Improved AlexNet with Inception-V4 for Plant Disease Diagnosis

Zhuoxin Li, Cong Li, Linfan Deng, Yanzhou Fan, Xianyin Xiao, Huiying Ma, Juan Qin, and Liangliang Zhu

School of Integrated Circuit Science and Engineering, Tianjin University of Technology, Tianjin 300384, China

Correspondence should be addressed to Juan Qin; jane.qin@tjut.edu.cn

Received 12 May 2022; Revised 19 July 2022; Accepted 21 July 2022; Published 10 September 2022

1. Introduction

Crop pests and diseases refer to the destruction of normal physiological functions of crops, which can be caused by the invasion of other creatures or environmental changes. As one of the major agricultural disasters, they are characterized by numerous species, high impact, and frequent outbreaks. Crop pests and disease identification are challenging due to the variety of types, the scarcity of technicians in rural areas, and the overreliance on insecticides. Traditional manual pest and disease monitoring rely on observation experience, which inevitably suffers subjectivity and inefficiency. Thus, automatic plant disease detection and control have been the primary concern of each country, especially in recent years, when due to the population increase, food demand is growing at a faster rate [1]. Therefore, it is of great significance to effectively analyze crop pests and diseases and ensure the use of pesticides. Motivated by a great advance in artificial intelligence, crop disease identification also can be conducted using deep learning models [2].

This paper exploits the deep learning model for plant disease recognition, motivated by the great success of deep learning techniques in other applications. The contribution of the research is summarized as follows:

(1) A large convolution kernel is used to obtain a large receptive field, enabling the model to focus more on shape than texture. Also, thanks to the employed large kernel, the depth of the model can be compact, which avoids the high computational complexity of the optimization process.

(2) Two complementary network structures, Inception-V4 and AlexNet, are combined to take advantage of both networks. The superposition of Inception-X (X represents A, B, C) modules in Inception-V4 is removed, which greatly reduces training and inference time with a sacrifice of negligible performance.

(3) The dataset is expanded to improve the generalization ability of the model.

The remaining paper consists of the following parts. Section 2 discusses the current status and limitations of existing research. Section 3 describes the experimental dataset, and Section 4 describes the proposed network structure, including the loss function and optimizer. Section 5 presents the experimental results and the analysis, verifying the feasibility of the proposed method. Lastly, this paper is concluded in Section 6.
2. Related Works

Multiple plant disease identification has been actively studied, including cassava, guava, and soybeans. Almadhor et al. [3] proposed an AI-based detection framework to classify the common guava fruit diseases. Alli et al. [4] proposed a deep residual convolutional neural network (DRNN) employing different block processing, where the unbalanced dataset was balanced, and gamma correction and decorrelation stretching were used to enhance the color separation of images with significant interband correlations. The DRNN outperformed the plain convolutional neural network (PCNN) on the cassava disease dataset from Kaggle [4]. The modified MobileNetV2 [5] showed a significant improvement in cassava leaf disease recognition on lower-quality images. Ozguven and Adem [6] proposed to detect the disease area of sugar beet leaf via adjusting Region-CNN (R–CNN), which was limited to a small number of sample images.

With the development of smart agriculture, more and more scholars have begun to study the identification of different diseases in different crops. The following papers conducted experiments for crop identification, including apples, corn, and tomatoes.

