

Classifying Corn Leaf Diseases using Ensemble Learning with Dropout and Stochastic Depth Based Convolutional Networks

Crop yields are severely impacted by a wide range of plant diseases, and if these diseases aren't detected in time, they can quickly spread and significantly reduce harvests. In our work, we looked into how deep learning works and made a convolutional ensemble network to help the model find corn lesion features better. To better recognize plant disease categories, we employed ensemble learning to combine three lightweight CNNs (Custom CNN with dropout, Custom CNN with Stochastic Depth, and DenseNet201) into a single network (Proposed Method). Model training embraced transfer learning and a two-step approach, with the initial stage involving the network weights. Using the weights learned in the first phase of training, the network was retrained in the second using the target dataset to obtain the best possible model parameters. On the local dataset, the proposed technique averaged 98.36% accuracy. The experimental results validate the suggested approach and show that it outperforms the current state of the art.

CCS Concepts: • **Computer systems organization** → **Embedded systems**; *Redundancy*; Robotics; • **Networks** → Network reliability.

Additional Key Words and Phrases: corn leaf disease, neural networks, ensemble learning, convolution

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1 INTRODUCTION

In order to feed the world's projected 9 billion residents by 2050, as stated in the 2020 World Population Data Sheet, farmers would need to maximize agricultural yields while reducing the impact of plant diseases via early diagnosis. As a consequence, there has been a lot of interest in the latest research on plant disease identification as it relates to food security. Numerous plant diseases pose severe risks to agricultural output, with some more pernicious ones rendering whole harvests impossible. Damage from plant diseases has been on the rise for a while now, and it's disturbing how quickly that's happened because of fundamental changes in how crop cultivation is conducted and the influence of hazardous organisms. The early detection and identification of plant diseases plays a crucial role in preventing their spread [2]. The majority of plant disease diagnosis methods, however, still rely on human specialists' visual observations. However, it's not always easy to get in touch with specialists in plant diseases. In most cases, farmers have to travel a significant distance to see a plant protection specialist, which adds both time and money to the consultation process. The development of pattern recognition and machine learning (ML) methods over the last several decades has created a new method for diagnosing plant diseases. In most cases, a dedicated classifier is used to identify plant illnesses, which sorts photos of plants into healthy and unhealthy categories.

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2 RELATED WORKS

In this analysis, we compare and contrast previous efforts on automated plants and on the classification of corn diseases. Some popular ML(Machine Learning) and DL(Deep Learning) approaches are investigated because they are very effective at accomplishing similar goals. These algorithms are a great tool in feature extraction and categorization, and would definitely be useful in agriculture as well due to the adaptable framework they give for making automated expert judgements.

The authors of the study [12] report that their suggested CNN model, TLNet, which employs normalization, augmentation, and class label encoding on a dataset of 11800 pictures, achieved 98.77% accuracy on seven classes of tomato leaf diseases. The CNN model used in the study reported in paper [1] achieves a 97.40% success rate in identifying rice leaf illnesses using K-fold cross validation. There are 900 photos in their dataset. The authors of study [3] used Haralick's method to extract characteristics and then classified them using logistic regression. Using these two techniques on a Kaggle dataset consisting of 14,000 images, they were able to reach an accuracy of 67.3%. Additionally, SVM was used to get 87.6% accuracy and Random Forest was utilized to get 70.05% accuracy. Using a decision tree approach on a dataset of 1000 photos (254 x 254 pixels) from kaggle.com, the authors of study [17] proposed an accuracy of 95% in recognizing four diseases across five different types of leaves. In [13] and [16], SVM was used for the detection of vine leaf illnesses and bacterial genome associations. In [6] and [21], SVM was utilized for the detection of citrus greening in lemon plants. Through the use of SVM in [14], researchers were able to detect yellow leaves and leaf curls on tomatoes with an accuracy of 90%.

