

Algorithms for Intelligent Systems

Series Editors: Jagdish Chand Bansal · Kusum Deep · Atulya K. Nagar

Manjaree Pandit

M. K. Gaur

Sandeep Kumar *Editors*

Artificial Intelligence and Sustainable Computing

Proceedings of ICSISCET 2022



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Algorithms for Intelligent Systems

Series Editors

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Manjaree Pandit · M. K. Gaur · Sandeep Kumar
Editors

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Preface

This book contains outstanding research papers as the proceedings of the 4th International Conference on Sustainable and Innovative Solutions for Current Challenges in Engineering and Technology (ICSISCET 2022). ICSISCET 2022 has been organized by Madhav Institute of Technology and Science, Gwalior, India and technically sponsored by Soft Computing Research Society, India. It was held on November 19–20, 2022 at Madhav Institute of Technology and Science, Gwalior. The conference was conceived as a platform for disseminating and exchanging ideas, concepts, and results of the researchers from academia and industry to develop a comprehensive understanding of the challenges of the advancements of sustainable and innovative solutions for current challenges in engineering and technology viewpoints. This book will help in strengthening congenial networking between academia and industry. The conference focused on collective intelligence, sustainable computing and information technology, computational intelligence and machine learning, embedded systems and VLSI design.

We have tried our best to enrich the quality of the ICSISCET 2022 through a stringent and careful peer-review process. ICSISCET 2022 received a significant number of technical contributed articles from distinguished participants from home and abroad. ICSISCET 2022 received 250 research submissions from 19 different countries. After a very stringent peer-reviewing process, only 59 high-quality papers were finally accepted for presentation and the final proceedings.

In fact, this book presents novel contributions in areas of computational intelligence and it serves as reference material for advanced research.

Gwalior, India
Gwalior, India
Bengaluru, India

Manjaree Pandit
M. K. Gaur
Sandeep Kumar

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Chapter 2

Lycopersicon Crop Leaf Disease Identification Using Deep Learning



Barkha M. Joshi and Hetal Bhavsar

1 Introduction

Crop disease identification is an art and science. The disease identification technique is integrally visual and requires intuitive judgment and the use of scientific approaches. Approximately 75% of India's population relies on farming, which is a major source of income for the nation. Disease in crops leads to a significant reduction in both the quality and quantity of agricultural products. In agriculture, plant diseases happen because of changes in climate like more or less rainfall, very hot or cold temperature, and weather cycles from one place to another. Climate change may affect the crops through bacterial infections, fungal, as well as viruses which damage the crop, develop the disease, and gradually collapse the crop quality. Crop diseases can affect entire crops by interfering with different manners like translocation as well as absorbance of nutrients and water, photosynthesis, fruit and flower development, plant development and growth, and enlargement and cell division. Plant diseases may damage the plant above and below the ground level as well. Diseases may develop in different parts of the plant body [1].

Crop disease control is a challenging task for farmers. Preventative actions may be taken early on, reducing both economic and production losses, if these illnesses are detected in their early stages [2]. For the purposes of plant disease research, visual patterns on the crop are considered to be the primary data source. Controlling and preventing the spread of disease across the whole farm is essential to ensuring the

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greatest possible yield and quality. Classifying a disease based on symptoms, determining its root cause, and then attempting to manage it is essential to stopping its spread. Crop disease monitoring and analysis were traditionally done manually by specialists in the field. Manually identifying the disease requires extensive work and also it consumes more time. The innovation in deep learning techniques like convolution neural networks may be used in plant disease identification which requires some resources but it identifies the correct disease automatically. This research work is mainly concentrated on a very essential part of the plant, the leaf. Leaf disease detection may be based on the symptoms including brown dots, spotting, yellow dots, etc. which have been caused due to bacterial, fungal, and viral infections. In most cases, farmers detect disease with their naked eye [10], but such a process is fairly taking too much time and is inappropriate in the farming area. Farmers may require the assistance of professionals in determining the disease's identity sometimes. It is easier to classify diseases because of the availability of automated methods that decrease the need for effective manpower and the expense of farmers. There is a great amount of complexity in the automated algorithms used to categorize plant leaf diseases using optical monitoring of signs on plant leaves [3]. Diagnosis of the disease in the plant leaves and at the same time deliver a healthier solution to control it, will be obliged to farmers to produce a good quality and quantity of the crop. Leaf makes food and the different part of plant uses that food for their growth. The disease control on a leaf is the major task in agriculture. There is no such common model that exist which identifies the disease which happens due to fungus, bacteria, and viruses [43–45]. The proposed model is identifying all the types of diseases which happen due to viruses, fungus, and bacteria for the *Lycopersicon* crop.

The research article is organized as follows: Sect. 2 covers the literature survey. Section 3 describes the material and methods. Implementation and results are described in Sect. 4. Conclusion and future work are covered in Sects. 5 and 6, correspondingly.