Srdjan et al. proposed a plant diseases detection model based on the CaffeNet model to identify 13 different types of sick leaves and distinguishing leaves from their surroundings [7]. Mohanty et al. evaluated the applicability of AlexNet and GoogLeNet in a one-leaf multimage problem [8], where the plant disease diagnosis system on mobile devices was developed and analyzed on the PlantVillage dataset. Gee-tharamani and Arun Pandian proposed a nine-layer DCNN for disease identification [9]. In [10], Triki et al. proposed a leaf detection and segmentation model, deep leaf, which was based on Mask-RCNN and used morphological characteristics in plant specimens. Liu et al. applied a long short-term memory network-based variational autoencoder to extract the sequential feature of the application running time [11]. Rao et al. used bilinear convolutional neural networks (bi-CNNs) for identifying different types of leaves, where VGG and ResNet were used as feature extractors [12]. Dyrmann et al. constructed a convolutional neural network (CNN) to distinguish seedlings in different stages of growth. However, due to the small number of data samples, the network suffered from low classification accuracy [13]. Ferreira et al. proposed a detection model and constructed a dataset for weed detection in soybean crops [14]. Ghazi et al. applied a pretrained AlexNet, GoogLeNet, and VGGNet to classify plant species in a dataset of given unconstrained photos, showing that the primary factor that affects the performance of fine-tuning was the iterations number [15]. Liu et al. proposed an end-to-end pest detection network, PestNet, where the Channel–Spatial Attention module was used to extract high-quality features for large-scale diseases [16]. Chao et al. proposed XDNet based on deep separable convolution and dense connection structure to identify apple leaf disease [17]. The XDNet used normalization and data enhancement to avoid overfitting and improve the stability of the network. Valeria et al. assessed the classification accuracy of tomato plant diseases based on AlexNet, GoogleNet, Inception V3, ResNet18, and ResNet 50 [18]. The results showed that GoogleNet is superior to other architectures in terms of accuracy, and AlexNet is the fastest model. Guo et al. proposed a plant disease detection and recognition model based on the RPN algorithm containing the feature of symptoms through the Chan–Vese (CV) algorithm [19].

Many studies have been conducted to improve recognition accuracy by optimizing the structure of deep learning networks, including batch normalization, dropout, and replacement of fully connected layers with pooling layers. Table 1 shows the summary of related studies with highlights of the proposed methods for data augmentation and classification. Some shortfalls of the existing plant disease classification models include data scarcity and class. Also, many works were focused on the efficient structure while avoiding overfitting, including dataset augmentation with mirroring, rotation, and additive noise. Among many deep learning models, AlexNet is one of the widely used models, mainly due to its simplicity, to identify defects of various crops and judge the speed of the germination process. The AlexNet network model is also widely used in agriculture, medicine, and power engineering fields.

Three types of convolution kernels are used in the Inception-V4 model: $7 \times 7$, $5 \times 5$, and $3 \times 3$. In this paper, a larger convolution kernel is used instead of increasing the depth of the network for more features. Also, in order to further reduce the depth of the network, this paper removes the superposition of Inception-X (X represents A, B, and C) modules in Inception-V4. Accordingly, the depth of the network is greatly reduced, shortening the training time as a consequence.

For the two reasons above, this paper combines two networks: AlexNet and Inception-V4, to identify diseases in corn, tomato, grape, and apple crops. Specifically, healthy, CercosporaGrayspot, Commonrust and NorthernBlight in corn, healthy, Bacterialspot, Lateblight and Septorialspot in tomato, Blackrot, healthy, Blackrot, sariopsisSpot and Measles in grape, healthy, Blackrot, Cedarrust and scab in apple. Experiments on the PlantVillage dataset show that the proposed model outperforms four compared networks in terms of identification accuracy. Further, the dataset is expanded to improve the generalization ability of the model to avoid overfitting caused by the small number of training samples, which is especially of significance in plant disease identification.

3. Dataset Processing

3.1. Dataset. The PlantVillage Project (https://www.plantvillage.org) is an open-source website for users that addresses all plant diseases [20]. This dataset includes 61,486 images with 39 different categories of plant leaves. In the study, four plant leaves from the PlantVillage dataset are selected as experimental subjects. In order to make the experimental data more universal, the images of plant diseases such as leaf curling, mutilation, and wilting were not discarded. Sixteen diseased and healthy samples of four plants are represented, as shown in Figure 1.
In the dataset, there are 16 types of diseased and healthy plants. The images are divided into training and test sets in an 8:2 ratios, whose detailed descriptions are given in Table 2.

