

# Potato Leaf Disease Detection using CNN - A Lightweight Approach

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## Abstract

Detection of potato leaf diseases at an early stage is of great significance to the agricultural industry. The conventional tactics of disease identification that exist are either unreliable or very complex or costly making them not suitable as viable techniques. However, with a boom in the field of Artificial intelligence, many procedures have come up over the recent years to help solve this problem. Data being the fuel for such procedures, it is very important to source reliable and accurate data for the training purpose of the AI based models. The task of disease detection for potato leaves is quite challenging as the symptoms show a lot of variations depending upon the species, climate and environmental factors. The popular pretrained models used for this purpose are VGG16, Inception V3, ResNet50 which help us to classify diseases of plants. In our research we have tried to build a custom Convolutional Neural Network classification model which is more robust and light weight as compared to the existing approaches. The model is built with a very simple approach and is trained using two standard publicly available datasets namely "PlantVillage" and PLD. The correctness of the suggested model has shown promising and consistent output with accuracy of 99.3% and 99.23%, while implemented on the two datasets respectively. To achieve the said accuracy, we have used image Enhancement algorithm: CLAHE at the preprocessing stage after the data acquisition.

## Keywords

Potato Leaf Disease, CNN, Image Enhancement, Image classification

## 1. Introduction

Since the dawn of human civilization, agriculture has played a crucial role in transforming people from roving hunter-gatherers to established citizens [1]. It has facilitated the growth of large human populations by providing a reliable and stable source of nutrition. The history of agriculture is a long continuum of groundbreaking innovations, evolving rapidly through industrial revolutions and advancements in modern science, particularly in the 20th and 21st centuries. Unlike a single, definitive moment, the origin of agriculture in human civilization unfolded over centuries and cannot be precisely dated. Researchers concur that early Homo Sapiens began transitioning from a nomadic lifestyle to settling down, domesticating animals, and cultivating cereal seeds during the early Neolithic period, known as the Neolithic Revolution [2]. This shift likely took place as glaciers retreated northward and the climate warmed, approximately 10,000 years ago—though some estimates place it at 12,000 or even 15,000 years ago. This further led to the development of complex societies as humans learnt the ways of trade and caused the growth of economy and exchange. From a contemporary standpoint, agriculture is a very dynamic industry that is essential to meet the basic need of food for entire population.

In a developing nation like India, agriculture is an important sector of its economy as it contributes about 15% of total GDP and renders employment to about 60% of its residing population [3]. However, despite being a formidable industry, due to the problem of crop diseases, the sector suffers havoc. Plant

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*The 2024 Sixth Doctoral Symposium on Intelligence Enabled Research (DoSIER 2024), November 28–29, 2024, Jalpaiguri, India*

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diseases can have a major effect on the leaves, fruits and different parts of crops, which degrades quality of crops and yield [4]. This, in turn, contributes to food scarcity and insecurity on a global scale. It is estimated that crop diseases cause an annual loss of around 16% in global crop yields, making them a major factor behind famines and rising production costs. According to predictions from the Food and Agriculture Organization (FAO), there will be 9.5 billion people on the earth by next thirty years [5], meaning that a 75% increase in food production is necessary to provide a consistent supply of food. A group of factors that impact plants and their products are diseases and illnesses. As opposed to disorders, which are mostly caused by factors such as rainfall, temperature, moisture, and nutritional deficiencies, illnesses are caused by biotic agents such as fungi, bacteria, and algae [6].

For the well-being of the crops, early and precise identification of diseases is necessary, so that the correct cure can be applied in time. Various methods are available for diagnosing plant diseases, with one of the simplest ones being visual inspection. Conventional diagnostic techniques frequently depend on the farmer's knowledge, which can be erratic and untrustworthy. Due to the extensive, time-consuming process needed and the restricted availability of experts in remote places [1], this strategy is frequently impracticable. To improve accuracy, researchers have introduced spectrometers to distinguish between healthy and infected plant leaves [7]. Another technique involves extracting leaf DNA using the PCR [8]. These methods are complex, costly, and time-consuming, requiring specialized skills, controlled experimental conditions, and extensive use of crop safety equipments. The role of artificial intelligence is immensely significant in this aspect. If the training of deep learning based models, is done on labeled samples, we can perform automated, efficient and accurate leaf disease detection [9]. We have chosen potato as the crop of our concern and our model serves to categorically classify blight disease both early and late, as well healthy leaf images. Potato (*Solanum tuberosum*) [10] is a temperate crop grown under subtropical conditions in India. Soils that are loose, muddy, and sandy and rich in organic matter are ideal for growing potato crops; alkaline and saline soils are not suited [11]. In addition to being a great source of fiber and heart disease prevention, potatoes are vital for overall health. Their high antioxidant content aids in the defense against diseases including excessive cholesterol and irregular blood sugar levels [12]. The nation has been growing potatoes for more than three centuries. It is currently one of the most widely grown crops in this nation for vegetable purposes. Potatoes are a cost-effective food that contributes inexpensive energy to the human diet.

For the purpose of training our model, we have made use of the publicly available dataset "PlantVillage" and PLD. Both these datasets contain potato leaves images for both blight diseases, Early and Late as well as healthy also. Pre-indication of the disease Early Blight can be seen initially towards the base of the plant, with roughly circular brown colored spots on the leaves and stems. This infection caused by Fungus can be deadly for tubers, leaves and stems, causing many problems like reduced tuber size, low produce and crop yield. One more fungal disease that affects potato crops is late blight, which first manifests as patches on the stems. They spread out very quickly, creating big, dark brown, and black areas that frequently look oily [1]. However, a marked variation in these symptoms can be observed based on the region it is taken from, the climate, the species etc., making it a difficult task to build a generalized classifier.

