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Plant disease detection using leaf images and an involutional neural network

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ABSTRACT

The human population and domestic animals rely heavily on agriculture for their food and livelihood. Agriculture is an important contributor to the national economy of many countries. Plant diseases lead to a significant reduction in agricultural yield, posing a threat to global food security. It is crucial to detect plant diseases in a timely manner to prevent economic losses. Expert diagnosis and pathogen analysis are widely used for the detection of diseases in plants. However, both expert diagnosis and pathogen analysis rely on the real-time investigation experience of experts, which is prone to errors. In this work, an image analysis-based method is proposed for detecting and classifying plant diseases using an involution neural network and self-attention-based model. This method uses digital images of plant leaves and identifies diseases on the basis of image features. Different diseases affect leaf characteristics in different ways; therefore, their visual patterns are highly useful in disease recognition. For rigorous evaluation of the method, leaf images of different crops, including apple, grape, peach, cherry, corn, pepper, potato, and strawberry, are taken from a publicly available PlantVillage dataset to train the developed model. The experiments are not performed separately for different crops; instead, the model is trained to work for multiple crops. The experimental results demonstrate that the proposed method performed well, with an average classification accuracy of approximately 98.73% (κ = 98.04) for 8 different crops with 23 classes. The results are also compared with those of several existing methods, and it is found that the proposed method outperforms the other

Introduction

Agriculture and agriculture-related activities provide a living for an enormous number of people across the world. Plant diseases are a serious threat to food security and economic losses (Vishnoi *et al.,* 2020; Vishnoi *et al.,* 2021). It is often difficult to obtain the desired crop yield due to various plant diseases. In countries such as India, many smallholder farmers depend on healthy crops for their livelihood. Detecting and treating plant diseases at the initial stage is crucial for preventing substantial losses in yield. Plant diseases lead to a loss of $20 billion worldwide annually due to a lack of timely treatment (Pantazi *et al*., 2019). Therefore, efficient disease management is crucial for preventing crop yield. Conventionally, people rely on expert knowledge to identify plant diseases. However, expert knowledge depends on experience, which can be subjective and sometimes biased. Modern computing techniques such as machine learning and deep learning, along with digital image processing, offer alternatives for detecting plant diseases without expert knowledge (Sujatha *et al.,* 2020). The process involves capturing digital images of the plants and analyzing features such as spots, wilting, color, and texture, etc., with the help of machine learning models. In recent years, various deep learning techniques have exhibited excellent performance. Deep learning is being widely used to develop image processing-based methods for plant disease identification due to its ability to learn features and high accuracy (Chen *et*