### 3.2. Dataset Augmentation

The original data from PlantVillage consists of a total of 21,035 images, which is an insufficient amount to train plant leaf diseases without overfitting when considering the number of diseases. For a richer and more generalized dataset, the original dataset was augmented via the affine transformation, superimposed Gaussian noise, and vertical flip [17], as shown in Figure 2.

In this study, each image was rotated 30 degrees counterclockwise and 1.2 times enlarged with an affine transformation. Also, the Gaussian noise (mean = 0, variance = 0.025) was added to the input images, which ensured that the brightness of the image remained unchanged during the shooting process, and the Gaussian noise of the image effectively simulated the noise interference phenomenon in the actual shooting process. Gaussian noise superimposed can reduce the dependence on certain properties and improve the robustness of the model [21]. Furthermore, a vertical flipping was randomly applied for each image. With these data augmentations, the final 168,280 images were obtained. Table 3 summarizes the quantity of the dataset after each data augmentation process.

### 3.3. Preprocessing

Preprocessing plays a great role in correct classification. First, all images in the dataset are resized to 227 × 227, normalized into the range of [0, 1], and finally standardized based on the arithmetical average (avg) and the standard deviation (std), as follows:

\[
\text{Standardized Image} = \frac{\text{image} - \text{avg}}{\text{std}} \tag{1}
\]

The preprocessed image has pixel values ranging from −1 to 1. Normalization and standardization reduce the adverse effects caused by singular sample data.
4. Network Structure

4.1. CNN. CNN has been the most popular deep learning network structure in the image recognition field. The classical networks include AlexNet, VGGNet, and GoogleNet. The advent of AlexNet opened the door to deep learning research, which was the basis of many subsequent deep learning models. The innovation of AlexNet was the employment of the nonlinear unsaturated function, ReLU, instead of the original Softmax function. Local response normalization (LRN) was also used to improve accuracy and generalization capability. Furthermore, a smaller stride was used than the polling size, which improved feature richness and minimized information loss since the outputs of the pooling layers overlapped and covered each other [22]. The first layer of AlexNet uses a large convolution kernel to better extract global information such as location. The front layer is large enough to get a larger receptive field and provide more information for the later layers. Due to a large amount of information, feature mapping and the pixel-by-pixel classifier can be closely connected, thereby enhancing the ability to deal with different transformations [23]. Although the AlexNet has large convolution kernels and deepens the depth of the network, it raises the risk of gradient disappearance and has low accuracy.

GoogleNet introduced the concept of the Inception structure. The GoogleNet proposed a local network structure (Inception module) with strong expressiveness but small computation, which can be stacked. Then, the BN layer and the decomposed network structure were added. This
structure improved a significant accuracy with a little computational complexity increase. The Inception-V3 model is the third generation model in the Google Inception series, which utilizes parallel pooling and asymmetric convolution. The stem module of Inception-V4 followed the basic principles in Inception-V3. Compared with the accumulation of simple multi-layer convolution kernel pooling in Inception-V3, Inception-V4 had a simpler architecture and more Inception modules with high accuracy [24].

### 4.2. Improved AlexNet Network Structure

In this paper, the AlexNet structure is combined with the Inception-V4 structure to take both cons of those two structures. The Inception-V4 module is added based on the AlexNet structure, strengthening the preprocessing ability of the network. The BN is also applied to accelerate the convergence, improve the generalization ability, and prevent the gradient from disappearing. During the phase of model training, each sample in the batch is normalized by calculating the mean $\mu$ and variance $\sigma^2$ per batch.

$$
\mu = \frac{1}{N} \sum_{i=1}^{N} x_i, \\
\sigma^2 = \frac{1}{N} \sum_{i=1}^{N} (x_i - \mu)^2, \\
\bar{x}_i = \frac{x_i - \mu}{\sqrt{\sigma^2 + \varepsilon}},
$$

where $N$ is batch size and $x_i$ is a sample in the batch. For a two-dimensional image input, the convolution output of the BN layer is $(N, C, W, H)$, where $C$ indicates the number of output channels, and $W$ and $H$ indicate the dimension of the