2 Literature Survey

Plant leaf sicknesses appear due to environmental and climate changes. Having a disease in the crop is a herbal issue. The ailment can appear within the crop for a unique reason. Fungi, microorganisms, phytoplasma, viruses, viroid, nematodes, and many others are examples of the sickness. Diseases like Canker, Aster yellows, fireplace blight, Rice bacterial blight, Bacterial wilt, Crown gall, Rot, Basal rot, and Scab are examples of bacterial sickness. The fungal diseases are a late blight, Anthracnose, Blight, Chestnut blight, Canker, Clubroot, Damping off, Black knot, Dutchelm disease, Ergot, Fusarium wilt, Panama disease, Leaf blister mold, Powdery mildew, Downy mold, o.k.wilt, Rot, Basal rot, gray mold rot, Rust. Mosaic, Curly pinnacle, Psoriasis, noticed wilt, and so forth are manifest because of the virus. Agriculture-related research has been extensive in identifying disease in many plant and crop parts, including root, fruit, leaf, soil, and weeds for instance. Smartphones,

Table 1 Lycopersicon crop leaf diseases [26]

Bacterial disease	
Common name	Scientific name
Bacterial spot	Xanthomonas Vesicatoria
Fungal disease	
Early blight	Alternaria Solani
Late blight	Phytophthora Infestans
Leaf mold	Fulvia Fulva
Septorial leaf spot	Lycopersicon
Target spot	Corynespora cassicola
Viral disease	
Mosiac virus	Lycopersicum virus 1
Yellow leaf curl virus	Solanum Lycopersicum
Two spotted spider mites	Tetranychus Urticae

internet penetration, and unmanned aerial vehicle technologies offer new tools for detecting plant disease in the field of automated image recognition that can aid in early detection at a large scale [4]. Once a disease is diagnosed, the reason for the disease should be investigated, and after those certain preventive actions are to be applied to stop the spread of the disease in the future [11]. Crops can have distinct causes and symptoms of the disease. This research work concentrated on the detailed study of diseases of Lycopersicon crops and the timely detection of such diseases using deep learning algorithms. Table 1 describes the different diseases with their scientific names on Lycopersicon crops [15, 16, 42].

The inception CNN was utilized by Amanda Ramcharan et al. to classify the infection in cassava leaves. The image processing was utilized to extract features, and then the CNN was used to identify diseases. For cassava leaf disease, this method is 93–98% accurate. The authors have identified the diseases based on fungus. The proposed model only works for the fungal disease of the cassava leaves. They’ve also created a smartphone app that can identify diseases quickly [4]. There are a variety of CNN architectures for crop disease detection and diagnosis, including Alex Net OWTBn, Alex Net, Over feat, VGG, as well as Google Net [3]. VGG has the greatest success rate and the best fit between laboratory data and actual data among all these models. The morphological idea has also been employed by authors to identify plant diseases. The proposed model only identifies the bacterial leaf disease of the various leaf-like banana, apples, cabbage, onion, orange, tomato, and potatoes. Classification of Leaf Diseases in Plants CNN and LVQ Algorithm was used to identify plant diseases using the “Learning Vector Quantization” approach for feature extraction [5]. Diseases including late blight, bacterial spots, yellow-curved leaf disease on tomato crops as well as Septoria leaf spots were discovered using this method. The algorithm is 86% and give an accurate result. Sometimes it identifies the wrong disease. Artificial Neural Network (ANN) and gray level co-occurrence matrix (GLCM) were used to classify pomegranate plant disease [6, 9, 12]. Diseases

