International Research Journal on Advanced Engineering Hub (IRJAEH)
e ISSN: 2584-2137
Vol. 03 Issue: 10 October 2025
Page No: 3869-3876
https://irjaeh.com
https://doi.org/10.47392/IRJAEH.2025.0562

Plant Disease Detection using a Deep Learning approach: a Custom CNN

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Abstract

With the global population expected to increase substantially, it raises a concern about feeding these populations, and it becomes essential to protect crops from diseases for food security. According to several studies, plant diseases and pests cause about 20–40% of the world's crop yield to be lost each year. Current plant disease detection methods include visual inspections, microscopy, culture-based procedures, molecular techniques, etc. These techniques are time-consuming, require specialized equipment and expertise, and are prone to human error. To address this problem, this study employs a customized Convolution Neural Network (CNN), which provides a more effective and scalable substitute for manual inspection and lab-based diagnostic techniques. The model uses CNN's sequential architecture along with softmax and ReLU activation functions. While ReLU introduces non-linearity in the model, which is essential for complex feature extraction, softmax helps in the normalization of vectors and multiclass classification. It has 3 blocks, each consisting of a convolution layer, a pooling layer, and a dropout layer. The model operates on a publicly available hybrid dataset taken from PlantVillage and DoctorP datasets, with a combined total of 5,721 images organized into sub-directories representing different diseases belonging to major groups like fungi, bacteria, virus, non-infectious conditions, nematodes and pests/insects. Images of each category were fed to the model, to identify diseases which are complex to be detected through images. Our model achieved an overall accuracy of 96.54%, illustrating the potential of CNN-based approaches for automated plant disease detection.

Keywords: *Agriculture; CNN; Architecture; SoftMax; ReLU; PlantVillage; DoctorP.*

1. Introduction

Increasing population growth of the world, which is estimated to reach 8.5 billion by 2030 [1], increases the concern of food and shelter for these people. Food and shelter for these populations have become a vital concern globally. According to the Food and Agriculture Organization of United States (FAO), Around 2.1 billion tons of fruits and vegetables were produced in 2023[2] and around 70-80% of plants produced annually are consumed all over the world for food. This raises concerns for global food security and sustainable agricultural practices. According to the Food and Agriculture Organization of United States (FAO), around 20-40% of global crop production is lost due to pests and diseases [3]. Efficient diagnosis of plant disease is vital to sustainable agrarian practices, and thus, global food security. Plant diseases pose enormous risk to crop productivity, causing annual loss of billions of dollars and starvation directly. Timely and precise detection helps facilitate focused, sustainable control as well as saving vegetation and reducing unintended ecological consequences. This problem introduces us to recognize plant diseases and study the cures to it. Plant disease detection is an essential method for the preservation of food availability and stability. Without efficient detection and management, diseases can spread rapidly and produce extensive crop failure and severe food shortages. There are several methods that are used traditionally to detect plant diseases, such as Polymerase Chain Reaction, Fluorescence in-situ Hybridization, Enzyme-Linked Immunosorbent Assay, Immunofluorescence, Flow

Cytometry, Thermography, Fluorescence Imaging, Hyperspectral Techniques, and Gas Chromatography [4]. These methods need special equipment like microscopes, various acids and solutions, sample of the diseased plant, and several other scientific tools. To use this lab equipment, it also requires specific knowledge and expertise. While these methods can provide accurate results, they are also costly, time intensive and esoteric, understood by only few specialists.It becomes crucial to come up with a solution for this problem that's pocket friendly, applicable to large-scale production, time saving with a provision of real-time detection for early or timely detection of plant diseases to prevent massive crop losses. To mitigate this challenge, our study implements plant disease detection using Convolutional Neural Networks (CNN) to process images and identify plant diseases to understand the root cause of the disease and examine its cure.This paper also discusses other pre-trained models utilized for plant disease detection along with their strategy for better accuracy and other parameters. Detection of diseases in plants have been carried out traditionally since decades, but this also unveils different problems like inaccuracy of human calculations, time consumption, requirement of expertise and early detection challenges. Our research resolves all these problems by digitizing the detection allowing real-time, consistent, cost-effective and accurate results for disease detection.

The foundation of this research is to contribute to agricultural technologies for automation in detection of plant diseases thereby influencing the power of AI in the field of agriculture to produce time saving, automated, intelligent and innovative ideas that change the future of farming system.