| Disease type | Label                  | Total number of pictures (sheets) | Training set (sheets) | Validation set (sheets) |
|--------------|------------------------|-----------------------------------|-----------------------|-------------------------|
| Corn         | Corn_healthy           | 1162                              | 930                   | 232                     |
|              | Corn_CercosporaGrayspot| 1000                              | 800                   | 200                     |
|              | Corn_Commonrust        | 1192                              | 954                   | 238                     |
|              | Corn_NorthernBlight    | 1000                              | 800                   | 200                     |
| Tomato       | Tomato_healthy         | 1591                              | 1273                  | 318                     |
|              | Tomato_Bacterialspot   | 2127                              | 1702                  | 425                     |
|              | Tomato_Lateblight      | 1908                              | 1526                  | 382                     |
|              | Tomato_Septorialspot   | 1771                              | 1416                  | 355                     |
| Grape        | Grape_healthy          | 1000                              | 800                   | 200                     |
|              | Grape_Blackrot         | 1180                              | 944                   | 236                     |
|              | Grape_IsariopsisSpot   | 1076                              | 860                   | 216                     |
|              | Grape_Measles          | 1383                              | 1106                  | 277                     |
| Apple        | Apple_healthy          | 1645                              | 1316                  | 329                     |
|              | Apple_Blackrot         | 1000                              | 800                   | 200                     |
|              | Apple_Cedarrust        | 1000                              | 800                   | 200                     |
|              | Apple_scab             | 1000                              | 800                   | 200                     |

### Table 2: Dataset of plant leaves.

### Table 3: Dataset augmentation process.

| Original data (sheets) | Operations                 | Final data (sheets) |
|------------------------|-----------------------------|---------------------|
| The first time         | Affine transformation       | 42,070              |
| The second time        | Superimposed Gaussian noise | 84,140              |
| The third time         | Flip vertically            | 168,280             |

Figure 2: An example of the dataset augmentation. (a) Original image. (b) Affine transformation. (c) Superimposed Gaussian noise. (d) Flip vertically.
feature map. Then, each sample in the batch can be expressed as $x_{c, w, h}$. The BN normalizes each sample separately, so the calculated number of $\mu$ is also $C \times W \times H$.

During the inference phase, the BN layer uses the mean $\bar{\mu}$ and variance $\bar{\sigma}^2$ calculated in the training phase, which is computed by the moving average method.

$$\bar{\mu}_n = \alpha \mu_{n-1} + (1 - \alpha) \cdot \frac{1}{N} \sum_{i=1}^{N} x_{i,n}$$  \hspace{1cm} (3)

where $x_{i,n}$ is a sample in the nth batch, $\alpha$ is the step size factor of the learning rate, and $\mu_n$ is the mean value obtained when training to the nth batch. Similarly, $\bar{\sigma}^2$ is approximated in the same way [25].

Finally, a scaling coefficient $\gamma$ and a translation coefficient $\beta$ are often added to the calculation of BN, and then the output is:

$$y_i = \gamma \frac{x_i - \mu}{\sqrt{\sigma^2 + \epsilon}} + \beta.$$  \hspace{1cm} (4)

The BN layer can speed up the training and convergence of the network, control the gradient explosion, prevent the gradient from disappearing, and avoid overfitting. The structure of the improved AlexNet is depicted in Figure 3.

As shown in Figure 3, the convolution layer first extracts the texture information of the input image from the shallow edge structure to the deep texture semantic structure. Then, the Inception-V4 further extracts features as a backbone network, which consists of multiple convolutions and pooling operations. Inception-X ($X$ represents A, B, and C) module learns image features through multiple parallel feature transfer structures, improving the feature utilization. Reduction-X ($X$ represents A, B) module, as a pooling layer, convert large feature maps into small feature maps, where the number of channels increases. In this way, too high computational complexity can be avoided without significant loss of information [26]. Then, the Average Pooling layer reduces the deviation of the estimated mean, improving the robustness of the model and reducing the number of parameters. Also, the Dropout layer is used in the two fully connected layers to prevent the overfitting problem, where a certain amount of neurons are temporarily discarded from the network during the training process. Lastly, the Softmax regression, as the output layer, maps the results to the (0, 1) probability interval [27]. The use of multiple parallel convolution paths reduces the number of network parameters. Compared with the network without deepening layers, the network with deepening layers can achieve a similar (or better) performance with fewer parameters. The initial layer only needs to focus on learning edge information and can learn efficiently with less training data. By deepening the network, feature information can be decomposed hierarchically, thus improving learning efficiency. The detailed structure of the network is given in Table 4.