A lightweight CNN model using serially decreasing dense layers in the fully connected classifying block is suggested by Mondal and Islam et al. [15]. The accuracy of their model, which has a lot fewer parameters than other ones already in use, is 98.18% in various plant leaf disease classification. Another lightweight model proposed by Islam et al. [9], use serially increasing number of nodes in convolutional layers having batch normalization and max pooling after each convolution layer. They have utilized monte carlo dropout for finding uncertain samples from the predictions. Our proposed CNN architecture style is inspired by [9, 15] for achieving our goal of an efficient lightweight architecture. High-parameter convolutional Neural Networks (CNNs) for identifying plant leaf diseases were demonstrated by the authors of [19] and [4] utilizing a variety of datasets. Each plant also has its own unique set of convolution and pooling layers employed. Many DL (Deep Learning)-related research publications are analyzed in [10]. After studying these methods, they attempted to solve a number of agricultural issues. Stochastic Pooling, Batch Normalization, Dropout, and a 14-layer convolutional Neural Network were used by the authors of [20] to achieve an astounding 98.77% accuracy in detecting cerebral Sclerosis. The feature layers in DenseNet [8] are fed all the features taken from their preceding layers are delivered to all future layers as feature maps., revealing the current state-of-the-art in feature extraction. Here, the interdependencies between channels are not taken into account since each layer simply joins feature maps acquired in earlier levels without taking into account the channel connection features. Lightweight network studies and deployments have attracted a lot of interest in recent years. MobileNet is a DWSC-based lightweight network design that has shown success in dealing with issues of varying sizes [18]. A better version of MobileNet was achieved by including the SE block into the original concept. The ultimate accuracy of a data-augmented 13-layer convolutional neural network (CNN) for categorizing fruits using momentum-based stochastic gradient descent was 94.94%, according to another research [22]. The authors of these publications [11] [7] employed deep CNNs to diagnose

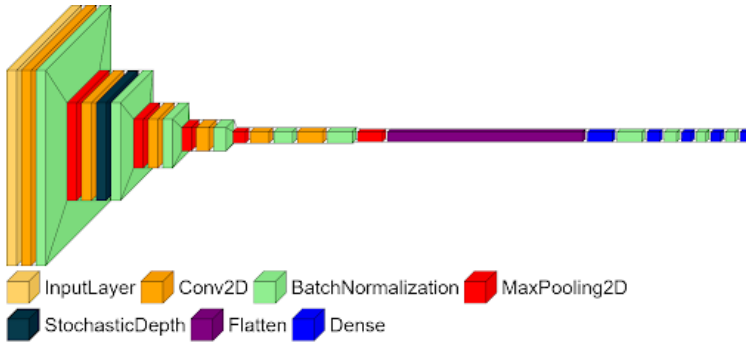


Fig. 1. Custom CNN with Stochastic Depth Model

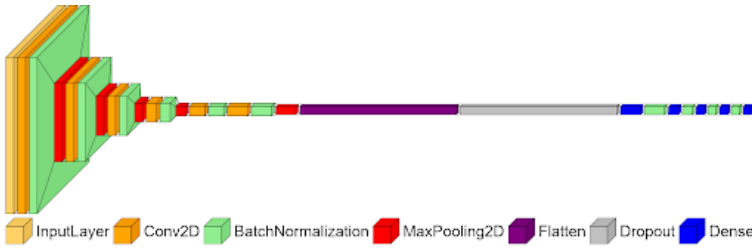


Fig. 2. Custom CNN with Dropout Model

a wide variety of plant illnesses; the technique may also be used to pest identification, as in [5] for tomatoes. The multi-temporal crop identification accuracy achieved in [23] was 85.54%.

3 METHODOLOGY

3.1 Pre-Trained

The forward connections between each layer are fed by the Dense Convolutional Network (DenseNet). They significantly reduce the number of parameters, improve feature propagation, promote feature reuse, and eliminate the problem of disappearing gradients. DenseNet is predicated on the assumption that convolutional networks can be taught to be substantially deeper, more accurate, and more efficient if the links between the layers near the input and the layers near the output are shorter.

3.2 Proposed Architecture

3.2.1 Custom CNN with Stochastic Depth. In this model we used Stochastic layer, which works in such a way that if a block survives with a certain probability then the result is kept, otherwise the block is skipped or avoided to carry further information.