Kamal et. al.[13] developed two models based on MobileNet architecture and applied the architecture on PlantVillage dataset. They have achieved an accuracy of 97.65% and 98.34% from Reduced MobileNet and Modified MobileNet respectively for classification of 55 classes in PlantVillage dataset. Liang et.al. Two different types of deep architectures where the first one based is on residual learning and the second one is based on attention mechanism, have been developed by Karthik and his co-authors [14]. The model based on the attention mechanism has attained an accuracy of 98% on the public dataset named plantvillage for the detection of diseased tomato leaf. Khamparia et. al. [15] designed a hybrid approach of developing an architecture for disease detection of potato leaves using Deep Neural Network and autoencoders and attained an accuracy of 97.50% on PlantVillage dataset. Islam et. al. [16] presented an approach which integrates the technique of image processing and machine learning to classify potato leaf diseases. They used the renowned machine learning algorithm SVM in their recommended solution and attained an accuracy of 95% over 300 images. For the identification and classification of cassava illness, Sambasivam and his team[17] developed a deep neural network that

was trained on a very small dataset with significant class imbalance. A possible solution to the illness identification accuracy problem with the least amount of time investment is the Kuan filtered Hough transformation based reweighted linear program boost classification (KFHT-RLPBC) technique, which was introduced by Nagarjan and his co-authors[18]. By using the PlantVillage dataset, they achieved an accuracy of 92%. Geetharamani et.al. [19] recommended a deep Convolutional Neural Network which can effectively identify and solve the problem of plant leaf diseases. They intended to carry out a more thorough analysis of the training procedure without utilizing the tagged photos after achieving an accuracy rate of 96.46% in the PlantVillage dataset. Table 1 discusses the synopsis of related works. Most of the current methods for crop leaf disease detection have used the popular transfer learning models, but these models often have a higher degree of parameters which leads to the problem of computational complexity. Other approaches have implemented custom Convolutional Neural Networks (CNNs) with reduced parameter counts; however, they generally fall short in achieving significant amount of accuracy. Thus, there is a need for a more efficient, lightweight model for crop leaf disease detection.

In order to detect diseases in potato leaves, we provide a novel lightweight Convolutional Neural Network (CNN) in this research that can recognize both simple and abstract patterns. The model architecture, illustrated in Figure 1, comprises convolutional layers, maxpooling layers for edge feature extraction, batch normalization to normalize the input neuron values, dropout layers to reduce overfitting, and fully connected layers for classification purpose. We have also used the Contrast Limited Adaptive Histogram Equalization (CLAHE) technique for image preprocessing. The major contributions are as follows.

- The model introduces a lightweight CNN architecture which is both less complex with respect to number of parameters and highly accurate for leaf disease detection of potato leaves.
- Through the use of convolution and max pooling layers, it is able to capture both intricate patterns and minute details.
- The addition of CLAHE raises the picture quality, which strengthens the model’s capacity to accurately detect damaged potato leaves.
- Data augmentation techniques used to make the training and testing datasets larger and more balanced. The classifier’s capacity for generalization increases with the use of various data augmentation strategies.

The study is organized as follows: the proposed CNN architecture is thoroughly explained in Section 2. The work is concluded in Section 4, while the experiments and comparison findings are presented in Section 3.

**Table 1**  
Summary of disease prediction of potato leaves

Author	Algorithm	Dataset	Plant	Accuracy
[13]	Modified Mobilenet	Plantvillage	Potato	98.34%
[20]	Resnet50	Plantvillage	Potato	98%
[14]	Attention Based Residual Network	Plantvillage	Tomato	98%
[17]	CNN	Cassava Challenge	Cassava	93%
[18]	Reweighted Linear Boost Program Classification	Plantvillage	Multiple	92%
[15]	CNN and Auto Encoders	Plantvillage	Potato, Maize, Tomato	97.5%
[19]	Deep CNN	Plantvillage	Potato	96.46%
[16]	Segment and Multi SVM	Plantvillage	Potato	95%

## 2. Proposed Methodology

Three subsections comprise this section: Data Preprocessing, Acquisition of Data, and Classification.

## 2.1. Acquisition of Data

The images of potato leaf diseases were sourced from two publicly available datasets: the PLD dataset[5] and the PlantVillage dataset[21]. Both datasets include two types of blight disease early, late as well as healthy images. The PlantVillage dataset provided a sum of 2,152 images— 1,000 each for both kind of blight diseases and 152 for healthy leaves (refer table-4). Owing to the limited quantity and imbalance of images, additionally, 3,251 photos from Pakistan's Central Punjab were included from the PLD dataset. This dataset contains 816 healthy images, 1,303 early blight images, and 1,132 late blight images after redundancy has been removed (refer to table-5). All photos are saved in uncompressed JPG style and have RGB color profiles.

## 2.2. Data Preprocessing

As preprocessing stage, we employed CLAHE [22] algorithm. CLAHE is an image processing technique designed to enhance image contrast. CLAHE operates on discrete areas of the image, known as tiles, as opposed to the full image at once, in contrast to conventional histogram equalization. Within each tile, CLAHE adjusts the contrast adaptively based on the local histogram, allowing it to enhance detail without overly amplifying noise. After processing each tile, neighboring tiles are merged smoothly to prevent visible boundaries. CLAHE is designed to prevent excessive contrast amplification by limiting it. The contrast amplification around each pixel is determined by a slope function transformation. To control this amplification, CLAHE clips the histogram at a predefined threshold before computing the cumulative distribution function, effectively constraining the enhancement to avoid noise exaggeration. By limiting contrast adjustments in uniform areas, CLAHE minimizes noise amplification, producing a balanced, enhanced image.