Combining different information obtained from different convolution layers obtains a discriminative image representation. Thus, the proposed model adopts convolution kernels of different sizes to extract features, stack the obtained features along the channel dimension, and transmit them to the next layer. The original first layer convolution of AlexNet provides a large amount of data for Inception-V4. It reduces the loss of information to some extent. At the same time, the small convolution kernel and deeper layer in the Inception-V4 network reduce the number of parameters and computation, improving the efficiency, and quality of

---

**Figure 3:** The structure of the improved AlexNet.

**Table 4:** The detailed structure of the AlexNet-Inception-V4 network.

| Layer name       | Tensor size |
|------------------|-------------|
| Input            | [3, 227, 227] |
| Conv             | [48, 221, 221] |
| Stem             | [384, 25, 25] |
| Inception-A      | [384, 25, 25] |
| Reduction-A      | [1024, 12, 12] |
| Inception-B      | [1024, 12, 12] |
| Reduction-B      | [1536, 5, 5] |
| Inception-C      | [1536, 5, 5] |
| Average pooling  | [1536, 1, 1] |
| Fully connected layers | [1536] |
| Output           | [4]         |
4.3. Dropout and Loss Function. Dropout aims to improve the generalization capability of the model by inactivating neurons with a particular probability throughout the training process. The use of the Dropout can reduce the dependence on the part of upper neurons. It also prevents overfitting by integrating multiple models with different network structures, as is shown in Figure 4.

The CrossEntropyLoss function is used as a loss function. The CrossEntropy function is often combined with the Softmax function to prevent the gradient from disappearing. It solves the problem of slow or stagnant updates of weights in the hidden layer.

The CrossEntropyLoss function is formulated as:

$$H(p, q) = -\sum_{i=1}^{M} p(x_i) \log(q(x_i)). \tag{5}$$

where $M$ represents the number of categories $p(x_i)$ and $q(x_i)$ represent the sample distribution and the prediction distribution, respectively $H(p, q)$ is used to compute the degree of deviation of the ground truth from the output values in the test set. The smaller the result value obtained by the function is, the closer the distribution of $p$ and $q$ is, and the better the performance is. However, in the backpropagation process, the greater the gap between the ground-truth value and the output value accelerates the parameter adjustment of the model.

4.4. Optimizer. The optimizer can promote the desired loss function by reducing the gradient and calculating the derivative of the multivariate function. Typical optimization algorithm includes adaptive moment estimation (Adam), stochastic gradient descent (SGD), and RMSProp. These three different optimizers were analyzed with the proposed model. The loss and accuracy for each epoch are depicted in Figure 5. Combined with AlexNet and inception-V4, the Adam optimizer adjusts the learning rate of each parameter to prevent the learning rate decay, stabilize the exponential gradient decay, improve the identification accuracy of the network, and reduce the loss.

5. Experimental Results and Analysis

5.1. Experimental Environment. Experiments were conducted on the computer with the CPU intel core i7 8565U and Windows 11. The models were implemented in Python 3.7.10 and Pytorch deep learning library. The model was trained for 200 epochs with the Adam optimizer and the initial learning rate $0.0001$.

5.2. Comparison of Different Network Models. The proposed model was evaluated with compared methods: AlexNet, VGG11, ZFNet, and VGG16. The loss is used to update the model parameters, while the accuracy is used to evaluate the performance of the model. Figure 6 compares the accuracy and loss for each epoch of the proposed model and the compared models, showing the superiority of the proposed model over the other models. With the increase in epochs, the proposed model converges better and faster.