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al., 2020; Li *et al.,* 2021; Cao *et al.,* 2021). In particular, convolutional neural networks (CNNs) are the leading methods used in classification and regression-based applications (Pradhan *et al.,* 2022; Pradhan and Kumar, 2022). Different layers in the CNN architecture can learn complex features without any additional techniques. Wang *et al.* (2019) developed an AlexNet-based CNN model for disease identification in tomato leaves and achieved an overall accuracy of 97.62%. Pradhan and Kumar (2021) also developed a CNN model for detecting tomato leaf diseases and reported an overall accuracy of 96.26%. Bernardo *et al.* (2021) used a CNN to detect Helminthosporium leaf spot disease in wheat crops with an accuracy of 91.43%. Afifi *et al.* (2021) developed two baseline models, a triplet network and a deep adversarial metric learning strategy, three different CNN architectures, ResNet18, ResNet34, and ResNet50. These models are trained on a large dataset and intended to identify novel diseases when a sufficient number of training images are not available. Thakur *et al. (*2023) proposed a lightweight model called VGG-ICNN that detected plant diseases with a good accuracy of 99.16%. A simplified CNN model with only 8 hidden layers was developed by Agarwal *et al.* (2020) that performed better than several existing methods, resulting in 98.4% accuracy. Zhang *et al.* (2019) modified the R-CNN for a faster version and identified rice diseases with good accuracy. Vishnoi *et al.* (2022) introduced a lightweight CNN model and proposed a disease detection method for apple leaves that takes advantage of augmentation techniques to train the model with a small number of images. The author reported an accuracy of 98%. Stephen *et al.* (2024) used a combination of different deep learning techniques to identify rice diseases. They extracted features with the help of a 3D2D CNN model, which were classified using an optimized deep generative adversarial network. Ahmad *et al.* (2023) assessed several deep learning models across various datasets and environmental conditions. They emphasized that background removal and data augmentation methods are effective at increasing model accuracy for field-deployed disease management systems. Tembhurne *et al.* (2023) analyzed the ability of deep learning algorithms to accurately identify and manage crop diseases. The authors developed an Android application named Plantscape based on MobileNet for monitoring plant health and reported an accuracy of 95.94%. Jung *et al.* (2023) developed a stepwise disease detection framework using a CNN to automate plant disease detection for better quality and yield. The model achieved a good accuracy of 97.09%. Shovon *et al.* (2023) presented a new deep ensemble model called PlantDet, which is based on the InceptionResNetV2, EfficientNetV2L, and Xception architectures. A high accuracy of 98.53% was reported for rice leaf diseases. Pavithra and Aishwarya (2024) proposed a novel method based on a modified Wiener filter, improved ant colony optimization, hybrid grasshopper optimization, and a modified artificial bee colony algorithm for plant disease classification and achieved a high accuracy of 98.53% on the PlantVillage dataset. Joseph *et al.* (2024) proposed a CNN model and evaluated its performance on maize, wheat, and rice crops with accuracies of 95.80%, 96.32%, and 97.28%, respectively. Despite the remarkable success, there are several issues with CNN -based methods. Most of the existing deep CNN techniques rely on fixed-size receptive fields, which may hinder their ability to efficiently capture data at various scales. Because receptive fields are fixed, they may perform less well when interacting with features or objects of different sizes within an image (Huang *et al.,* 2022). CNNs frequently include many parameters, especially in deeper layers. In addition, CNNs typically gather data from the receptive field to capture the local context. It might be difficult to effectively capture the global context or long-range dependencies, which are essential for comprehending complex scenes or capturing relationships between far-off objects. To address some of these issues, involution neural networks (INNs), which are computationally efficient and more parallelizable, are used as alternatives to CNNs (Chen *et al.,* 2021). Unlike standard convolution kernels, which are spatially agnostic and channel specific, involution kernels are more suitable for capturing long-range spatial information while minimizing network parameters. Xu *et al.* (2017) demonstrated that involution can enable fast and efficient plant disease detection. Huang *et al.* (2022) proposed an involution-based method that uses bottleneck blocks of residual networks instead of convolution neural networks. They developed a feature selection feature pyramid network that enables flexible and adaptable feature selection to effectively diagnose plant diseases. A number of methods have been developed to automate plant disease detection. However, most of the existing methods are tested on individual crops. A more realistic system should work for multiple crops. In this work, an involution-based plant disease detection method was developed. Other techniques are also used in the overall framework to effectively utilize the relevant information. The developed method is not crop specific and works for multiple crops. Several experiments were carried out to evaluate the proposed method on various crops, including apple, cherry, corn, grape, peach, pepper, potato, and strawberry.

Materials and methods

A deep learning approach is used in this work to detect and diagnose plant diseases using leaf images. The workflow of the procedure for identifying plant diseases is shown in Figure 1. The first step involves capturing images of plant leaves and labeling them according to the health of the leaves. However, this step is performed with the help of experts in the field. The collected images may contain some unwanted information in the background. Therefore, a segmentation operation is applied to remove the background. The refined set of images is divided into training and test sets. The involution model is trained using the training set of images. Once the training is completed, the trained model can be used to detect diseases in any leaf image. The performance of the model is analyzed with the help of the test set.