such as fruit spots, fruit rot, bacterial blight, and leaf spot are identified by these algorithms. The algorithm was only applied to the laboratory dataset for bacterial disease identification. The masking technique was utilized by Monzurul Islam et al. to extract features and train an SVM for disease detection [2]. SVM was formerly used to detect infections in potato plants, such as early blight and late blight. The model only works for the potato leaf of the bacterial disease identification process. The model identified the disease that is for the small dataset. The detection of infection in beans, rose, banana, lemon, tomato, mango, and jackfruit crops is shown by the classification of sick areas of plant leaves utilizing Genetic Algorithm as well as Image Processing [7, 41]. The classification as well as feature extraction technique use a genetic algorithm. The algorithm only works for the synthetic dataset. References [31, 39, 40] identified the disease using transfer learning process and identified disease using convolution neural network with transfer learning approach. Features extracted from pepper plants via masking gray pixels and threshold-based segmentation were employed by Jobin Francis et al. for classification using a neural network [8, 13, 14]. Authors discovered problems including rapid wilt and berry spot. In addition, the researchers have discovered the cause of the infection and taken preventative measures to stop it from spreading. An anomaly detection and plant leaf disease detection of the tomato crop is provided by Robert G. de Luna et al. [18]. Fully-Region CNNs are used to identify plant anomalies, whereas CNNs are utilized to identify diseases. After determining the disease's categorization, they recommended a particular treatment. This prototype may be used for any *Lycopersicon* crop since it automatically captures pictures via the box. Leaf Miner, Target Spot, as well as Phoma Rot, may all be accurately detected with this technique. The algorithm works for the fungal disease of the pepper plant leaf. In [19], Plant leaf disease detection was suggested by utilizing image classification and processing by the authors. Uses GLCM ("Gray Level Co-occurrence method") and k-means clustering for feature extraction, and an SVM to classify images. In the case of citrus leaves, this algorithm is utilized. The algorithm only works for the specific angle for the laboratory dataset. The algorithm work for the disease happens in the crop leaf or not without specifying the actual disease name. Srdjan Sladojevic et al. introduced the convolution neural network for the disease identification model. The initial step in this approach is to gather all of the photographs and delete those that are duplicates [20, 38, 40]. The images are carefully resized using the pre-processing procedure. For example, the augmentation technique may be used to increase the data size and add a little distortion to the pictures. For the augmentation procedure, the Python OpenCV package is utilized. To detect diseases including grapevine wilt, apple powdery mildew, peach powdery mildew, and Caffe Net framework was utilized for the CNN classification [25]. Reasonable outcomes may have been achieved by the use of Augmentation processes. The algorithm gives a good result for the synthesis dataset. In [17, 27] discuss the unique application of mastering systems based on agricultural production. Researchers have explored the fields of crop control, which include programs on yield prediction, disease detection, weed detection, crop fines, and species recognition, and farm animals' control, which includes packages on animal welfare and livestock manufacturing, water control, and soil control management. Articles are

organized according to category and filtered according to filtering, which indicates how machine mastering can benefit agriculture [33, 35–37]. In the era of machine learning and sensor data, farm management systems are becoming AI-enabled, real-time programs that support and guide farmer decision-making. The author [28] of this study presented a technique that led to a description of the chemistry of *S. marianum* flora by using subject spectroscopic evaluations and hierarchical self-organizing maps. There are three supervised hierarchical self-organizing concepts or models used for the identification of the systemically inflamed *S. marianum* flowers: the Kohonen community, the counter propagation synthetic neural network, and the XY-Fusion community. Pre-processing of the spectra protected normalization, 2nd spinoff, and primary element extraction. Identification of *S. marianum* with SKN and CP-ANN offered high overall accuracy and even performed better than XY-F [22–24]. Through hierarchical self-organizing maps, it was possible to identify systemically inflamed *S. marianum* flowers with an excessive degree of accuracy throughout vegetative growth. The main objective of the [29] observation is to locate thrips on the crop cover photos using the SVM type approach. For sorting parasites and detecting thrips, SVM with different kernel characteristics is utilized. It uses the ratio of a big diameter to a small diameter as a location index along with hue, saturation, and intensity as color indices. Additionally, suggest square mistakes, the root of suggesting square errors, suggest absolute errors, and imply percent errors were used for evaluating the classification. With the use of the SVM approach, its results demonstrated that an average percentage error of less than 2.25% is achieved in the high-quality category when the area index and intensity are used as color indexes. At 3 weeks of age, seedlings afflicted with Bakanae disease [30, 32, 34], may be distinguished from healthy seedlings using a machine vision technique. Healthy as well as infected seedlings could be differentiated with an accuracy of 87% using the suggested method.

An overview of plant leaf disease identification research is provided through a literature review. Table 2 covers the used algorithms in the different disease identification processes. Even though a great deal of study has been done in this field, there are still certain limits that must be overcome like developed models may require a lot of resources. AlexNet, VGG, and GoogleNet have generated very much high parameters so all those models required more time for training, developed models only work on a single dataset and identify the limited number of the disease means fungal, bacterial, or viral, no such model is available which identify all the type of disease on synthetic data and real data. This research work proposed a model which solved the problem of resources. The proposed model efficiently detects the different types of fungal, bacterial, and viral diseases using deep learning concepts.

Table 2 Literature review summary

Author	Result accuracy	Used algorithm
Ramcharan et al. [4]–2017	93–98%	CNN, SVM, KNN
Ferentinos et al. [3]–2018	99.53%	CNN applied on the VGG, AlexNet, and GoogleNet Architecture
Sardogan et al. [5]–2018	86%	CNN, LVQ
Dhakate et al. [6]–2015	90%	Image Processing K-means, GLCM and neural network
Islam et al. [2]–2017	95%	Image Processing and machine learning
Singh et al. [7]–2015	–	Image processing and classification
Francis et al. [8]–2016	–	Image segmentation and neural Network
de Luna et al. [18]–2018	–	CNN
Meena Prakash et al. [19]–2017	–	Image processing and classification
Liakos et al. [27]–2018		Machine learning algorithms, models, statistic measures,
Pantazi et al. [28]–2017	95.16%	ANN/XY fusion
Hassan et al. [31]–2021		CNN and transfer learning
Joshi [26]–2020		AlexNet, VGG and GoogleNet
Proposed model	93–95%	Convolution neural network