5.3. Analysis of Dataset Augmentation. In order to alleviate the overfitting problem during the training [17], the dataset was augmented with affine transformation, Gaussian noise, and vertical flip. Figure 7 compares the accuracy and loss with and without the data augmentation for corn, tomato, grape, and apple data. As shown in Figure 7, the data augmentation significantly improves the performance for all types of data (corn, tomato, grape, and apple): 0.945, 0.948, 0.923, and 0.965 with the data augmentation vs. 0.787, 0.826, 0.854 and 0.828 without the data augmentation.

5.4. Comparison of Training Data and Test Data. Figure 8 compares the accuracy and loss obtained from the training and test datasets, showing that for epochs >60, the accuracy...
and loss curve have converged. The accuracy of the test data reaches 0.94, and the loss reaches 0.16. The fluctuation degree of the two curves is small. Also, it can be seen that there is little difference between the training set and the test set, proving good adaptability and stability of the proposed model.

5.5. Confusion Matrix. The confusion matrix is mainly used to determine the merits of classifiers. Due to the complexification of the patterns displayed in each class, the system tends to obfuscate in multiclass classification [28]. Figure 9 presents the confusion matrix of the ultimate classification results. The diagonal elements represent the quantity of judged correct and are proportional to the global precision of the training model.

As shown in Figure 9, the recognition accuracy of the grape is the highest (0.95). The Grape_Measles and Grape_Blackrot leaves of grapes are the least easily confused, with a probability of the two being misidentified by only 0.1. The recognition capability of the proposed model can be intuitively assessed through the confusion matrix, which helps further to analyze the confusion degree of various plant disease identification.

The performance of the proposed method is evaluated in terms of accuracy, precision, recall, and F1 Score, which are computed based on the true positive (TP), true negative (TN), false positive (FP), and false negative (FN). The calculation formulas are as follows:
In the case of 1,200 samples, accuracy, precision, recall, and $F_1$ Score of Corn_healthy are 0.964, 0.927, 0.930, and 0.928, respectively. To further demonstrate the generalization of the proposed model in plant disease identification, relevant parameters in different plant diseases are listed as follows.

Table 5 shows that the top three accuracies were Grape_Measles (0.972), Grape_Blackrot (0.970), and Corn_CercosporaGrayspot (0.970) in a case of 1,200 samples. Meanwhile, its precision and recall reached the level of 0.87 or more. After 200 epochs, the highest accuracy of corn, tomato, grape, and apple reached 0.945, 0.948, 0.923, and 0.965, respectively, and the highest $F_1$ scores of corn, tomato, grape, and apple reached 0.938, 0.910, 0.945, and 0.924, respectively.

The analysis and comparison demonstrate the practicability of the proposed model in the plant disease identification and classification field. Extensive experiments show that the proposed model trained on a large-scale plant leaf...
A dataset can obtain accurate and stable results. It indicates that the proposed model can be used to diagnose plant diseases to take action in time and achieve healthy growth of crops.

5.6. ROC & AUC. The receiver operating characteristic (ROC) curve is an analysis tool that is depicted on a two-dimensional plane, where the abscissa of the ROC is false positive rate (FPR), and the ordinate is true positive rate (TPR). The AUC indicates the area under the ROC curve. The TPR and FPR are defined as follows:

\[
\text{TPR} = \frac{TP}{P}, \quad \text{FPR} = \frac{FP}{F},
\]

where \(P\) represents the number of positive samples and \(F\) represents the number of negative samples. For a
classifier, FPR and TPR can be obtained according to their performance on the test sample. The ROC curve and corresponding AUC of the proposed model are shown in Figure 10.