2. Literature Review

Existing studies provide similar approach for plant disease detection. Pre-trained models like EfficientNet, DenseNet, ResNet, etc gaining good accuracy on plant diseases [5]. These approaches effectively detect plant diseases but can be complex and may have higher computational costs. An in-depth analysis of current scientific approaches to detect plant diseases was done by author [4] discussing various methods like Polymerase Chain Reaction, Fluorescence in-situ Hybridization, Enzyme-Linked Immunosorbent Assay, Immunofluorescence, Flow Cytometry, Thermography, Fluorescence Imaging, Hyperspectral Techniques, and Gas Chromatography. These methods require pipettes, buffers, antibodies (or enzymes), tubes, fluorescent dyes and microscopes. Extending beyond tangible considerations to include scientific knowledge and expertise in these procedures. An advanced version of detecting plant diseases was proposed by author [6] using Machine Learning. He utilised PSO-SVM (Partial Swarm-Optimisation, Support Vector Machine) to compare it with BPNN (Backpropagation Neural Network) and Random Forest algorithms for classification. This model includes several steps for classification like image acquisition, image denoising through the mean function, image enhancement using the contrast limited adaptive histogram equalization (CLAHE) method, image segmentation (Fuzzy C means), feature extraction using Haar Wavelet Transformation (HWT) and disease classification using PSO SVM / BPNN / Random Forest. It was concluded that PSO SVM gives the best accuracy among all the three approaches for classification. Different technologies like Neural network architecture search technology, DropConnect, Focal loss function, Adam optimizer are used in research studies to enhance the model's performance to detect plant diseases using Convolutional Neural Network [5]. This study discusses how minor optimization in depth, width, and resolution can result into problems such as gradient loss, gradient explosion, a large amount of calculation, and so on. He used the Focal loss function to replace the traditional CrossEntropy (CE) loss function, which makes classification easy by reducing weights of easy classification samples and increasing the weight of hard classification samples so that the model is more focused on hard classification samples in the training phase. He compares different models and found that FL-EfficientNet has the highest accuracy with the use of focal loss. He concludes that ResNet50 can't guarantee the recognition accuracy well in a short period of training time, DenseNet169 cannot guarantee the training time but ensures the recognition accuracy and EfficientNet has the highest recognition accuracy and has the shortest training time. FL-Efficient is better than comparison network in terms of convergence speed and recognition accuracy, with an average accuracy of 99.72%. Author [7] used Plant Village dataset that is publicly available with final 2,085 images of subclasses like fully healthy, early stage healthy, middle stage healthy and end stage disease images. Preprocessing techniques like resizing, rescaling, and normalization are used. He explains how ReLU is much faster than other existing activation functions. He achieves a validation accuracy of 81.4% with 10 convolution layers. The accuracy achieved after parameter tuning is better than the existing model which is 84.0% to 93.5%. The best relevant outcomes in the VGG16 model having accuracy of 93.5%. This result concludes that transfer learning can give better result even if there are insufficient data. Author [8] MobileNetV2 architecture for better efficiency and better extraction of features of the images. He also integrated Squeeze and-Excitation (SE) module and incorporated residual skip connections to develop its performance and collectively refine feature representation. He evaluated the model with online random images, to demonstrate its significant adaptability and effectiveness in overcoming key challenges, such as achieving high accuracy and meeting the practical demands of agricultural applications. These approaches resulted in model's effectiveness, achieving an accuracy of 98% and F1 score of 98.2%. Since, he used random images from the internet, he used various techniques for dataset preprocessing which include resizing, data augmentation, and normalization techniques. He utilized various data augmentation techniques like random changes in object orientation, adjustments in aspect ratio, and variations in luminance to tackle issues related to real-world applications. To enhance the efficiency of the MobileNetV2 model, he also made use of depth-separable convolution which can further reduce parameters during group convolutions that feature diversity. A study focused significantly on potatoes, apples, and corn for early detection of leaf diseases utilized Enhanced- Convolutional Neural Networks(E-CNN) [9]. For ECNN, this model used several loops of convolution, pooling, and dropout layers to extract detailed features of images. Further it was concluded with flatten, dense, dropout and lastly 10 units of dense with ReLU Activation. This model reached an accuracy of 98.17% with a dataset of multiple plants. Author concludes that they were able to achieve this accuracy with the help of activation functions (Softmax, softplus, ReLU and sigmoid). For transfer learning, comparing several models of CNN like VGGNet, ResNet50, Inception-v3 includes slight changes in the size of the filters used. Inception-V3 model is an improved model for better efficiency, and it can be further improved with a smaller number of parameters. ResNet is made by using one over other remaining basic building blocks. These basic building blocks consist of number of convolution layers with loose connection or no connection in some of the blocks. Another similar approach includes few-shot learning. It enables image classification even on samples fewer than 10 are available. These methods rely on identifying similarities between images. Author [10] eight models with strong reported accuracies and robust evaluation records. They were ConvNeXt_Small, EfficientNet_B3, Inception_V3, MNASNet1_3, MobileNetV2, MobileNet_V3_Large, RegNet_X_1_6GF, ResNet101, ResNeXt50_32X4D. Experiments were carried out in two stages, in the initial stage basic transfer learning was employed to evaluate accuracy and training time costs [10]. In the second stage, similarity learning was utilized using different loss functions based on Siamese and angular distances were experiment with. These loss functions were Contrastive, Triplet, Quadruplet, SphereFace (A-softmax), CosFace, ArcFace. Different metrics like Mean Epoch Processing Time (MEPT), accuracy, weighted averages of precision, recall and F1-score were utilised for model evaluation. Based on metrics, ArcFace loss may not be the optimal choice for plant disease detection while, the effect of normalization remains ambiguous Shown in Table 1 Summary Table of Related Works.