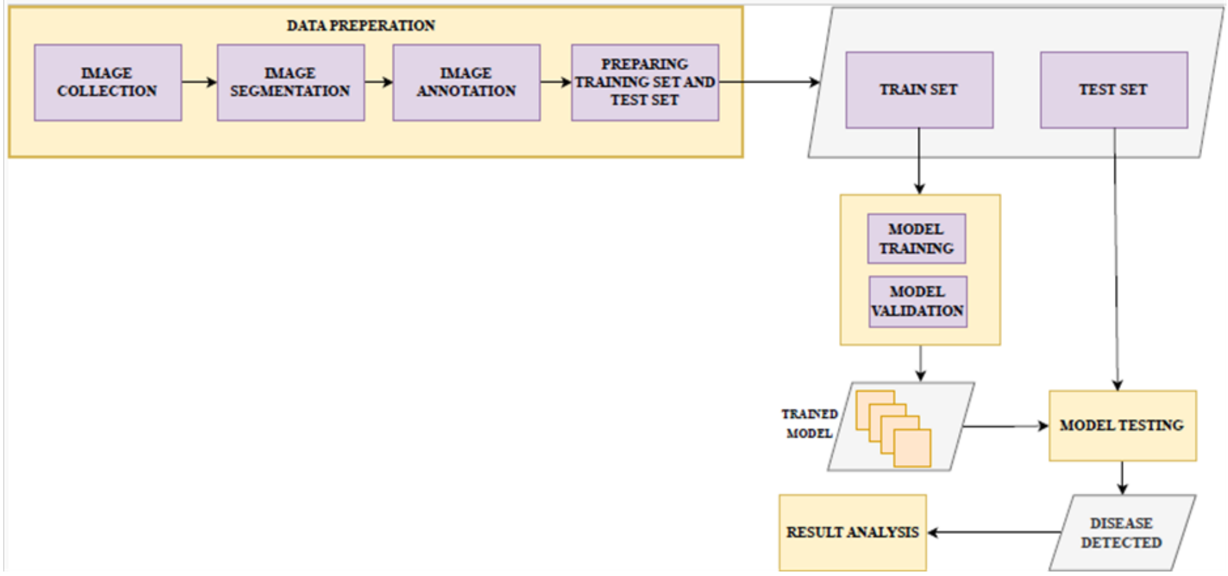

Figure 1. Workflow for automated leaf disease detection using an involution neural network

Dataset

The leaf images for different crops are obtained from a publicly available PlantVillage repository that contains over 54,000 images across 38 crop categories. Eight crops of 23 different classes were selected: apple (*Malus domestica*), cherry (*Prunus avium*), corn (*Zea mays*), grape (*Vitis vinifera*), peach (*Prunus persica*), pepper (*Capsicum*), potato (*Solanum tuberosum*), and strawberry (*Fragaria xananassa*). A total number of 21,768 images are distributed across different health classes, as shown in Figure 2. Table 1 provides the distribution of images for each class in the dataset. For each class, 75% of the samples are taken for training, and the remaining samples form the test set.

Image segmentation

The main purpose of segmentation is to identify specific regions of interest and eliminate unwanted background in an image. It helps to isolate the affected area and make the image simpler to analyze. GrabCut (Qi F *et al.,* 2022) is a well-known image segmentation algorithm based on the Gaussian mixture model. It estimates the color distribution of the target region and background to create a Markov random field over pixel labels. It is formulated as an energy minimization problem (Xiong *et al.,* 2020). The energy function is defined as follows:

$$E(S) = E_d(S) + E_{sm}(S) \tag{1}$$

where S represents the segmentation mask, E_d measures the difference in colors between the foreground and background pixels, and the smoothness term E_{sm} is used for spatial coherence. The data term is expressed as follows:

$$E_d(S) = \sum_{i \in S_f} D(i) + \sum_{i \in S_b} D(i) \tag{2}$$

where i is the pixel index, S_f represents the foreground region, S_b is the background region, and $D(i)$ is the color vector. The terms $\sum_{i \in S_f} D(i)$ and $\sum_{i \in S_b} D(i)$ are the measures of similarity of the foreground and background models, respectively. The smoothness term $E_{sm}(.)$ is given by

$$E_{sm}(S) = \lambda \sum_{i,j \in N} w(i,j)\big(1 - S(i)S(j)\big) \tag{3}$$

where parameter λ controls the trade-off between $E_{sm}(\cdot)$ and $E_{sm}(\cdot)$, N is the set of neighboring pixel pairs, $w(i, j)$ is the spatial weight, and $S(\cdot)$ is the segmentation value of a pixel. The algorithm works iteratively and updates the segmented regions until it converges. Figure 3 shows a sample image segmented via the GrabCut method.