## 2.3. Classification

Image processing, recognition, and classification are the main applications for CNNs, a kind of deep learning method. The architecture of the human brain served as the model for CNN's design. The similarity of both can be understood as human brain has neurons and in the neural networks, it is the neurons which are the backbone of the entire system. A CNN consists of several layers namely convolutional, maxpooling, dropout and fully connected.

The convolution operation for a 2D convolutional layer can be represented as:

$$y_{p,q,r} = \sum_{i=1}^M \sum_{j=1}^N \sum_{k=1}^C x_{p+i,q+j,k} \cdot w_{i,j,k,r} + b_r$$

- $y_{p,q,r}$ : Output feature map at position  $(p, q)$  in channel  $r$ .
- $x_{p+i,q+j,k}$ : Input feature map at position  $(p + i, q + j)$  in channel  $k$ .
- $w_{i,j,k,r}$ : Convolution filter weight of size  $(M \times N)$  for channel  $k$  and output channel  $r$ .
- $b_r$ : Bias term for channel  $r$ .

For max-pooling, the operation can be written as:

$$y_{p,q,r} = \max_{i,j} (x_{p+i,q+j,r})$$

- $y_{p,q,r}$ : Output of max-pooling at position  $(p, q)$  in channel  $r$ .
- $x_{p+i,q+j,r}$ : Input feature map over a pooling window defined by  $(i, j)$ .

The following is an expression for a Fully connected layer's output.

$$y_j = \sum_{i=1}^N w_{j,i} x_i + b_j$$

- $y_j$ : Output of the  $j^{\text{th}}$  neuron in the layer.
- $x_i$ : Input from the  $i^{\text{th}}$  neuron in the previous layer.
- $w_{j,i}$ : Weight connecting the  $i^{\text{th}}$  neuron in the previous layer to the  $j^{\text{th}}$  neuron.
- $b_j$ : Bias term for the  $j^{\text{th}}$  neuron.

Softmax function, used to convert final layer's logits into probabilities, is given by:

$$\sigma(z)_i = \frac{e^{z_i}}{\sum_{j=1}^N e^{z_j}}$$

- $\sigma(z)_i$ : Softmax output for class  $i$ .
- $z_i$ : Logit (raw output) for class  $i$ .
- $N$ : Total number of classes.

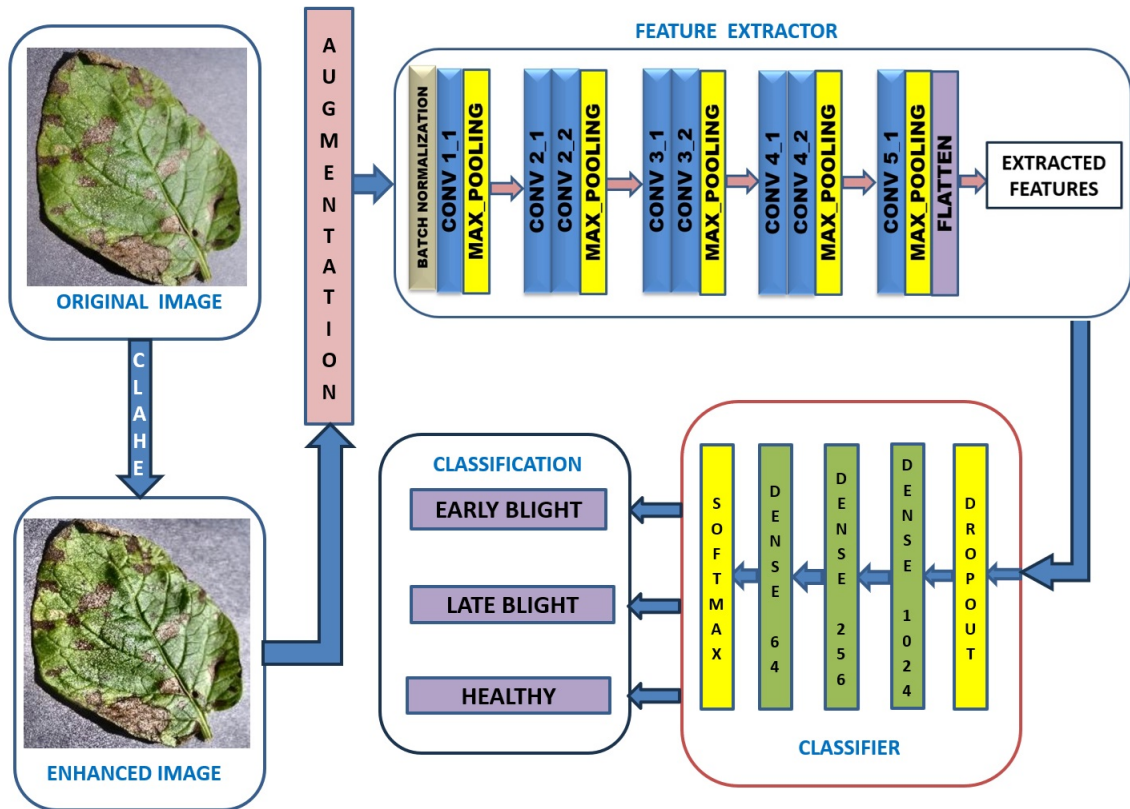
The function of these layers is to detect the features like edges and complex patterns. To extract features and different kinds of edges, various types of filters will be used as per the requirement. For Potato Disease Detection, we used the three well known transfer learning models: VGG16, InceptionV3 and ResNet-50.