Table 1 Summary Table of Related Works

Author(s)	Year	Model/Method Used	Dataset Used	Accuracy / Result
Yi Fang & Ramaraja P. Ramasamy	2015	PCR, FISH, ELISA, Biosensors (QD-FRET)	Various lab samples	**100% sensitivity** (QD-FRET); PCR (CFU/mL)
Sharaf Alzoubi, Malik Jawarneh, et al.	2023	**PSO-SVM** + Image Processing (CLAHE, Fuzzy C Means)	Custom Fig Leaf Dataset	**Exceptional performance** (Fig leaf disease detection)
Xuewei Sun, Guohou Li, et al.	2022	**FL-EfficientNet** (Focal Loss, NAS)	New Plant Diseases Dataset (NPDD)	**99.72% accuracy** (10 diseases/5 crops)
A.V. Panchal, S.C. Patel, et al.	2021	Convolutional Neural Network (CNN)	PlantVillage (images)	**90.4% accuracy** (38 diseases/14 crops)
Asadulla Y. Ashurov, Mehdhar S. A. M. Al-Gaashani, et al.	2025	**Modified Depthwise CNN** (SE + Residual Skip)	Comprehensive dataset	**98% accuracy** / **98.2% F1 score**
Mudassir Iftikhar, Irfan Ali Kandhro, et al.	2024	Enhanced CNN (E-CNN) & fine-tuned models	PlantVillage + Custom sets	**98.17% accuracy** (Fungal classes)
Emmanuel Moupojou, Appolinaire Tagne, et al.	2023	Deep Learning Models (Dataset validation)	**FieldPlant Dataset** (field images)	Dataset creation: **27 disease classes** (field images)

3. Dataset

Table 2 Disease Categories and their Corresponding Disease Names

Disease Category	Disease Names
Fungi	Alternaria leaf blight, Anthracnose, Ascochyta blight, Black rot, Botrytis, cinerea, Cherry leaf spot, Coccomyces of pome Fruits, Corn downy, Mildew, Downy Mildew, Dry rot, Esca, Eyespot, Grey Mold, Late blight, Monilia, Northern leaf blight, Polypore, Powdery Mildew, Rust, Scab, Sooty Mold, Verticillium wilt.
Pests-Insects	Ants, Aphid, Caterpillars, Colorado beetle, Cyclamen mite, Gryllotalpa, Lear miners, Pear blister Mite, Scale, Slugs, Spider Mite, Thrips, Whitefly, Wireworm.
Bacteria	Bacterial spot, Black chaff, Canker, Leaf spots.
Nematodes	Gall
Virus	Mosaic virus
Non-Infectious	Aphid effects, Anthocyanosis, Black spots, Blossom end roots, Burn, Colorado beetle effects, Edema, Frost cracks, Gryllotalpa effects, Healthy, Leaf deformation, Leaves Scorch, Lichen, Loss of foliage turgor, Marginal leaf necrosis, Mechanical damage, Nutrient deficiency, Pest damage, Slugs Caterpillar effects, Spot hole, Shute, Tubercular necrosis, Wilting, Wireworm effects, Yellow Leaves.