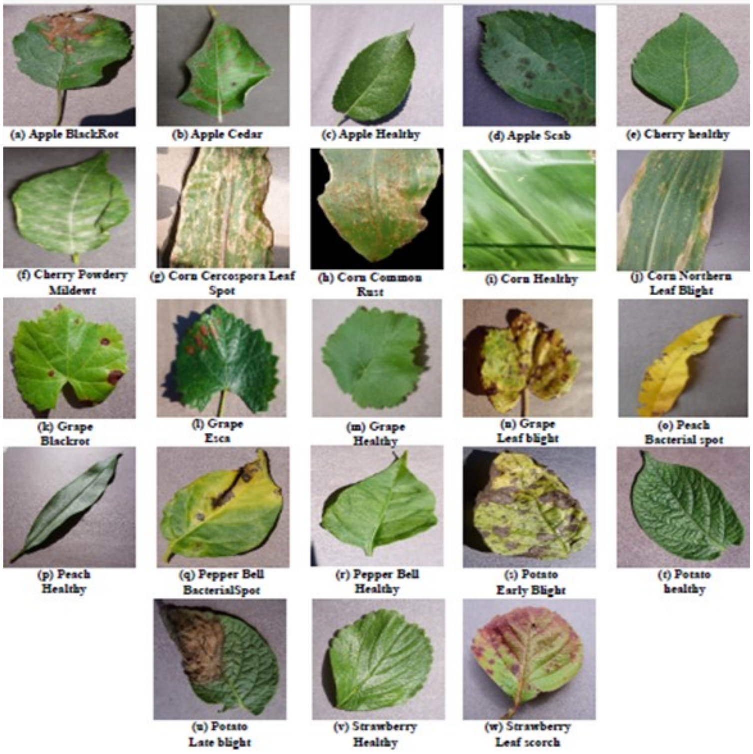

Figure 2. Dataset image sample of 23 different crops classes, including healthy and unhealthy crop leaves

Table 1. Plant Leaf Disease Dataset (Training Set and Test Set)

Name of Crop	Scientific Name of Crop	Crop Disease/ Health Class	Total	Training Set (75%)	Test Set (25%)
Apple	*Malus domestica*	Scab	504	378	126
		Apple Black Rot	497	373	124
		Apple Cedar Rust	220	165	55
		Apple Healthy	1316	987	329
Cherry	*Prunus avium*	Cherry Healthy	513	171	684
		Powdery Mildew	632	211	842
Corn	*Zea mays*	Gray Leaf Spot	411	308	103
		Common Rust	954	716	239
		Corn Healthy	930	698	233
		Northern Leaf Blight	788	591	197
Grape	*Vitis vinifera*	Grape Black Rot	944	708	236
		Esca	1107	830	277
		Grape Healthy	339	254	85
		Grape Leaf Blight	861	646	215
Peach	\ *Prunus persica*	Peach Bacterial Spot	1838	1379	460
		Peach Healthy	288	216	72
Pepper	*Capsicum*	Bell Bacterial Spot	798	599	200
		Pepper Healthy	1183	887	296
Potato	*Solanum tuberosum*	Early Blight	800	600	150
		Potato Healthy	122	92	31
		Potato Late Blight	800	600	150
Strawberry	*Fragaria ananassa*	Strawberry Healthy	365	274	91
		Leaf Scorch	888	666	222

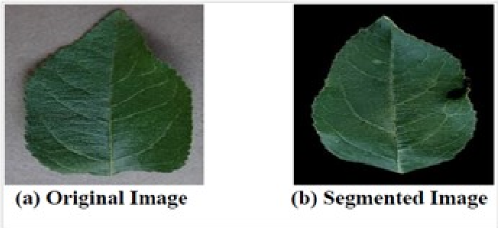

Figure 3. (a) Original image and (b) segmented plant leaf using the GrabCut segmentation technique

