

# Image Classification For Plant Disease Prediction Using Ensemble Deep Transfer Learning

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#### Abstract:

Plant diseases continue to pose a significant threat to global agriculture. Plant diseases have a serious impact on crop production and food security. Early and accurate detection of these diseases is crucial for minimizing yield losses and ensuring food security. In this study, we explore the efficacy of transfer learning, a powerful technique in deep learning, for plant disease prediction through image classification. We show that transfer learning can significantly improve the accuracy as well as efficiency of disease classification by using pre-trained convolutional neural network architectures and fine-tuning them on a variety of plant image datasets. Our experimental results show that the effectiveness of transfer learning in accurately classifying various plant diseases, thereby offering a promising solution for timely disease detection.

**Keywords:** Deep Learning, Plant diseases, Image Processing, Transfer Learning, CNN, Dense121, ResNet50, Ensemble Technique.

#### Introduction:

Agriculture plays a pivotal role in sustaining the global population. However, plant diseases pose a substantial threat to crop yields and quality. Plant diseases continue to be a major challenge in global agriculture, leading to substantial crop losses and reduced yields. Traditional methods of disease diagnosis are often time-consuming and may not yield accurate results. The impact of plant diseases on agricultural productivity underscores the need for innovative and efficient disease management strategies.

A lot of research has been done in the last decade to identify plant diseases using computer vision and deep learning. As computer vision continues to advance, many methods are also being developed to solve plant disease identification problems. (Khan et al., 2020) proposed a novel method based on an improved saliency method and deep features selection for cucumber leaf disease detection and classification involving contrast enhancement, diseased space segmentation, deep features extraction and selection and classification. Several techniques have been proposed by researchers to classify and accurately detect plant diseases. Some use conventional image processing methods that involve manual feature extraction and segmentation through hand-crafted techniques. (Poornappriya & Gopinath, 2020). In recent years, the emergence of deep learning techniques with the availability of large-scale image datasets has led to more accurate and automated disease prediction as well as the availability of GPU machines and software makes it easier to express the basic features of an image for automatic classification and feature extraction. At present, Convolution neural networks (CNNs) are capable to extract low-level complex features from images, which has attracted widespread attention. Therefore, CNN is being preferred for replacement of traditional methods to achieve better results in automated plant disease detection. (K. R. et al., 2020).

There are several open-source plant disease image datasets that are used for research and development and collection of these databases known as an electronic library of plant disease. In a study (Namdeo et al., 2021) state that scientists, researchers and faculty members use electronic databases to identify the disease of plants and other properties of plants. The brief outline of these databases is given bellow:

#### PlantVillage

It is a well-known platform for plant disease identification and research, and offer a variety of datasets and resources related to plant diseases. It is a collection of 54303 images of healthy and unhealthy leaf of plant leaves and divided into 38 classes/categories by species and disease. Datasets may include images and information on various plant species, including vegetables (Hughes & Salathe, 2015)

#### PlantDoc

This dataset has been created to visually detect plant diseases. It contains a total of 2,598 data points from 13 plant species and 17 classes of diseases. (D. Singh et al., 2020)

## Plant-Pathology-2020 dataset

This dataset contains 3651 high quality annotated RGB images displaying various apple diseases, such as cedar apple rust and apple scab, as well as images of leaves displaying complex disease symptoms and healthy apple leaves. (Thapa et al., 2020)

## VegNet

It contains a collection of 6850 images of four different vegetable crops. The dataset is organized into four main subfolders, representing bell peppers, tomatoes, chili peppers, and New Mexico chili. Within each vegetable category, there are five additional subfolders for further classification, including raw, ripe, old, dried, and damaged.