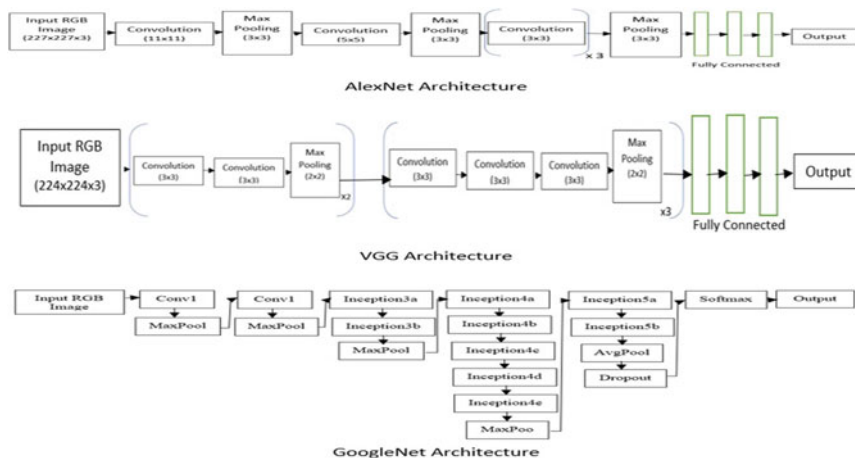
3 Material and Methods

Interest in Convolution Neural Networks has currently heaved, and deep gaining knowledge of is the most famous approach wherein exclusive styles of structure fashions can research suitable capabilities from input photographs at one-of-a-kind convolutional levels comparable, to the feature of the human mind. This version of DL includes convolutions, pooling layers, fully linked layers as well as activation capabilities to deal with composite issues correctly and quickly with high accuracy. As shown in Table 3, different CNN architectures such as AlexNet, VGG, and GoogleNet have various layers and parameter sizes.

The standard model uses different types of filters. The basic architecture diagrams of the CNN model like AlexNet, VGG, and GoogleNet are demonstrated in Fig. 1. The standard architecture model used the convolution layers, max-pooling layers fully connected layers for disease identification. The model used a different number of layers for disease identification. The standard model generates very large parameters due to that reason it takes more time to execute and it required a large number of resources. Hence proposed model used the less number of layers and generate fewer parameters so that computation time and resource cost will be reduced. In this research work we compared the result with the standard model.

Table 3 CNN model parameters and filters

Invented year	Name of architecture	Total noof layers	Parameters	Filters	Limitation
2012	AlexNet	8	60 M	$11 \times 11, 5 \times 5$ and 3×3	1. Hard to apply the high-resolution Images 2. Overfitting problem
2014	VGG	16	134 M	3×3 and 2×2	1. It takes more time to train the model 2. It takes a lot of disk space and bandwidth making it inefficient 3. Vanishing gradient problem 4. More complex than AlexNet. expensive
2014	GoogLeNet	22	360 M	$1 \times 1, 3 \times 3, 5 \times 5$	1. Required more computing power to train the model 2. Overfitting problem 3. More time is required for training and expensive

**Fig. 1** CNN models architecture

4 Proposed Work

Though AlexNet, VGG, and GoogLeNet architectures are powerful and accurately identified the disease, this architecture requires very large resources and computation time to identify the disease. Hence disease identification using deep learning required such a model which identifies the disease very accurately in less amount of time with a limited number of resources. The suggested model utilizes the max-pooling layer, convolution layer, activation function, as well as fully connected layer for the

classification of the specific disease. The proposed model uses the five convolution layers with single fully connected layers which is covered in Fig. 3.

Dataset: An open-access Plant Village dataset of 50,000 infected and healthy plant leaves [2, 21] was utilized for testing and training purposes. All of the photos in the database were taken in laboratory conditions from 14 distinct species of plants. We used *Lycopersicon* crops with healthy and unhealthy leaves in our experiment. The dataset size of *Lycopersicon* is 16012. In Fig. 2, we show color images of *Lycopersicon* crop leaves. The disease names, but no images, are displayed in Table 4. The experiment used RGB color images for disease identification.

All the diseased classes are imbalanced, we have used the augmentation process to make the number of images size balanced in all the types of disease. A total of two sets of leaf images were used, a testing and training set. For evaluation, leaf images were split into 80% training images and 20% testing images.

Pre-processing: There are five approaches applied on the dataset for the experiment of disease diagnosis. The augmentation technique is used for a horizontal and vertical shift, flip, random rotation, brightness, and zoom of the images. Different types of methods made the dataset balanced for the disease identification process.