Pathogens are the organisms that cause diseases in plants. Four main types of pathogens responsible for diseases are Bacteria, Fungi, Viruses and Nematodes. In this study, dataset comprising of multiple classes including different diseases and healthy plant images are used to extract each feature of the image with all the common diseases known such as powdery mildew, rusts, scabs, blights, leaf spots, black rots, etc. Our dataset is hybrid dataset taken from publicly available datasets. Initially it was taken from DoctorP Dataset with 4001 images [11] but later incorporating more images from another dataset i.e. PlantVillage dataset [12] to increase the number of images so that it can provide efficiency on disease identification. Dataset has different directories, each belonging to a specific disease class. 70 diseases which were further classified majorly into Fungi, Bacteria, viruses, pests/insects, nematodes and non-infectious diseases. These classes consist of 70 diseases namely Shown in Table 2. It consists of total 5,721 images with 128 x 128 pixels. In this study, dataset is divided into 6 major categories mentioned above to observe each category in detail. Training and validation dataset with the ratio of 8:2 affirming a balanced evaluation of model's performance.

4. Model Architecture

Deep learning uses neural networks for extraction of complex patterns and to learn them using multiple hidden layers. Neural networks work with interconnected neurons to transmit information just as our brain works. There are different approaches of neural network like Convolutional neural network (CNN), Recurrent neural network (RNN), Transformers, Artificial neural network (ANN), etc. Opting for CNN for disease detection was necessary to extract all the features of the images and guarantee better identification and classification of the image. The network was implemented using Sequential architecture which allowed the model to be straightforward and stack each layer one by one. Sequential architecture works as the output of the current layer becomes the input for another layer. This is the simplest and most common type of model architecture. The input layer consists of images with a dimension of 128 x 128 pixel with three colour channels (RGB). This step ensured numeric stability and reduced training time during optimisation. The model was embedded with 3 Convolution-Pooling blocks to extract discriminative features of the images. In the first block, 32 filters with 3 x 3 kernel size and a stride of 1 were used to preserve spatial dimensions. ReLU function was utilized as activation function to introduce non- linearity. The role of ReLU is to learn complex features of the image. After applying the convolution to the input layer with filters, we get a feature map which can have both positive and negative values. ReLU is then applied to this feature map. If the values are negative, they are switched with 0, and the positive values remains the same.

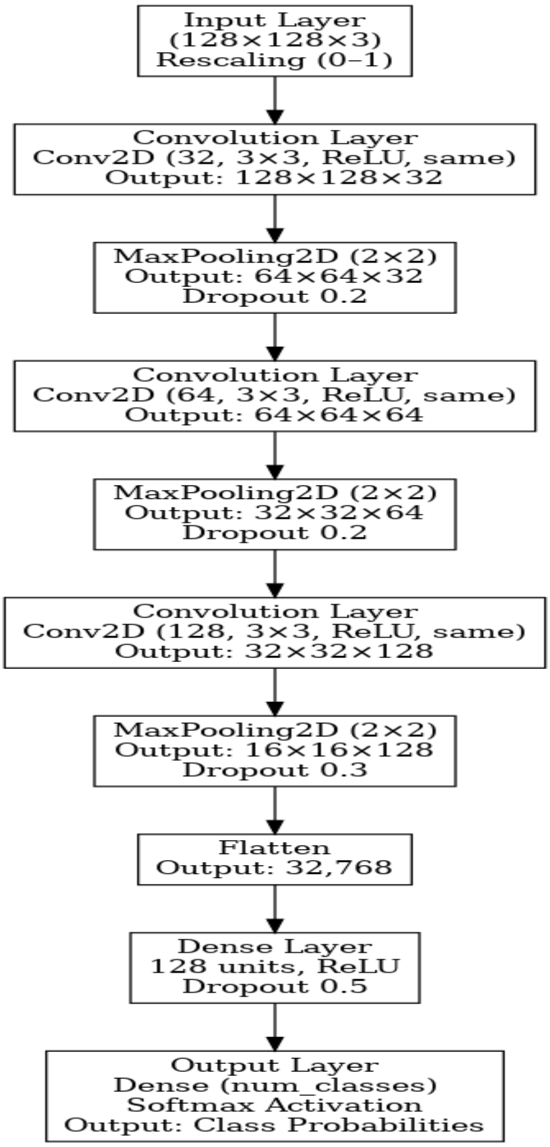

Figure 1 **Architecture of the Proposed Custom CNN Model**

International Research Journal on Advanced Engineering Hub (IRJAEH)
e ISSN: 2584-2137
Vol. 02 Issue: 10 October 2025
Page No: 3862-3868
https://irjaeh.com
https://doi.org/10.47392/IRJAEH.2024.0561