VGG16 [23] is a deep CNN architecture which has been introduced for image classification in the year 2014. Its architecture is based on the input size 224x224 pixels of RGB images. It consists of total 16 layers comprises with 13 convolutional and 3 fully connected layers. Activation function relu is employed in all the layers. VGG16 is trained on ImageNet dataset and is competent enough for the classification of images into 1000 classes. categories and detecting objects from 200 classes. The convolution layer has 3x3 filters with increasing number of filters to detect the complex hierarchal patterns in the images. Max pooling layers of size 2x2 with a stride of 2 have been used to extract features that select the maximum valued pixel within each small region. After the feature extraction layers, there are 2 fully connected layers of 4096 neurons and finally there is a fully connected layer of 1000 neurons for classification purpose.

The 48-layer deep pretrained CNN InceptionV3 [24] was trained on the ImageNet dataset and can categorize images into 1000 different categories. The network is based on the input size of 299x299 pixels of RGB images. The layers architecture of InceptionV3 consists of Inception modules where each module is combined of 1x1, 3x3, and 5x5 convolutions. InceptionV3 has fewer no. of parameters because of factorizing convolutions. A convolution of 5x5 filter can be replaced by two 3x3 filters. In this context, for a 5x5 filter it requires 25 parameters but for two 3x3 filters it requires 18 parameters. It will reduce the no. of parameters by 28% without losing the ability to capture patterns by a 5x5 filter. Because of this light weight architecture, it is computationally efficient to work on.

ResNet-50 [25] is a popular deep CNN architecture, which is a part of the ResNet (Residual Networks) family, which was developed to tackle the problem of vanishing gradient in deep networks by introducing residual blocks. It was first introduced in the year 2016. Convolutional layers, batch normalization, ReLU activations, and skip (residual) connections make up this 50-layer deep model. 48 convolutional layers, one max-pooling layer, and one average-pooling layer make up the layers. There are many residual blocks in each of the four main stages of the model. Each residual block in ResNet-50 has a shortcut connection that skips single or multiple layers, enabling the gradient to pass back through the network without vanishing. They consist of three convolutional layers with 1x1, 3x3, and 1x1 convolutions. The final fully connected layer in ResNet-50 typically has 1,000 output units for 1,000 classes in the ImageNet dataset, which the model was originally trained on. However, ResNet-50 can be modified to handle any number of classes by adjusting the number of output units in the final layer. This modification is common in transfer learning, where the network is adapted to different datasets with fewer or more classes.

For our experiment of potato disease detection, we proposed a custom CNN which comprises with 20 layers Table-3. The architecture of the proposed CNN model is depicted in following steps. Figure 1 and Figure 2 are representing the model architecture and detailed layerwise flow diagram respectively.



**Figure 1:** Paradigm of proposed model

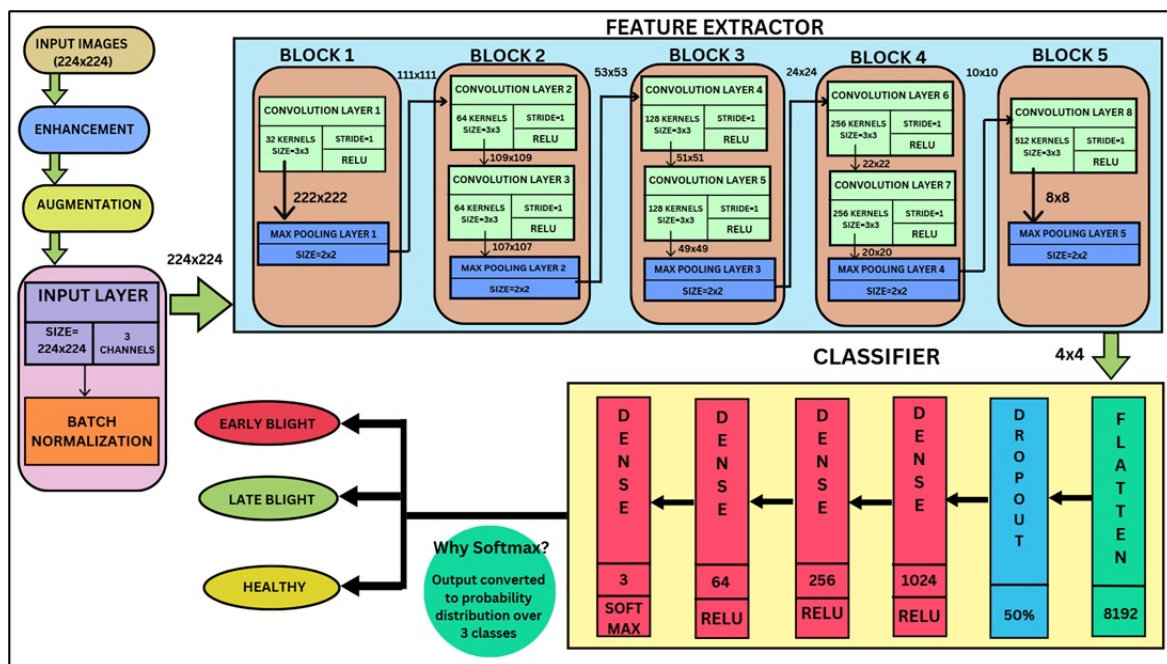
- The images of the datasets PlantVillage and PLD are enhanced using **CLAHE** for better clarity, noise reduction and ease of feature extraction.
- Enhanced images undergo **augmentation** using a variety of techniques that make use of the dataset and improve the generalization capacity of the model.
- Images are passed to the **Input Layer** which accepts an input of size 224 X 224 and 3 channels.
- Images are subsequently **batch normalized** to normalize the output from neurons by calculating the mean and variance across the mini batch during training, for better convergence and improvement of training accuracy.
- Normalized images are then fed to our customized **feature extractor** comprising 5 blocks, each consisting of **Convolution** and **Maxpooling** layers. The Convolution layers are used to capture minute details for fine feature extraction. The Maxpooling layer on the other hand reduces the spatial dimensions by selecting a maximum value within a kernel, retaining the most prominent features. A stride of 1 has been maintained throughout, and activation function **ReLU** has been employed with the convolution layers to incorporate the absence of linearity. Only positive feature values are activated, allowing the model to learn intricate patterns.
- Uniform kernel size of 3x3 has been used for the convolution layers, and all the Maxpooling layers used are of size 2x2. **Block 1** consists of 1 Convolution layer of 32 filters, followed by a Maxpooling layer. **Block 2** consists of 2 convolution layers of 64 filters each and a Maxpooling layer. **Block 3** contains 2 convolution layers of 128 filters each and a Maxpooling layer. Two convolution layers of 256 filters and a Maxpooling layer is contained in **Block 4**. In **Block 5**, the last and final block, there are 2 convolution layers of 512 filters each and a Maxpooling layer.
- The output from the Feature Extractor is fed into **customized Classifier** which first flattens the vectors to a single dimension comprising 8192 neurons, followed by a Dropout layer to avoid overfitting of the model. After this, dense layers are used which steps down the sizes from 1024 to 256 to 64 neurons consecutively. The dense layers also employ the ReLU activation function.

