convolutional Layers:** The VGG16 architecture is characterized by the repeated stacking of convolutional and pooling layers, which allows it to learn features at different scales.
- **ImageNet Pretraining:** VGG16 was pretrained on the ImageNet dataset, which contains millions of labeled images across thousands of categories. This pretraining provides the model with a broad understanding of various visual concepts.
- **Transfer Learning:** VGG16's pretraining makes it an excellent choice for transfer learning. You can fine-tune the model on a specific task, like brain tumor detection, by replacing the last few layers while keeping the pretrained layers' weights intact.
- **Deep Network:** VGG16 is relatively deep compared to its predecessors and is capable of learning intricate features and patterns from images. However, this depth also results in increased computational complexity.

The VGG16 model has been widely adopted for various image-related tasks, including object recognition, image segmentation, and medical image analysis, such as brain tumor detection. Its architecture, though somewhat resource-intensive due to its depth, provides a strong foundation for building accurate and powerful convolutional neural networks. It remains a valuable tool in the field of deep learning and computer vision. Based on the predicted disease, provide the fertilizer information to users.

5. EXPERIMENTAL RESULTS

In simulation, from key features datasets, the sign facts are acquired which are employed to measure the usefulness of the suggested method. Using F-measure, Recall and Precision the performance of the system is being evaluated.

$$\text{Precision} = \frac{TP}{TP+FP}$$
$$\text{Recall} = \frac{TP}{TP+FN}$$
$$\text{F measure} = 2 * \frac{\text{Precision} * \text{Recall}}{\text{Precision} + \text{Recall}}$$

Accuracy (ACC) is found as the fraction of total number of perfect predictions to the total number of test data. It can also be represented as 1 – ERR. The finest possible accuracy is 1.0, whereas the very worst is 0.0.

$$ACC = \frac{TP+TN}{TP+TN+FN+FP} \times 100$$

Fig 3 shows the training and validation accuracy for proposed model

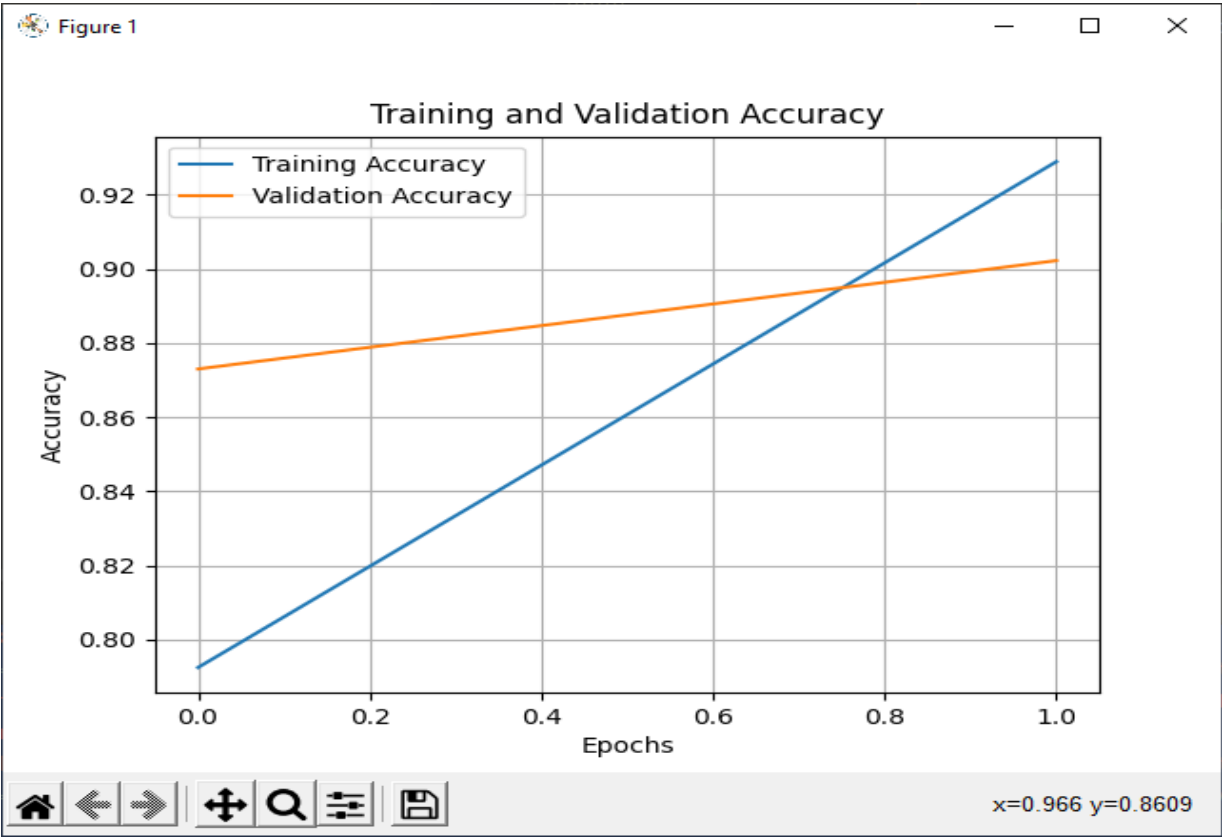


Fig 3: Training accuracy and validation accuracy

A confusion matrix represents the prediction summary in matrix form. It shows how many predictions are correct and incorrect per class. It helps in understanding the classes that are being confused by model as other class.