For example, Before ReLU: [-9, -5, 0, 8, 3] → after ReLU: [0, 0, 0, 8, 3] MaxPooling2D layer follows after ReLU with pool size of 2 x 2 to reduce the spatial features while preserving the foremost features of the image. And a Dropout layer of size 0.2 to avoid any possible overfitting issue. In the second block, a convolution layer of 64 filters with 3 x 3 kernel and ReLU activation was applied, followed by a MaxPooling2D layer (2 x 2) and a Dropout layer of 0.2. In the third block, a deeper convolution layer with 128 filters of kernel size 3 x 3 and ReLU activation followed by MaxPooling2D (2 x 2) was implemented. This gradual increase in the filters over the convolution layers helped in extracting the features in different levels. The final architecture of the model looks like Shown in Figure 1. Initially low-level features like edges and texture were obtained while, deeper layers acquired intricate design of the images like shape, patterns and potential disease patterns. Further, a layer of Dropout with the size of 0.3. From the final block of convolution layer, the output feature maps are then flattened into 1D vectors in the flatten layer. This layer helps the features to be passed into the fully connected layers, linking convolutional feature extraction and final decision making. Further two dense layers were used, one to allow studying the complex relationships between the patterns by using 128 units and ReLU activation along with Dropout layer with a size of 0.5 and the final fully connected dense layer with units equal to number of classes and softmax activation was used, generating class probability distribution. Softmax activation is used for multiclass classification in the final layer of the CNN model. It processes with the vectors produced in the previous layer. The final output produces probability all over classes Shown in Figure 2 & 3.

For example:

For input vectors = [0, 5, 1]
↓
SoftMax: [0.006, 0.975, 0.017]

5. Result

Since the dataset is divided into six categories of diseases. Our model was implemented on these six categories. The final training and validation accuracies of each category are Shown in Table 3:

Table 3 Training and Validation accuracy of individual Categories

Diseases Category	Training Accuracy	Validation Accuracy
Fungi	99%	82%
Bacteria	100%	100%
Virus	100%	100%
Nematodes	100%	100%
Pest and Insects	99%	97%
Non-Infectious	99%	91%
Overall Accuracy	96.54%	95.7%

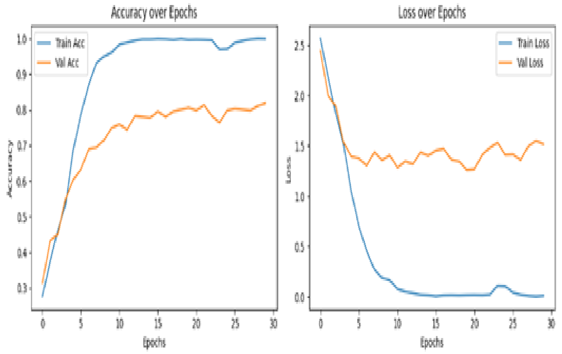

Figure 2 Accuracy and Loss Graph of Fungi

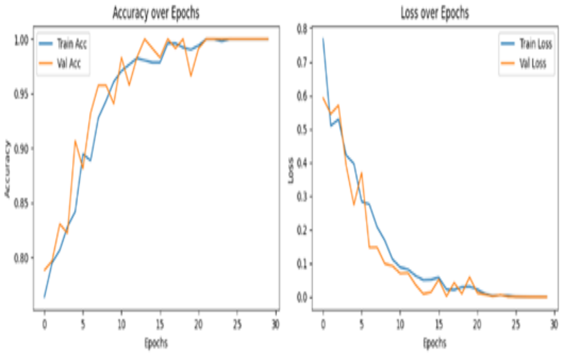

Figure 3 Accuracy and Loss Graph of Bacteria

As summarized in the table, Bacteria, Virus and Nematodes achieved the highest accuracy i.e. 100% on both training and validation dataset. While other categories like Fungi, Pests/Insects and Non-

Infectious achieved accuracy of 99% on training dataset and 82% to 97% percentage accuracy on validation dataset. To visualize the training dynamics that led to these final results, figure 9 to 13 represent the accuracy vs epochs and loss vs epochs graphs of each category Shown in Figure 4 ,5 & 6.