PlatVillage has used (Chen et al., 2020; Ferentinos, 2018; Sravan et al., 2021; Wang et al., 2017) and other researchers have used the well-known PlantVillage public database (collection of 54303 images of healthy and unhealthy leaf of plant leaves and divided into 38 classes/categories by species and disease) and reached high accuracy in detection to 99.7% on a held-out test set (Mohanty et al., 2016). But PlantVillage images were collected and processed under special controlled conditions, so they are synthetic and differ from real life images. If we want good result we need real life database. Although many related successful studies are known using their self-collected databases (Fuentes et al., 2017; Lu et al., 2017; R. R. & Park, 2018; Ramcharan et al., 2017) but there are no references to used databases, unfortunately. Because of most of the symptoms of plant disease can be seen on the leaves and spotted so we collect our database of vegetable plant leaves from open source images and then reduce their size and extract only the meaningful parts. Ultimately, we have a very small number of 1070 images of three vegetable plants named cauliflower, chilli and brinjal divided into nine disease categories and three categories of healthy plants. We used this database to test some models and try some new approaches.

To achieve better results in plant disease detection, deep learning methods require larger amounts of data. But we have a small database and do not contain enough images, which is a necessity for high-quality decisions. So we used the ensemble transfer learning method. Among various deep learning approaches, transfer learning has emerged as a powerful strategy to address challenges associated with limited labeled data, computational resources, and model convergence. Transfer learning has evolved as a powerful approach to leverage pre-trained models for specific tasks. Transfer learning is a method that enables the knowledge gained in one task to be transferred to another task. This method offers great potential for increasing the accuracy and efficiency of disease classification models.

In ensemble learning, multiple models are trained instead of a single model and predictions from these models are combined. This reduces the variation of predictions and reduces generalization errors. The results are predictions that it is better than any one model.

### **Related Work:**

Previous research has demonstrated the efficacy of transfer learning in various image classification tasks, including plant disease prediction. Transfer learning allows researchers to benefit from the knowledge captured by models trained on extensive datasets while fine-tuning them to specific domains. This approach has proven effective in reducing the need for massive datasets and computational resources, while still achieving competitive results.

Several studies have demonstrated the efficacy of transfer learning in the field of predicting plant diseases.(Qiang et al., 2019) analyze plant leaf diseases based on inception V3 transfer learning and fine-tuning. Their results show that the neural network can effectively differentiate crop diseases using a deep learning model based on Inception-V3.

(Goncharov et al., 2018) shows that the accuracy of neural models can be severely affected when processing real-life images if the images in the collection are synthetic in nature. They developed Deep Siamese Convolutional Network to solve the problem of small image database and achieved high accuracy. AlexNet model for fast and accurate detection of leaf diseases in maize plants. The model achieved high accuracy (99.16%) using the PlantVillage dataset.

(Vallabhajosyula et al., 2021) presents a classification of pre-trained neural networks and a weighted ensemble for plant leaf disease detection, showing that DENN outperforms state-of-the-art models and effectively classifies plant diseases. The development of a plant disease detection system employing ensemble learning techniques. Their system consists of six base models and their performance has been evaluated on a substantial dataset of 87,000 images. Their study highlights the effectiveness of ensemble learning in the context of plant disease detection, resulting in a highly accurate and robust system for identifying diseased plants in images.

(Acharya et al., 2020) discussed the application of Convolutional Neural Networks (CNNs) in an ensemble fashion for detecting plant diseases in paddy crops. They created five pre-trained convolutional neural network (CNN) architectures GoogleNet, ResNet, ShuffleNet, ResNext and Wide ResNet with different weights to detect three rice leaf diseases like blast, bacterial leaf blight and brownspot. Their results showed that when models were compared, the combination model achieved greater accuracy than individual architectures in detecting disease from crop leaves. (Saleem et al., 2019) performed a review and offered an in-depth examination of deep learning models applied to visualize various plant diseases. Additionally, his research points to specific areas of investigation to increase the transparency of detecting plant diseases before symptoms become apparent.

(Sagar & Jacob, 2020) has shown how deep neural networks can be used for plant disease identification in the context of image classification. Their research involved a comparison of five different architectures, namely VGG16, ResNet50, InceptionV3, InceptionResNet and DenseNet169, with the best results obtained from the ResNet50 model.