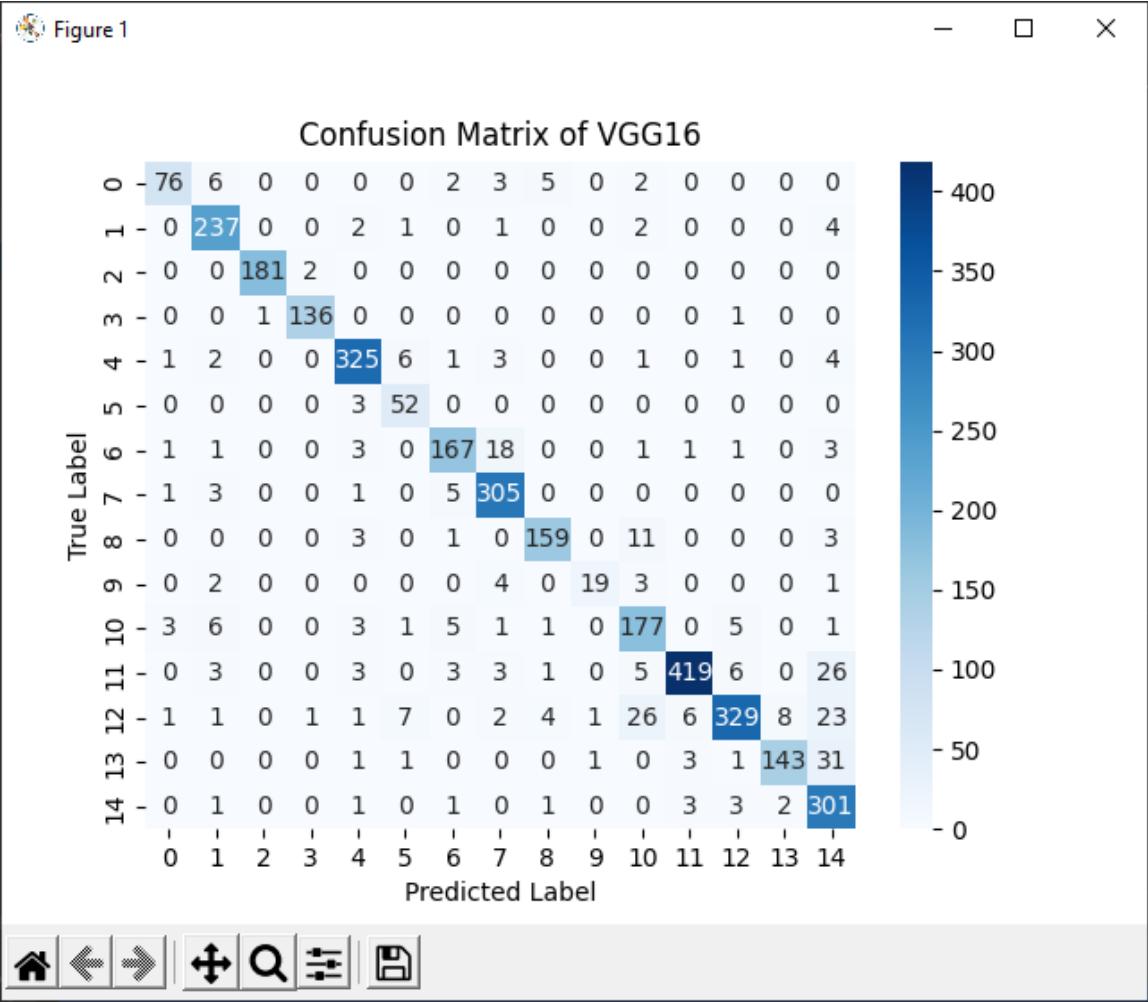


Fig 4: Confusion matrix

6. CONCLUSION

Finally, the proposed system for tree leaf-based disease prediction with fertilizer recommendation using the VGG16 convolutional neural network represents a significant advance in precision agriculture and environmental monitoring. The incorporation of deep learning techniques, specifically the VGG16 architecture, provides a powerful tool for early detection of tree diseases. The system demonstrates the ability to accurately classify leaves as healthy or diseased by leveraging a diverse dataset of tree leaf images and applying meticulous preprocessing, including resizing and augmentation. The VGG16 model's adaptability for feature extraction, combined with the customization of its top layers for disease prediction, improves the system's ability to generalize across different tree species and disease types. And also provide the remedies about predicted disease with improved accuracy rate.

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