- The output of the last dense layer, which consists of three neurons representing the three classes, is then sent through the Softmax activation function to classify the image as either Healthy, Early Blight, or Late Blight.

**Table 2**  
Augmentation parameters

Sl No.	Operation used	Range
1.	Rotation	30 Degree
2.	Zoom	0.15
3.	Width shift	0.2
4.	Height shift	0.2
5.	Shear	0.15
6.	Horizontal Filp	True

Softmax is generalization of sigmoid function for multiclass classification which generates probabilistic output between 0 and 1. Relu activation adds non-linearity to the model in each convolution and max pooling layer by setting just the negative variables to zero while leaving the positive ones unaltered. Details about hyperparameters are depicted in Table-9.



**Figure 2:** Flow diagram of proposed model

### 3. Experimental Result

All the experiments have been done using an IntelR CoreTM i5-1135G7 CPU, an NVIDIA Tesla T4 GPU with 16 GB VRAM, 32 GB of RAM, and a Windows operating system. The deep learning implementation was carried out using the TensorFlow 2.16.1 framework, Python 3.12.2, to accelerate neural network operations. The proposed methodology has been implemented using the two public dataset namely PLD and Plantvillage. Keras, framework of neural networks written in Python, has been used to implement the model. There is total 2152 images from PlantVillage Dataset and 3251 images of PLD dataset which have been used. To artificially increase the dataset and flexibility of the model, data augmentation

**Table 3**

An overview of the suggested neural network model

Layer	Output Shape	Param #
Batch_normalization	(None, 224, 224, 3)	12
Convolution2D_1	(None, 223, 223, 32)	896
MaxPooling2D_1	(None, 111, 111, 32)	0
Convolution2D_2	(None, 109, 109, 64)	18,496
Convolution2D_3	(None, 107, 107, 64)	36,928
MaxPooling2D_2	(None, 53, 53, 64)	0
Convolution2D_4	(None, 51, 51, 128)	73,856
Convolution2D_5	(None, 49, 49, 128)	147,584
MaxPooling2D_3	(None, 24, 24, 128)	0
Convolution2D_6	(None, 22, 22, 256)	295,168
Convolution2D_7	(None, 20, 20, 256)	590,080
MaxPooling2D_4	(None, 10, 10, 256)	0
Convolution2D_8	(None, 8, 8, 512)	1,180,160
MaxPooling2D_5	(None, 4, 4, 512)	0
Flatten	(None, 8192)	0
Dropout	(None, 8192)	0
Dense_1	(None, 1024)	8,389,632
Dense_2	(None, 256)	262,400
Dense_3	(None, 64)	16,448
Dense_4	(None, 3)	195

technique has been employed in the dataset [26]. For both datasets, we have used the same techniques. We used ImageGenerator class in Keras for augmentation purpose Table 2. We applied the parameters to rotate the image about an angle of 30 degree and transform the images horizontally, vertically and zoom into or out in a range of 15% randomly. With the learning rate set to 0.001 and the number of epochs set to 200, batch size 32 has been utilized Table 9. Categorical cross-entropy is the loss function, and the Adam optimizer is employed.

For the Plant Disease detection, we have used the publicly available PlantVillage Dataset [27] and PLD Dataset. The PlantVillage dataset is a widely available and comprehensive benchmark dataset for crop leaf disease classification. It includes 54,306 samples across 14 plant species, covering a total of 32 classes. Among them, 26 classes are from diseased plants, while the remaining 12 classes belongs to healthy plants. We selected three different kinds of potato leaf disease samples—late blight, early blight, and healthy—from the "PlantVillage dataset" because our study focuses on potato leaf diseases prediction. In all, 2152 images of potato leaves were used in our experiment; 1000 of these images showed early blight, 1000 showed late blight, and the remaining 152 showed healthy in Table 4. Potato crops are susceptible to a fungal ailment called early blight. The PlantVillage dataset has not an adequate number of images and exhibits an uneven class distribution, so the PLD dataset has been used which has been created in Pakistan's Central Punjab region. From that dataset, we have rejected some images of potato leaves due to redundancy. There is a total of 3251 images of potato leaves used amongst which 1303 pictures are from Early blight section, 816 pictures are from healthy section and 1132 from Late blight section Table 5.