Proposed Model Architecture: Proposed model uses the $227 \times 227 \times 3$ RGB images as an input. All the images are passed through the different layers. The proposed model contains the 5-convolution layers. All the layers are followed by the max-pooling layers. A single fully connected layer is used for the classification of the disease. We have used 11×11 , 3×3 , and 1×1 filters on different layers for the feature selection.

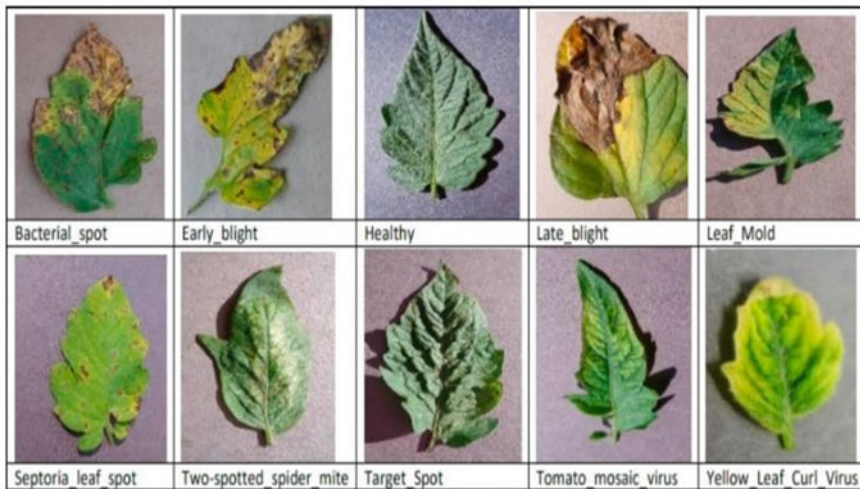


Fig. 2 Lycopersicon crop leaf classification

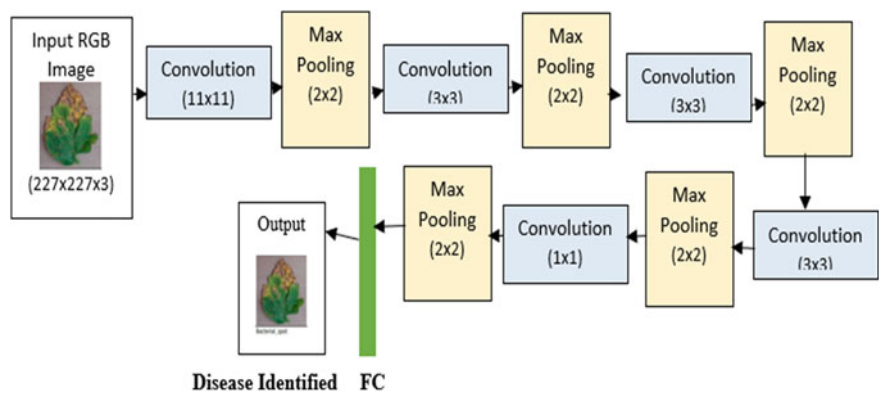


Fig. 3 Proposed CNN architecture

Table 4 Lycopersicon crop leaf disease images

Crop name	Class no	Number of images	Class name
Lycopersicon leaf	1	1404	Target spot
	2	373	Mosaic virus
	3	3209	Yellow leaf curl virus
	4	2127	Bacterial spot
	5	1000	Early blight
	6	1591	Healthy
	7	1909	Late blight
	8	952	Leaf mold
	9	1771	Septoria leaf spot
	10	1676	Two spotted spider mite

Convolution layer: Width, Height, and Depth are all learnable filters in a convolutional algorithm. An image matrix is used to represent the input picture and the filter slides through it to produce a filtered image, which is the result of the filtering process. In the case that a filter is applied to a picture, the output matrix will be smaller than the original. The output matrix would be smaller than the original picture if a filter were applied to the input one. To ensure that the output size matches the input size, padding is required. Convolution is used to extract features from a dataset. Input data will be transformed linearly by convolution based on spatial information in the data. Convolution kernels may be trained based on CNN input by adjusting the weight of that layer's weight.

Activation function: The activation function of the ReLU has been enhanced with the inclusion of the Leaky ReLU. For the ReLU activation function, the gradient is 0 for all input values that are less than zero, which would deactivate the neurons in that area and may lead to the death of ReLU neurons. To deal with this issue, the term “leaky ReLU” is used. A small linear component is defined as a negative value of the ReLU activation function, rather than zero, for negative inputs (x).

$$f(x) = \max(0.01 * x, x)$$

Pooling Layer: The pooling layers have been utilized to gradually decrease the image sizes. The pooling layer resizes the input by applying the pooling function to each layer of the input. The max-pooling layer has been used in the proposed model. Every depth slice in the input is down-sampled by two along with both height and width in Pooling layer 2×2 size, resulting in a loss of 75% of the activations.