### 6. Conclusion

This paper proposes an improved AlexNet with Inception-V4 for plant disease diagnosis, where the AlexNet convolutional layers were appropriately adjusted, and Inception-V4 was added as a backbone network. Extensive experiments on the PlantVillage dataset showed superior performance (accuracy = 0.965) of the proposed method over the compared models: AlexNet, VGG11, VGG16, and ZFNet. Furthermore, analysis of different optimizers and data augmentation were conducted to confirm that the Adam optimizer and data augmentation improved the performance and robustness of the model. Also, the proposed model was evaluated in terms of accuracy, precision, recall, F1 Score, ROC, and AUC. The experimental results show that the proposed model performs well in plant disease detection. However, still, the proposed model cannot distinguish different plant diseases in crops that have similar features. No clear boundary between different levels of the same plant disease causes misidentification, leading to the lower identification accuracy of the plant disease. Also, the used dataset is single-leaf oriented upward images with a homogenous background. In the real world, the background is more complex, and some plant diseases do not even appear on the surface of the leaves but exist in other roots, stems, and other parts of the plant. Thus, future works will investigate to address these limitations.

### Data Availability

The data that support the findings of this study are available from the corresponding author upon reasonable request.

### Conflicts of Interest

The authors declare that they have no conflicts of interest.

### Authors’ Contributions

Juan Qin was responsible for the methodology of projects and supervision. Zhuoxin Li was responsible for writing the original draft. Cong Li was responsible for software code. Linfan Deng was responsible for data set expansion. Huaying Ma, Xianyin Xiao, and Yanzhou Fan were responsible for data preprocessing, validation and writing-review. Zhu
Liangliang was responsible for validation and project administration.

Acknowledgments

The authors acknowledge support from the Tianjin University of Technology’s Innovation and Entrepreneurship School-level Training Program (project no. 20210060046).

References

[1] RR. U. Khan, K. Khan, W. Albattah, and A. M. Qamar, “Image-based detection of plant diseases: from classical machine learning to deep learning journey,” Wireless Communications and Mobile Computing, vol. 2021, pp. 1–13, Article ID 5541859, 2021.

[2] D. Wang and X. J. Chai, “Application of machine learning in plant diseases recognition,” Journal of Chinese Agricultural Mechanization, vol. 40, no. 9, pp. 171–180, 2019.

[3] A. Almadhor, H. T. Rauf, M. I. U. Lali, R. Damaševičius, B. Alouffi, and A. Alharbi, “AI-driven framework for recognition of guava plant diseases through machine learning from DSLR camera sensor based high resolution imagery,” Sensors, vol. 21, no. 11, p. 3830, 2021.

[4] A. Alli, O. Oluwakemi, D. Robertas, M. Sanjay, and M. Rytis, “Cassava disease recognition from low-quality images using enhanced data augmentation model and deep learning,” Expert Systems, vol. 38, no. 4, pp. 1–21, 2021.

[5] D. O. Oyewola, E. G. Dada, S. Misra, and R. Damaševičius, “Detecting cassava mosaic disease using a deep residual convolutional neural network with distinct block processing,” PeerJ Computer Science, vol. 7, no. 2, p. e352, 2021.

[6] M. M. Ozguven and K. Adem, “Automatic detection and classification of leaf spot disease in sugar beet using deep learning algorithms,” Physica A: Statistical Mechanics and Its Applications, vol. 535, Article ID 122537, 2019.

[7] S. Sladojevic, M. Arsenovic, A. Anderla, D. Culibrk, and D. Stefanovic, “Deep neural networks based recognition of plant diseases by leaf image classification,” Computational Intelligence and Neuroscience, vol. 2016, Article ID 3289801, 11 pages, 2016.

[8] S. P. Mohanty, D. P. Hughes, and M. Salathé, “Using deep learning for image-based plant disease detection,” Frontiers of Plant Science, vol. 7, p. 1419, 2016.

[9] G. Geetharamani and J. Arun Pandian, “Identification of plant leaf diseases using a nine-layer deep convolutional neural network,” Computers & Electrical Engineering, vol. 76, pp. 323–338, 2019.

[10] A. Triki, B. Bouaziz, J. Gaikwad, and W. Mahdi, “Deep leaf: Mask R-CNN based leaf detection and segmentation from digitized herbarium specimen images,” Pattern Recognition Letters, vol. 150, pp. 76–83, 2021.