The model's performance is calculated using standard validation metrics. To evaluate how well the suggested model discriminated, the model's accuracy, recall, precision, and f1-score were calculated. A tabular method of displaying the prediction model's performance is the confusion matrix. The number of predictions the model made when it properly or erroneously identified the classes is indicated by an entry in a confusion matrix.

A classifier's True Positive (TP) is the number of predictions in which it correctly identifies the positive class as positive. Conversely, True Negative (TN) refers to the quantity of predictions in which the classifier correctly identifies the negative class as negative. False Positives (FP) are the quantity of



hypotheses in which the classifier incorrectly predicts the negative class as positive. False Negative (FN) is the frequency with which the classifier incorrectly predicts the positive class as negative. Accuracy provides the model's overall accuracy, or the percentage of all samples that the classifier successfully classified. Equation (1) can be used to determine accuracy.

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

Precision indicates the percentage of positive class predictions that came true. Equation (2) can be used to determine precision.

$$Precision = \frac{TP}{TP + FP} \quad (2)$$

Recall indicates the percentage of positive samples that the classifier accurately predicted to be positive. Other names for it include probability of detection, sensitivity, and true positive rate (TPR). Equation (3) can be used to determine precision.

$$Recall = \frac{TP}{TP + FN} \quad (3)$$

The F1 score, a mixture of the two measures, is frequently used by practitioners in machine learning to balance the precision-recall score. It merges recall and precision into one metric. In terms of mathematics, it is the harmonic mean of recall and precision. It can be computed by using Equation (4).

$$F1 - Score = 2 * \frac{precision * Recall}{precision + Recall} \quad (4)$$

**Table 4**  
PlantVillage Dataset

Sl No.	Class	Sample size
1.	Healthy	152
2.	Late Blight	1000
3.	Early Blight	1000

**Table 5**  
PLD Dataset

Sl No.	Class	Sample size
1.	Healthy	816
2.	Late Blight	1132
3.	Early Blight	1303

**Table 6**  
Comparative study of parameters with various Transfer Learning Model

Transfer Learning Model	Number of Parameters		
	Trainable	Non-Trainable	Total
VGG16	75,267	14,714,688	14,789,955
INCEPTIONV3	153,603	21,802,784	21,956,387
RESNET50	301,059	23,587,712	23,888,771
Proposed Model	11,011,849	6	11,011,855

**Table 7**

Comparative study of accuracy Measures of Suggested model with well-known Pretrained Models

Model	Type	Precision	Recall	F1-score
VGG16	Micro Average	0.97	0.97	0.97
	Macro Average	0.98	0.90	0.93
	Weighted Average	0.97	0.97	0.97
ResNet50	Micro Average	0.98	0.98	0.98
	Macro Average	0.98	0.97	0.97
	Weighted Average	0.97	0.97	0.98
InceptionV3	Micro Average	0.77	0.77	0.77
	Macro Average	0.80	0.60	0.61
	Weighted Average	0.79	0.77	0.75
Proposed Model (PlantVillage)	Micro Average	0.99	0.99	0.99
	Macro Average	0.99	0.99	0.99
	Weighted Average	0.99	0.99	0.99
Proposed Model(PLD dataset)	Micro Average	0.99	0.99	0.99
	Macro Average	0.99	0.99	0.99
	Weighted Average	0.99	0.99	0.99

**Table 8**

Comparative study of accuracy measures with State of the Art Models

Reference	Technique	Crop	No. of Diseases	Accuracy
Divyansh[28]	SVM, KNN and Neural Net	Potato	2	97.8%
Zhang[29]	Faster RCNN	Tomato	4	97.1%
Barman[30]	SBCNN	Potato	2	96.75%
Rozaqi[31]	CNN	Potato	2	92%
<b>Proposed Model(Plantvillage dataset)</b>	CNN	Potato	3	99.3%
<b>Proposed Model(PLD dataset)</b>	CNN	Potato	3	99.23%