Fully connected layer: Final layer is called the Fully connected layer. This layer is used for the dimensionality reduction process. These two-dimensional arrays are transformed into a single long linear vector by this layer. This proposed model uses a single fully connected layer, which generates the less number of parameters.

Output: At the output layer SoftMax activation function is used for the normalized the output. Once the output is normalized it is classified as healthy or unhealthy with specific diseases.

5 Model Implementation and Result

The Proposed CNN model has been implemented in Python language. Model is implemented in the TensorFlow environment. Keras is one of the best libraries for the convolution network, which is installed on the TensorFlow environment. There are many libraries like pandas, NumPy, OpenCV, matplotlib, and scikit used to implement the convolution-based proposed model. The proposed model uses the 11×11 , 3×3 and 1×1 filters on the convolution layer for the feature extraction. Each convolution layer is followed by the max pool layer, which is used to reduce the dimension of the images. Proposed model used the 500 epochs because after 500 the graph curve is pretty flat and after some time it goes downward means overfitting of the data. Learning rate is 0.0001 for the training and testing. This rate accurately trains the model with good accuracy. For the training purpose I am using the Google colab which provides 25 GB free RAM with GPU support because of that, I have chosen the 32 batch size for the training of the dataset. In the proposed model we have used the single fully connected layer which generates the least number of parameters over the AlexNet, VGG, and GoogLeNet architecture. Table 5 describes the hyperparameters are considered for the proposed model.

Table 5 Hyperparameter of proposed model

Hyperparameter	Description
No. of convolution layer	5
No. Fully connected layer	1
Dropout rate	0.5
Activation function	LeakyRelu
Learning rate	0.0001
Number of epochs	500
Batch size	32

The number of parameters may be computed with $[(\text{Shape of a width of filter} * \text{the shape of the height of filter} * \text{previous layer filter or feature map}) + 1] * \text{Number of filter for current layer}]$ formula. Parameter comparison of the proposed model over AlexNet, VGG, and GoogleNet is depicted in Fig. 4. The proposed model generates less number of parameters due to a single fully connected layer. Class wise prediction of diseases are displayed in Fig. 5 and its accuracy in terms of precision, recall and f1-score is shown in Table 6. AlexNet, VGG, GoogleNet and Propose models have been executed in a Google cloud environment with Tesla T4 GPU. The model wise accuracy comparison chart is depicted in Fig. 6. The results demonstrated that the proposed model gives more accuracy than the other three models. The proposed model gives 93% to 95% training and testing accuracy. The proposed model generates the least number of parameters so it requires less amount of time to identify the disease accurately. Figure 7 describes the chart for the training testing accuracy. As results show that the training and testing accuracy increases when the epochs increase. Accuracy increases till the threshold value is 500 epochs.

We must get good training and testing accuracy but at the same time, we have to consider the loss. Figure 8 depicts the comparison of the error rate over the AlexNet, VGG, and GoogleNet of the proposed model over the other three models. Results proved that the loss is less than the other standard model. Figure 9 displays the training and testing loss of the proposed model. The model has been executed on the google cloud environment with the Tesla T4 GPU. The research work has been carried out on the plain background plant leaf images Convolution neural networks used some hyperparameters to train the model accurately without overfitting and underfitting problems.

Though deep learning model requires a long time to train the model, more resources and highly configured machines, the proposed model uses a single fully connected layer so, it generates the least number of parameters. Due to less number of parameters, it requires comparatively less amount of time than the other three models. Figure 10 describes the time comparison chart over AlexNet, VGG, and GoogleNet. The model has been tested on the testing dataset. Figure 11 shows the leaf disease has been identified by Python application of Lycopersicon crop leave test data. All the diseases are classified based on their symptoms.