#### Materials and Methods:

Predicting plant diseases through deep transfer learning involves using pre-trained deep learning models and fine-tuning them to detect disease in plants. Here's a step-by-step methodology for building a plant disease prediction system using deep transfer learning:

**Dataset:** In this experiment, we have selected three vegetable plants viz. Cauliflower, Chilli and Eggplant. We collected our database of vegetable plant leaves from PlantVillage dataset and also downloaded images from Google Images using the internet. The dataset contains 280 images of cauliflower diseases such as Bacterial Spot Rot disease, Black Rot disease, Downy Mildew disease and 50 images of healthy cauliflower plants. Similarly the dataset includes 300 images of chilli diseases like Leaf Curl, Leaf Spot, Chilli Yellowish and 100 images of healthy plants and 240 images of Eggplant diseases like Cercospora Leaf Spot, Tobacco Mosaic Virus, Verticillium Wilt disease and contains 100 images of healthy plants. Thus, the dataset contains 1070 images, including nine categories of diseases and three categories of healthy. Following figure shows some samples from dataset.



**Image Pre-processing and Augmentation:** In the fields of computer vision and image analysis, image pre-processing and enhancement are essential techniques. These techniques are used to improve the quality of images, enhance the performance of machine learning models, and ensure robustness in various applications such as object detection and image classification.

**Image Pre-processing:** Image pre-processing involves a series of operations performed on raw or unprocessed images to make them suitable for analysis and model training. The key objectives of image pre-processing are:

**Normalization:** In this process, we re-scaled the pixel values of each image to a range of 0-1 to make the images more consistent for model training by reducing the effect of varying brightness and contrast levels.

**Resizing:** In the collected dataset, all images have RGB coefficients in the range 0-255. It is necessary to resize images to a normal size for training a neural network. This ensures that the model can consistently process images of similar dimensions. So we resized all images into the shape of 224x224x3 pixels.

**Image Augmentation:** Image augmentation involves creating new training examples by applying various transformations to existing images. This technique is especially useful when working with limited datasets, as it artificially increases the diversity of data available for model training. Image augmentation techniques, including random rotation, horizontal flipping, and random cropping, were applied to augment the training dataset, improve the model's generalization ability and reduce overfitting. In our study we implemented image augmentation techniques using the Keras deep learning library in Python. Specifically, for general category images, we applied both horizontal and vertical flipping operations. Additionally, we set the image random rotation value to 0.2 degrees.

#### Method:

We adopt a two-step transfer learning approach. First, we initialize our model with pre-trained weights from wellestablished convolutional neural network architectures, such as DenseNet121 and ResNet50. These architectures have demonstrated exceptional performance on general image classification tasks. Next, we fine-tune the model on our plant disease dataset. This involves training the final layers while retaining the learned representations from the pre-trained layers. The ensemble model aggregates the predictions of these models to make the final decision, resulting in enhanced classification accuracy and improved overall performance.

## 4. Model building:

## 4.1. CNN without transfer learning:

It is a basic Convolutional Neural Network (CNN) designed for multi-class classification, with some hyper parameters fine-tuned to enhance its performance. CNNs are constructed from three basic types of layers: convolutional layers, pooling layers, and fully connected (FC) layers. These layers are combined (stacked) to form the overall CNN architecture. Additionally, two other important components are the dropout layer and the activation function.

Our CNN model comprises a total of twenty layers. These include four convolution layers, four max pooling layers, three batch normalization layers, three dropout layers, and three fully connected layers followed by the output layer. The input images are standardized to a size of 224x224x3. The schematic representation of the model used in our proposed system is depicted in the figure below-



Figure-The architecture of custom CNN model

**Convolutional layer:** A convolutional layer is a fundamental building block in a convolutional neural network (CNN). It serves as the initial layer that is responsible for extracting diverse features from the input images using filters with adaptively learned parameters (weights). The mathematical operation of convolution is the main operation in this layer, which consists of the input image and a filter of a specific size, often denoted as MxM. The process of convolution occurs by systematically sliding a filter over the input image. In each case, a dot product is calculated between the filter and the corresponding part of the input image, with dimensions defined by the size of the filter (MxM). This operation helps to identify and highlight specific patterns and features in the input data, which become important for subsequent layers in the CNN to learn hierarchical representations.

Activation function: The activation function is one of the most important parameters of a CNN model. They introduce non-linearity into the model, allowing it to learn and predict complex, non-linear relationships within the data. These functions determine what information should be activated (i.e., allowed to pass through the network) and what information should be suppressed. Activation functions such as ReLU, Softmax, tanH, and sigmoid serve different purposes and are used in different parts of neural networks depending on the specific requirements of the task and network architecture.