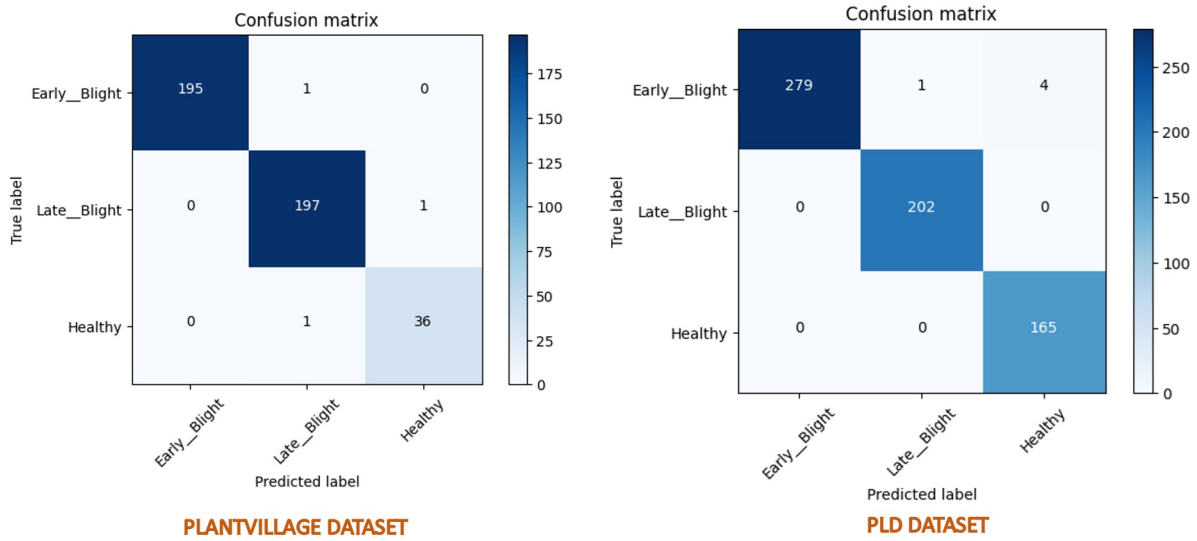
**Table 9**

Hyperparameters

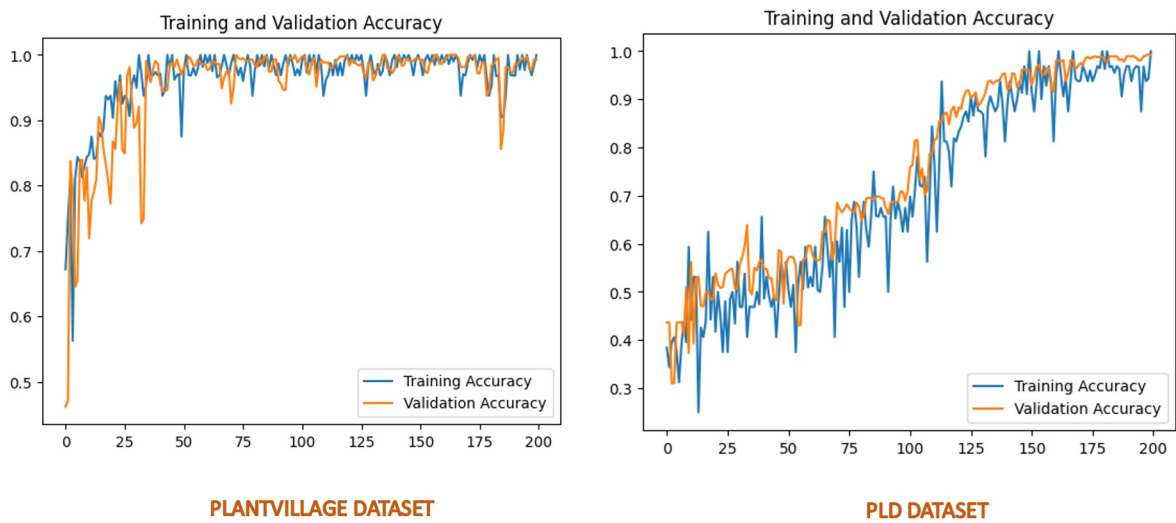
Hyper-parameter	Description
Convolution Layers	8
Max-pooling Layers	5
Dropout	0.5
Activation function	Relu
Number of epochs	200
Batch size	32
Learning rate	0.001

A binary classifier's diagnostic performance can be assessed visually using a ROC curve. Across a range of threshold values, it compares True Positive Rate (TPR) against the False Positive Rate (FPR). The FPR shows the percentage of actual negatives that are mistakenly categorized as positives, whereas the TPR, or sensitivity, shows the percentage of actual positives that are accurately detected.

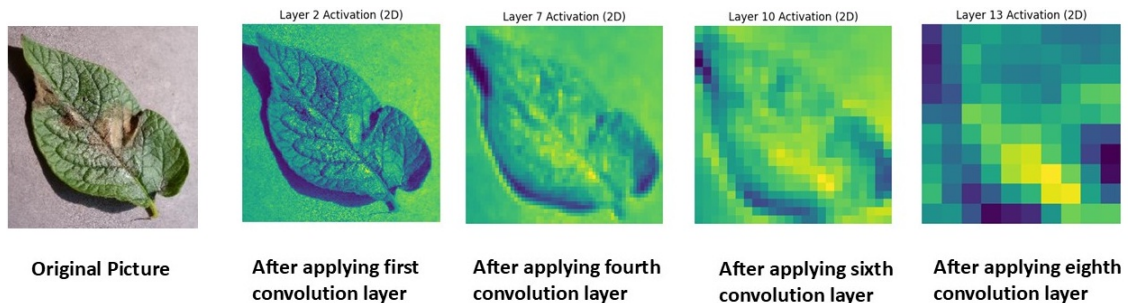
The trade-off between sensitivity and specificity is illustrated by the ROC curve. Better performance is indicated by a model whose curve is closer to the plot's upper-left corner. This performance is frequently measured using the Area Under the ROC Curve (AUC), where a value of 0.5 indicates no discriminatory capacity and a value of 1 indicates flawless classification.