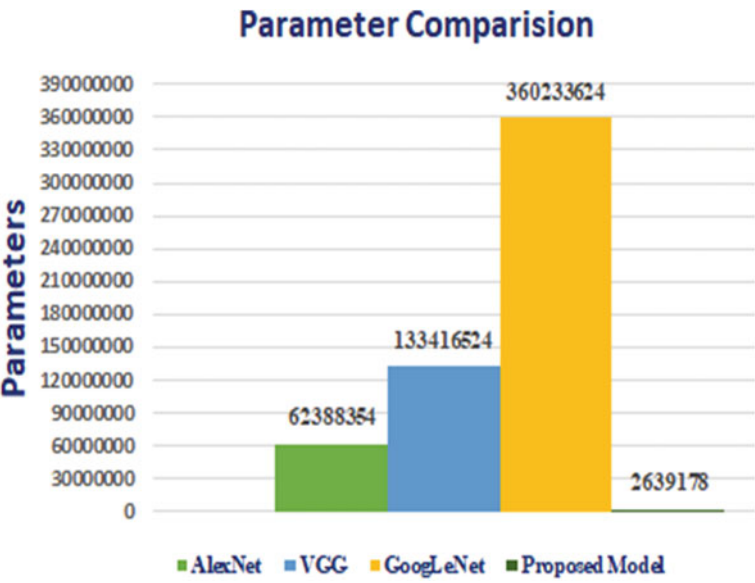


Fig. 4 Parameter comparison

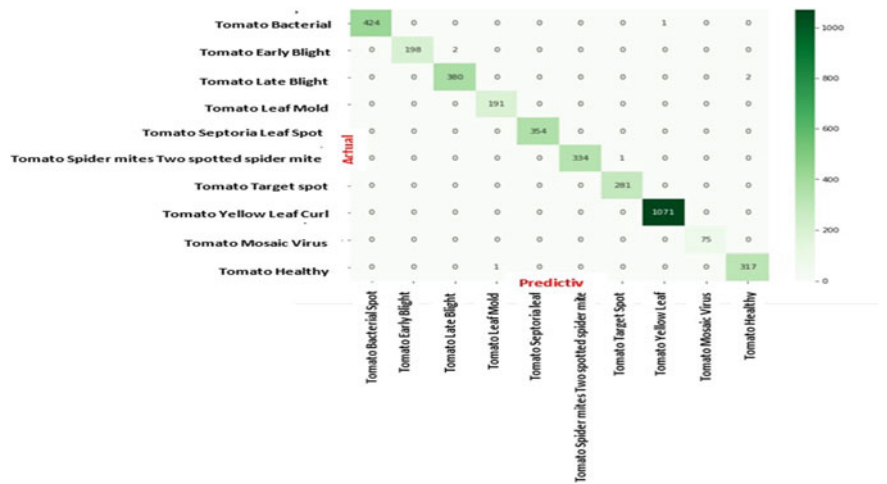


Fig. 5 Confusion matrix of lycopersicon crop diseases

Table 6 Accuracy matrix

	Precision	Recall	f1-score	Support
0	1.00	1.00	1.00	425
1	0.95	1.00	1.00	200
2	1.00	0.93	1.00	382
3	0.94	0.94	0.95	191
4	1.00	1.00	1.00	354
5	0.94	0.95	1.00	335
6	1.00	1.00	0.94	281
7	1.00	1.00	1.00	1071
8	1.00	1.00	0.95	75
9	0.95	1.00	1.00	318
Accuracy			95.23	3632
Macro avg.	0.94	0.94	0.94	3632
Weighted avg.	0.94	0.94	0.93	3632