[11] M. Liu, S. Wei, and P. Jiang, “A hybrid modeling of mobile app dynamics on serial causality for malware detection,” Security and Communication Networks, vol. 2021, Article ID 9994588, 10 pages, 2021.

[12] D. Srinivasa Rao, R. Babu Ch, V. Sravan Kiran et al., “Plant disease classification using deep bilinear CNN,” Intelligent Automation & Soft Computing, vol. 31, no. 1, pp. 161–176, 2022.

[13] M. Dyrmann, H. Karstoft, and H. S. Midtiby, “Plant species classification using deep convolutional neural network,” Biosystems Engineering, vol. 151, pp. 72–80, 2016.

[14] A. dos Santos Ferreira, D. Matte Freitas, G. Gonçalves da Silva, H. Pistori, and M. Theophilho Folhes, “Weed detection in soybean crops using ConvNets,” Computers and Electronics in Agriculture, vol. 143, pp. 314–324, 2017.

[15] M. Mehdipour Ghazi, B. Yanikoglu, and E. Aptoula, “Plant identification using deep neural networks via optimization of transfer learning parameters,” Neurocomputing, vol. 235, pp. 228–235, 2017.

[16] L. Liu, R. Wang, C. Xie et al., “PestNet: an end-to-end deep learning approach for large-scale multi-class pest detection and classification,” IEEE Access, vol. 7, Article ID 45301, 2019.

[17] X. F. Chao, G. Sun, H. K. Zhao, M. Li, and D. J. He, “Identification of apple tree leaf diseases based on deep learning models,” Symmetry, vol. 12, no. 7, pp. 1065–1082, 2020.

[18] V. Maeda-Gutiérrez, C. E. Galván-Tejada, L. A. Zanella-Calzada et al., “Comparison of convolutional neural network architectures for classification of tomato plant diseases,” Applied Sciences, vol. 10, no. 4, p. 1245, 2020.

[19] Y. Guo, J. Zhang, C. Yin et al., “Plant disease identification based on deep learning algorithm in smart farming,” Discrete Dynamics in Nature and Society, vol. 202011 pages, Article ID 2479172, 2020.

[20] J. Tie, J. Luo, L. Zheng, H. F. Mo, and J. J. Long, “Citrus disease recognition based on improved residual network,” Journal of South-central University for Nationalities, vol. 40, no. 6, pp. 621–630, 2021.

[21] S. M. M. Hossain, K. Deb, P. K. Dhar, and T. Koshiba, “Plant leaf disease recognition using depth-wise separable convolution-based models,” Symmetry, vol. 13, no. 3, pp. 511–529, 2021.

[22] S. A. Wagle and H. R, “Comparison of plant leaf classification using modified AlexNet and support vector machine,” Traitement du Signal, vol. 38, no. 1, pp. 79–87, 2021.

[23] A. Elaraby, W. Hamdy, and M. Alruwaili, “Optimization of deep learning model for plant disease detection using particle swarm optimizer,” Computers, Materials & Continua, vol. 71, no. 2, pp. 4019–4031, 2022.

[24] M. Türköglu and D. Hanbay, “Plant disease and pest detection using deep learning-based features,” Turkish journal of Electrical Engineering and Computer Sciences, vol. 27, no. 3, pp. 1636–1651, 2019.

[25] S. Ioffe and C. Szegedy, “Batch normalization: accelerating deep network training by reducing internal covariate shift,” in Proceedings of the International conference on machine learning, pp. 448–456, PMLR, Long Beach, California, US, June 2019.

[26] M. Mehdipour Ghazi, B. Yanikoglu, and E. Aptoula, “Plant disease and classification,” Frontiers of Plant Science, vol. 19, p. 4161, 2019.

[27] Y. Guo, J. Zhang, C. Yin et al., “Plant disease identification based on deep learning algorithm in smart farming,” Discrete Dynamics in Nature and Society, vol. 202011 pages, Article ID 2479172, 2020.