3.2.2 Custom CNN with Dropout. First this model contains an input layer, then we have in total six 2D Convolutional Layers for extracting information from the image. Moreover, this model also has six Batch Normalization layers for normalizing the data. To complete our model we got 5 2D Max Pooling layers which helps to reduce the computational power. Then it contains a Flatten layer to convert our data to 1 dimensional. Dropout of 30% is used after the flatten layer. Finally Dense layers are used and the final dense layer contains 4 nodes as we have 4 classes to identify from our dataset.



Fig. 3. Sample images from dataset

3.3 Stacked Ensemble Procedure

Model Averaging: To obtain a more accurate result, many models' forecasts are integrated. The forecast of the different models are combined. This might also be viewed as a flaw in the model as there may be instances where one model outperforms the other while receiving equal weight. Each model has weights set in order to address this issue. Each model is given a weight, and the model with the better performance is given more weight than the model with the worse performance. The forecast is then finalized after calculating a weighted average.

3.4 Dataset

We utilized the freely accessible PlantVillage dataset. It comprises 38 different classes in all, but we only used the ones that pertain to corn. There are a total of four classes featuring both healthy and malignant photos. The three diseased classes are Corn Cercospora Leaf spot Gray leaf spot, Corn Common Rust, and Corn Northern Leaf Blight, while the Corn healthy class contains only photographs of healthy corn. When we combine all four classes, there are a total of 4354 photos. However, all of these photos were randomly divided into training, validation, and testing sets containing 3,498 images, 428 images, and 428 images, respectively, as depicted in figure 2. The distribution of photos for each class in the training, validation, and testing set is displayed in Table 1. Figure 1 illustrates two images for each class in our dataset.

4 EXPERIMENTAL ANALYSIS

We performed the studies mostly with Python 3.8. For algorithm execution, Tensorflow, and Keras libraries are applied. The hardware configuration consists of an Intel® i5 7500 processor, 24G of memory, and a GeForce RTX 3060 graphics processing unit.

4.1 Experiment on the Corn Images from Plant Village Dataset

All our models used in this research were trained with Corn images from the Plant Village dataset. We divided our dataset into 3 sets as follows Training, Validation and Testing set. All the images were randomly assigned to those sets. 80% of images were in Training and other images were equally distributed to Validation and Testing set. Specifically, to study further the effectiveness of the suggested approach we considered popular DenseNet201 and two custom model one with Dropout and another with Stochastic Depth based Convolutional Networks. We also compared it

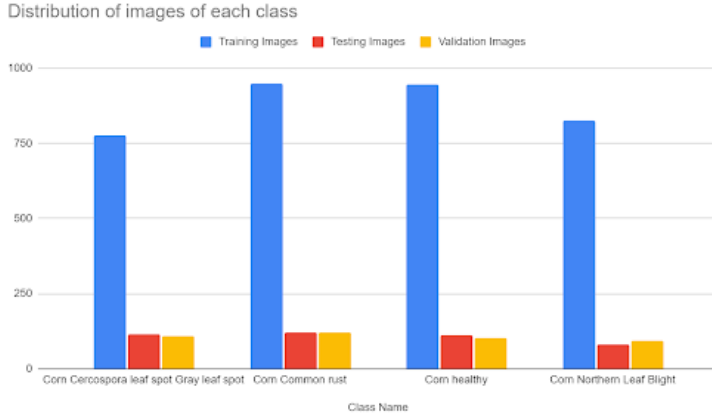


Fig. 4. Distribution of images each class

with other pretrained models like VGG16, InceptionV3 and ResNet50.

The findings generated by these CNN models were subjected to a comprehensive examination, and the efficacy of the corn disease detection model was evaluated using the individually produced metrics Accuracy, Recall, F1-Score, and Precision.

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

$$Recall = \frac{TP}{TP + FN} \quad (2)$$

$$F1 - Score = \frac{2 \times Recall \times Precision}{Recall + Precision} \quad (3)$$

$$Precision = \frac{TP}{TP + FP} \quad (4)$$

Here, TP (true positive) reflects the amount of properly identified crop images for each disease or healthy class, TN (true negative) symbolizes the sum of successfully predicted crop samples for all other forms excluding the related ones, FP (false positive) indicates the number of specimen that does not belong to the class but were incorrectly classified as such, and FN (false negative) signifies the number of incorrectly identified samples. Table 1 demonstrates the Testing accuracy and metrics of all models compared to our own suggested model.