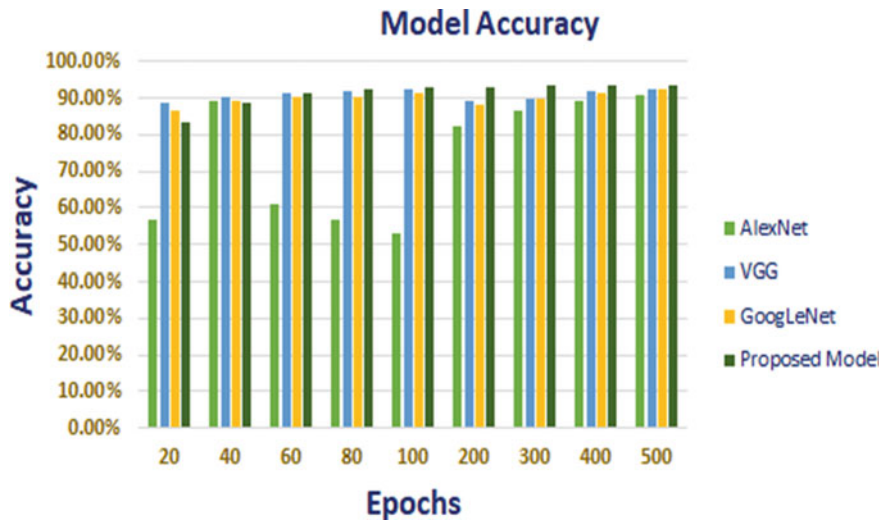


Fig. 6 Accuracy comparison chart

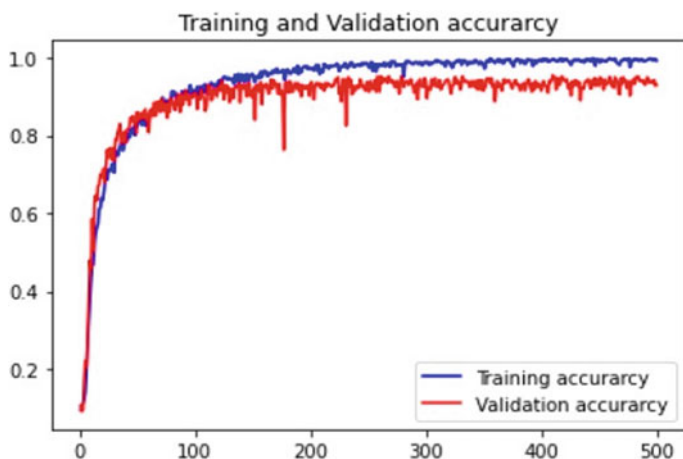


Fig. 7 Training Testing accuracy

Fig. 8 Error comparison chart

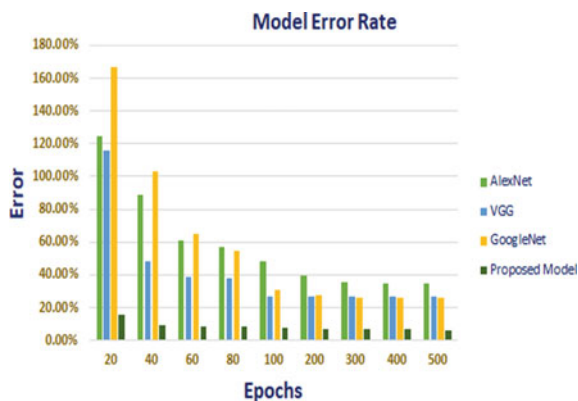


Fig. 9 Training Testing Loss

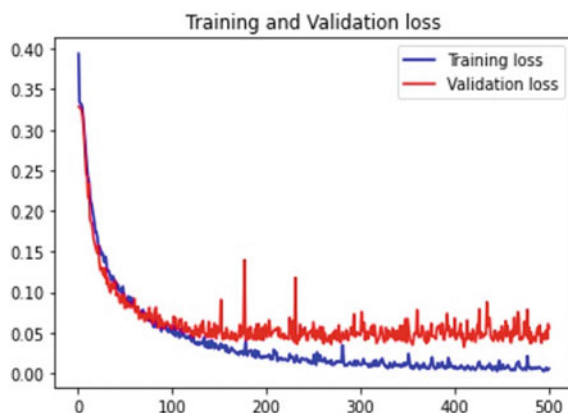




Fig. 10 Time comparison

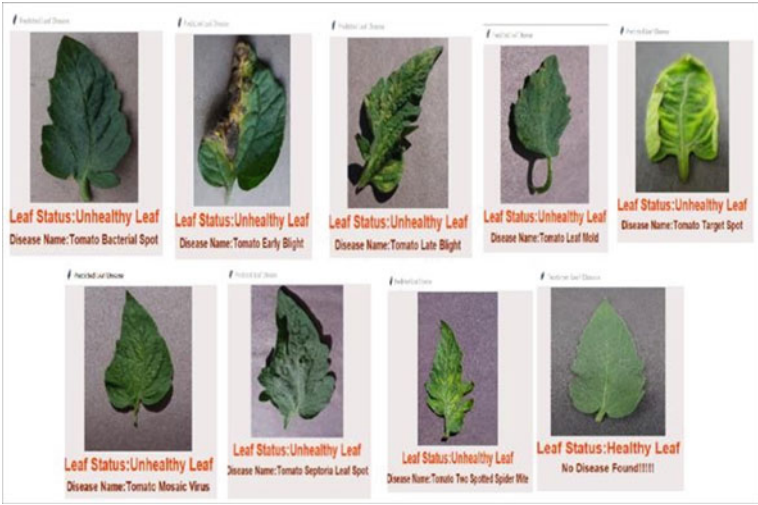


Fig. 11 Proposed model testing dataset accuracy (93–95%)

6 Conclusion

The research work has been proved that the proposed model gives remarkable results. The proposed model training and the testing accuracy is almost 93% to 95%. The model accurately identifies healthy and unhealthy leaves. The model also classifies the unhealthy disease name very accurately and also suggests the treatment for the disease so that the same disorder will not occur in the nearer future. The model generates a 5–8% of mean absolute error. The result has been proved that the proposed model generates less parameter than the other models hence it requires less amount of recourse and less computational power.

7 Future Work

Though the deep learning techniques are expensive and time-consuming they give very remarkable results. Hence proposed algorithm will apply to the other crops of nightshade family for disease identification. The model also suggests remedial measures so that the same disease will not happen in the nearer future. The algorithm also applies to the ground truth dataset for finding the accurate result.

Declarations

Funding—Not Applicable.

Conflicts of 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.

Ethics approval—Not Applicable.

Consent to Participate—Not Applicable.

Consent for Publication—Dataset images we have used from the plant village repository.

Availability of data and material—Data and material is available when it requires.

Code availability—Proposed CNN model has been implemented in Python with the OpenCV environment and executed on Google colab environment.

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