**Figure 3:** Confusion matrix generated by proposed methodology

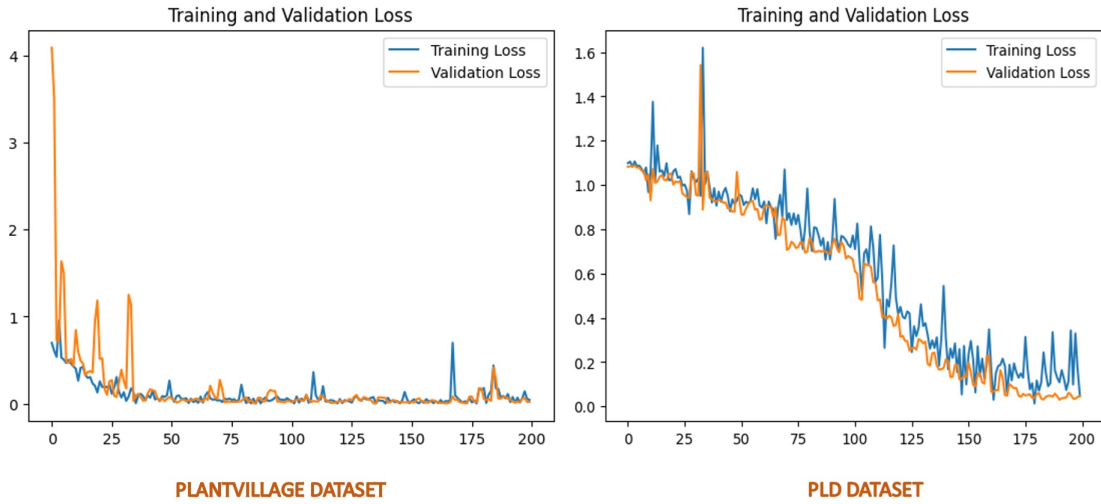


**Figure 4:** Training validation accuracy of proposed methodology

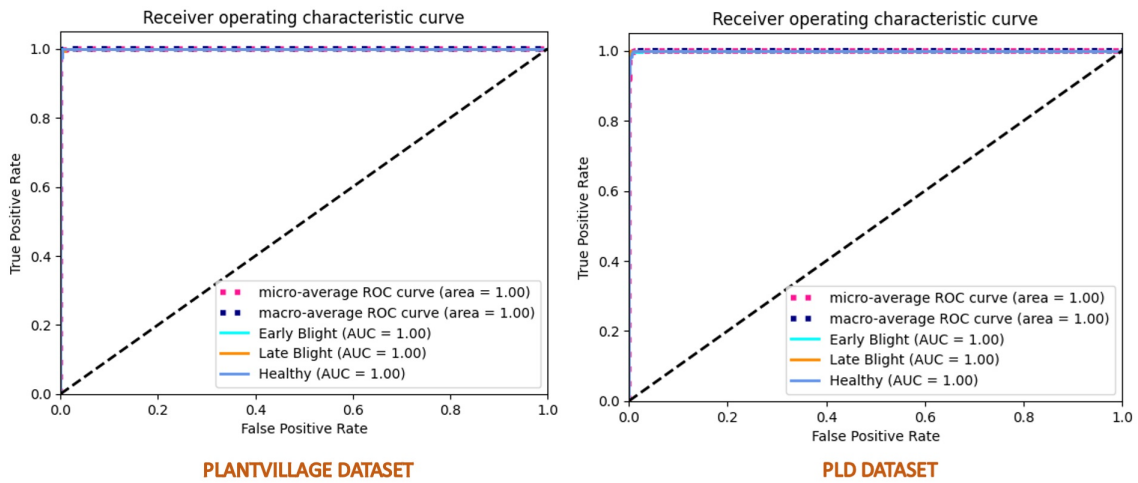


**Figure 5:** Feature extraction output of different convolution layers

The confusion matrix for both PlantVillage and PLD dataset is given in Figure 3. If we have a look at



**Figure 6:** Training validation loss of proposed methodology



**Figure 7:** Receiver Operating Characteristic curve proposed methodology

the graphs of the accuracy and loss for both the datasets PLD and PLantVillage 4, then it gives us the idea of the convergence speed of the model. The training and validation loss graph for both the datasets PlantVillage and PLD is given in Figure 6. The proposed model has outperformed the 3 transfer learning models VGG16, ResNet50 and InceptionV3 comprehensively and has achieved a test accuracy of 99.3% on PlantVillage dataset and 99.23% on the PLD dataset Table 8. The implementation process requires way less hardware because of the presence of fewer parameters unlike the deep CNN architectures Table- 6. The model also outperformed the other state-of-art models in terms of accuracy Table 8. The performance of the proposed model as compared to the other transfer learning models in terms of Precision, Recall and F1-score is given in Table 7. The two ROC curves for the two datasets PlantVillage and PLD is given in Figure 7. Thus, the model gives us an efficient way to solve the problem of potato leaf disease detection with a better accuracy than the pretrained models and less computational hazards.

#### 4. Conclusion and Future Scope

Agriculture holds the most important economical aspect of our country as majority of the common people have been heavily relied on Agriculture. Identifying illnesses that damage economically valuable

crops early on is crucial to preventing farmers from suffering financial losses related to these crops. Potato is one of the most staple crops and our experiment is based on [26] the detection of the potato leaf diseases. Our unique Convolutional Neural Network categorizes potato leaves into three groups for that purpose, blight disease namely early and late along with healthy. Due to presence of fewer layers and parameters than the other transfer learning and CNN models, it is highly efficient and resourceful in the computationally constrained environments. It achieved more than 99% precision in PlantVillage, as well as in the PLD data set.

The vision of our research is to improve the model's adaptability and resilience so that it can identify diseases in a variety of crops besides potatoes. A mobile and web application for the benefit of the farmer community and contribution to this sector overall will be developed, along with an attempt to further minimize the parameters to make the model more efficient.

## Acknowledgments

Thanks to the developers of ACM consolidated LaTeX styles <https://github.com/borisveytsman/acmart> and to the developers of Elsevier updated L<sup>A</sup>T<sub>E</sub>X templates <https://www.ctan.org/tex-archive/macros/latex/contrib/els-cas-templates>.

## Declaration on Generative AI

The author(s) have not employed any Generative AI tools.

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