As demonstrated in table 1, our suggested model has produced a better performance improvement over existing state-of-the-art techniques. After just 30 epochs of training, the training and validation accuracy have reached 99.57 and 98.32 percent, respectively, and our proposed model has also obtained the greatest testing accuracy of 98.36 percent. Integrating the benefits of several networks using stacking-based convolutional ensemble learning and averaging the output of all three models, which improves the feature extraction of plant lesion symptoms, is the primary reason for the proposed method's impressive performance. In addition, the method of training in two-stage enable the proposed model to gain ideal weight parameters, so assisting the model in

Table 1. Comparison of testing Accuracy & Metrics

NAME	TESTING	LOSS	PRECISION	RECALL	F1
VGG16	90.89	0.238	92.12	90.03	91.06
ResNet50	74.77	0.6053	76.57	70.24	73.27
Inception V3	88.32	0.3251	90.38	87.13	88.73
DENSENET 201	94.39	0.245	94.27	94.27	94.27
Custom CNN	95.79	0.1441	95.98	95.98	95.98
CUSTOM CNN STOCHASTIC	94.86	0.1323	94.94	94.72	94.83
ENSEMBLE	98.36	0.0701	98.44	98.44	98.44

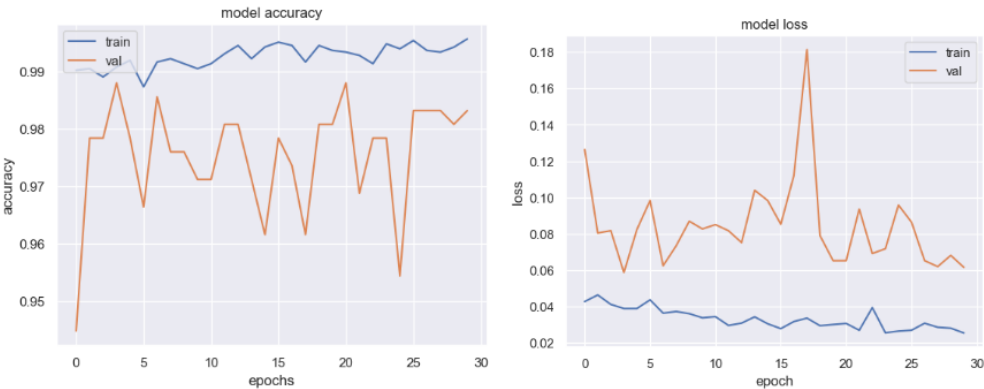


Fig. 5. Accuracy and Loss Comparison of Proposed Ensemble Model

achieving satisfactory outcomes.

5 CONCLUSION

Identification of agricultural diseases in a timely and precise manner is crucial for guaranteeing a high crop yield. A practical, easy-to-use, and rapid instrument for automatically recognizing various Plant diseases have a huge demand and play an important role in practical scenarios. In this research, a deep convolutional neural ensemble learning approach for identifying crop disease kinds is suggested.Using a stacking technique, two lightweight networks, including a custom CNN model with dropout and a custom CNN model with stochastic depth, are involved, with the well-known DenseNet201 serving as the third model. These three models were used to construct a new convolutional ensemble network as the backbone extractor. In the first phase, the network weights were initiated by training just the weights on the newly increased layers and the parameter of the bottom convolutional layers were frozen. In the second phase, using the targetted dataset our model retrained the network by the weights from the first step. Moreover, the optimal weight parameters for the ensemble convolutional network were obtained and averaged. On our dataset, experimental results demonstrate that the suggested approach for crop disease identification is highly effective. In the future, rather than focusing on a single plant, we will collect a larger spectrum of plant disease

images under live on-field environmental conditions in order to quickly identify the broad spectrum of plant disease images. In addition, we wish to expand the methodology to other important fields, such as online flaw identification, computer-assisted evaluation, etc.

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