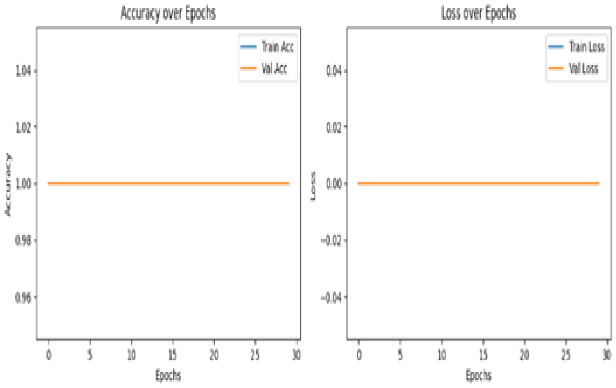

Figure 4 Accuracy and Loss Graph of Virus

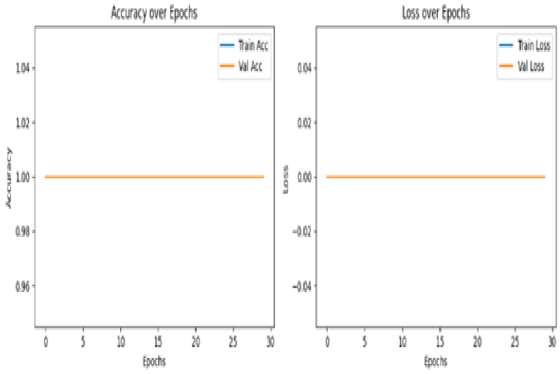

Figure 5 Accuracy and Loss Graph of Nematodes

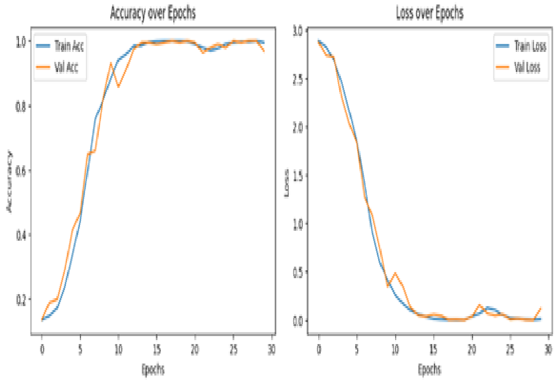

Figure 6 Accuracy and Loss Graph of Pests/Insects

Our model achieved a final accuracy of 96.45%. While softmax helped in increasing the accuracy, it also helped in normalizing the output data for better performance on validation dataset Shown in Figure 7 & 8.

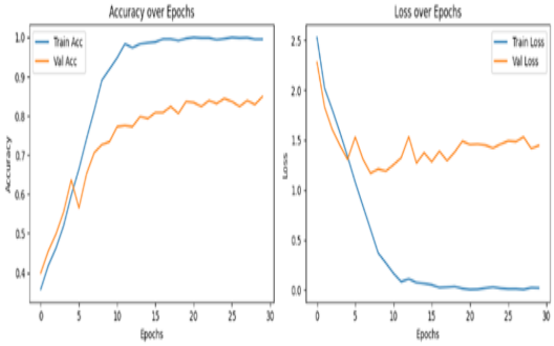

Figure 7 Accuracy and Loss Graph of Non-Infectious

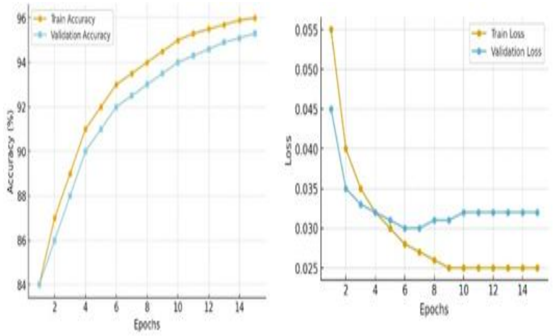

Figure 8 Accuracy & Loss Graph of Overall Dataset

Conclusion

Final accuracy of the proposed custom CNN is 96.54%. After the observation, it can be concluded that this research efficiently derives the massive potential of AI to bring great innovations in the field of agriculture and thereby solve major problems faced such as soil degradation, pests and diseases outbreak and sustainability concerns during agricultural practices. The implementation of CNN using conv2D, flatten and dense layer effectively extracts the complex features of diseases which contributes to automation of disease detection over traditional methods. This study not only resolves immediate agricultural needs but also contributes to innovative, intelligent, and automative farming system that can accommodate global food security demands.

Acknowledgement

Mr. Jitendra Upadhyay along with all student authors would like to express their sincere gratitude to the B. U. Tarsadia Learning Resource Centre (Library and all their staff), for offering such a wonderful space and resources that made our work possible.

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