Here we have used ReLU(Rectified Linear Unit) function. ReLU is the widely used activation function in Convolutional Neural Networks (CNNs) & Multilayer perceptrons. It introduces non-linearity by setting all negative values to zero, allowing positive values to pass through. This helps mitigate the vanishing gradient problem and accelerates training.

**Pooling Layer:** The pooling layer, also known as the pooling operation, is a key component in Convolutional Neural Networks (CNN). Pooling in Convolutional Neural Networks (CNN) is a form of down-sampling that reduces the spatial dimension (width and height) of a feature map while maintaining important information. Pooling layers help reduce the computational complexity of the network, make it more robust to translations and distortions in the input, and capture the most important information in the feature map. Two common types of pooling operations used in CNN are Max Pooling and Average Pooling.

The most common type of pooling layer is Max pooling. Here we have used (2x2) Max Pooling layer. It operates by taking the maximum value from a small window (usually 2x2 or 3x3) and moving it across the input feature map. At each position of the window, the maximum value is selected and forms the output of that window. Max pooling effectively preserves the most prominent features in each region and reduces the spatial resolution. It is less sensitive to small spatial translations in the input.

**Batch Normalization:** Batch normalization (BatchNorm) is a technique commonly used in Convolutional Neural Networks (CNNs) and other deep learning architectures to improve training stability and speed up convergence. It was introduced by Sergey Ioffe and Christian Szegedy in their 2015 paper titled "Batch Normalization: Accelerating Deep Network Training by Reducing Internal Covariate Shift."

During the training phase, for each mini-batch of data that is passed through the network, batch normalization normalizes the activations of each layer. The normalization is done per feature map (channel) independently. For each channel, it calculates the mean and standard deviation across the mini-batch and then scales and shifts the activations

using learned parameters (gamma and beta) so that they have a mean close to zero and a standard deviation close to one. This helps in reducing internal covariate shift, which is the change in the distribution of activations that occurs as the network trains.

$$z^{N} = \frac{z - m_{z}}{s_{z}}$$

here  $m_z$  = mean of the neurons' output and  $s_z$  = standard deviation of the neurons' output.

**Dropout:** A dropout layer is a regularization technique frequently employed in Convolutional Neural Networks (CNNs) and various deep learning structures. Its primary purpose is to mitigate overfitting and enhance the network's ability to generalize effectively. It was introduced by Geoffrey Hinton and his colleagues in 2012.

Throughout the training process, as the network undergoes each forward pass, the dropout layer randomly sets a fraction of the neurons (units) in the preceding layer to zero. This fraction is typically defined by a dropout rate, a hyperparameter commonly chosen within the range of 0.2 to 0.5. The dropout rate signifies the likelihood of a neuron being "dropped out" or rendered inactive.

We have used dropout regularization technique to drop out randomly selected nodes with probability of 0.2 in our model.

Similarly in our model the flattening layer is used to convert the data into a single dimensional array which is used as input to the fully connected layer. The image classification model comprises three sets of fully connected layers, with 128, 64, and 12 neurons, responsible for categorizing images into distinct classes. In the final fully connected layer, we've applied a softmax activation function. This function yields probabilities for each class, with the target class being the one associated with the highest probability.

**Transfer Learning in Image Classification**: Transfer learning in image classification is a machine learning technique that leverages pre-trained neural network models to improve the performance of image classification tasks. Transfer learning uses neural network models pre-trained on large and diverse datasets such as ImageNet. These models have learned to extract meaningful features from images through extensive training. By fine-tuning these pre-trained models to specific tasks with small datasets, training time and resource requirements can be significantly reduced.

The proposed ensemble learning approach integrates two deep learning models: DenseNet121 and ResNet50. These models were pre-trained on the ImageNet dataset to leverage their learned feature representations and then fine-tuned using the vegetable plant disease dataset. Predictions from these base models were aggregated using the ensemble model weighted average method to make the final decision. During the training process, we applied overfitting mitigation techniques such as dropout and batch normalization. The evaluation compared the performance of individual base models and ensemble models, which would demonstrate the superiority of the ensemble learning approach for plant leaf disease detection.

Ensembling the pre trained Deep learning models:

Ensemble learning in Convolutional Neural Networks (CNNs) is a technique that combines multiple CNN models to improve the overall performance, robustness, and generalization of a machine learning system. Ensemble methods leverage the idea that multiple diverse models, when combined, can often outperform a single model. ensemble learning method has four main classes such as Bagging (Bootstrap Aggregating), Boosting, Stacking and Random Forest



An Ensemble Convolutional Neural Network with a weighted average ensemble combines the predictions of multiple individual CNN models using weighted averaging. Each individual CNN model has its own set of weights, and these weights are used to assign different levels of importance to each model's prediction. Here's an equation that represents this ensemble:

Let's say we have N individual CNN models, and for each model i (where i ranges from 1 to N), the prediction is denoted as P\_i. Additionally, we have a set of weights w\_i (where i ranges from 1 to N) that determine the importance of each model's prediction. The weighted average ensemble prediction P\_ensemble is calculated as follows:

Ν

$$P_{ensemble} = \sum wi \cdot Pi$$
  
 $i=1$ 

Where:

Pensemble is the final prediction of the ensemble.

*wi* is the weight assigned to the prediction of model i. These weights should satisfy the condition that  $\sum_{i=1}^{N} w_{i=1}^{N}$ , meaning that the weights should sum up to 1 to ensure that the ensemble predictions are properly weighted. We calculated the predictions of each individual CNN model, assigned weights, and then calculated the weighted average to obtain the final predicted prediction.

## **Experimental Setup:**

We conducted experiments on a computing platform equipped with an appropriate GPU runtime specified by Google Colaboratory for accelerated training. The code was Implemented using Python and deep learning libraries like TensorFlow and Keras. The dataset is divided into training, validation and testing sets to assess the performance of the model. Hyperparameters including learning rate and batch size and dropout rates are fine-tuned using grid search and cross-validation.

### **Results and Discussions:**

We combined a custom CNN model and DenseNet121 and ResNet50 models for plant leaf disease detection in our proposed ensemble model. During testing, the ensemble model achieved 90.63% accuracy, while the individual DenseNet121, ResNet50 and custom CNN models achieved 96.09%, 91.41% and 91.41% accuracy, respectively. This significant improvement in accuracy clearly reflects the synergistic effect of combining the powers of DenseNet121, ResNet50 and the custom CNN architecture, enabling the model to leverage diverse feature representations and multi-scale feature extraction capabilities to make more accurate predictions. The holistic approach effectively reduces bias and variation, leading to better generalization and overall performance.

To further highlight the superiority of our ensemble model, we conducted a comparative analysis with other individual models widely used in plant leaf disease detection. The table below summarizes the results:

Table - Comparison of Different Models			
Model Name	<b>Training Accuracy</b>	Validation Accuracy	Test Accuracy
Weighted Ensemble Model	99.43	96.88	93.75
Ensemble Model	99.43	95.83	90.63
Multi Class CNN	99.21	96.88	91.41
DenseNet121	99.89	98.96	96.09
ResNet50	99.77	97.92	91.41



**Limitations and Future Work:** While the proposed model shows promising results, its performance can be further enhanced by considering techniques such as transfer learning and ensemble methods. Additionally, efforts to collect larger and more diverse datasets can help address class imbalance issues and improve the model's generalization.

**Conclusion:** The proposed model of plant disease prediction using ensemble deep transfer learning represents a significant advancement in the field of agricultural technology and disease management. This model harnesses the power of deep learning, transfer learning, and ensemble techniques to enhance the accuracy, robustness, and practicality of plant disease prediction. The ensemble deep transfer learning model combines the strengths of multiple pre-trained neural networks, enabling it to extract intricate features from plant images and achieve higher prediction accuracy compared to individual models. Leveraging transfer learning, the model benefits from the knowledge and feature representations learned by deep neural networks on large-scale image datasets, making it more adaptable to plant disease prediction tasks. Ensemble methods reduce overfitting and improve the model's ability to generalize to diverse and dynamic real-world conditions. This robustness is crucial for accurate predictions in the presence of variations in disease symptoms and environmental factors. The successful implementation of this model can significantly impact global

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