Convolution Neural Network

A CNN model consists of a layered architecture that consists of different types of layers stacked together in a cascade (Xu Y *et al.,* 2017). The output of one layer is input to the next layer in the stack. An input image is processed by multiple layers to extract useful information. Convolutional and pooling are the two major layer types in a CNN. These layers perform some typical mathematical operations on the input data to produce feature maps. Several nonlinear activation functions also operate on feature maps (Saleem *et al.,* 2021). An activation function adds nonlinearity to the model and helps to adjust the size of the feature maps. A convolutional layer typically convolves an input image with a set of filters. The convolution operation is defined as follows:

$$h_j^l = f\left(\sum_{i \epsilon T_j} h_i^{l-1} * v_{i,j}^l + s_j^l\right) \quad (4)$$

Where h_j^l

Represents the output feature maps that are convolved with kernel $v_{i,j}$ for a set of input maps T_j and s_j is the bias term at layer j. The height-to-length ratio F of the resulting feature map is determined as follows:

$$F = \frac{W - K + 2P}{s} + 1 \quad (5)$$

where K is the filter size, W is the height/length ratio of the input, P is the padding size, and S represents the stride. The edges of the input can be padded with zeros to maintain the output size. An activation function is used to reduce vanishing gradients and speed up model training. ReLu is one of the most suitable activation functions for multiclass classification. It transforms any negative activation values to zero and can be expressed as follows:

$$f(m) = \max(0, m) \quad (6)$$

In addition, the fully connected layers integrate the features determined at the previous layer to simplify the classification process. This layer generates an N-dimensional vector at the output for an N-class problem. The last layer in the model is the output layer, which uses a classifier such as softmax that assigns class labels based on the probability distribution. Effective training requires a large number of high-quality samples, which may not always be available. Transfer learning can help address this matter by leveraging the knowledge gained from solving one problem to another. A CNN that was previously trained for a similar task can be fine-tuned with data from the current task. This helps reduce computing time and resources, as well as avoid the need for more extensive training. Some models have been trained and are now publicly available for use. DenseNet, InceptionResNetV2, InceptionV3, ResNet, VGG16, and VGG19 are among the popular pretrained models and can be reused across domains via the transfer learning approach.

Involution Neural Network

A conventional convolutional layer applies a small filter or kernel that slides over the entire image to calculate the weighted sum of the nearby pixels. It is good at capturing local features, but it may find it difficult to effectively capture the global context. Unlike convolution, involution uses different kernels at different locations. The dimensions of an involution kernel depend on the dimensions of the input image. However, these kernels can be shared across spectral bands. Therefore, involution kernels (Xu *et al.,* 2017) are known as location-specific and spectral-agnostic kernels that are able to handle long -range interactions. These kernels are adaptive and can adjust their weights according to the input. The kernel generation function $\phi(\cdot)$ (Liang and Wang 2021) is used to determine the kernel size for a pixel *(i, j)* in involution as follows:

$$v_{i,j} = \phi(X_{i,j}) \quad (7)$$

The involution inverts the inherence of the convolution, which can adjust to the specific details to highlight the most significant features. Involution can particularly handle local features with a reduced computational cost compared to convolution operations. The process of involution is shown in Figure 4. Involution has shown better performance than convolution for several computer vision tasks, such as classification and object detection. Overall, involution is a promising technique that complements convolution for image processing tasks with better accuracy.

Proposed framework for disease detection

Figure 5 illustrates the proposed method in the form of a flowchart. As shown in the figure, first, the input image is segmented to remove undesirable background details. The segmentation is performed by applying the GrabCut method. The segmented image is then input to the involutional neural network. The proposed involutional neural network architecture consists of one MobileNetV2 block, one MobileNet Involution block, and two basic blocks. The basic block consists of a convolutional layer with a 3x3 kernel. It uses a stride of 1, a padding of 0, and the ReLU activation function. The MobileNetV2 block is a group of four basic blocks with kernels of sizes 3x3, 1x1, 3x3, and 1x1. The MobileNet Involution block consists of four convolutional layers and one

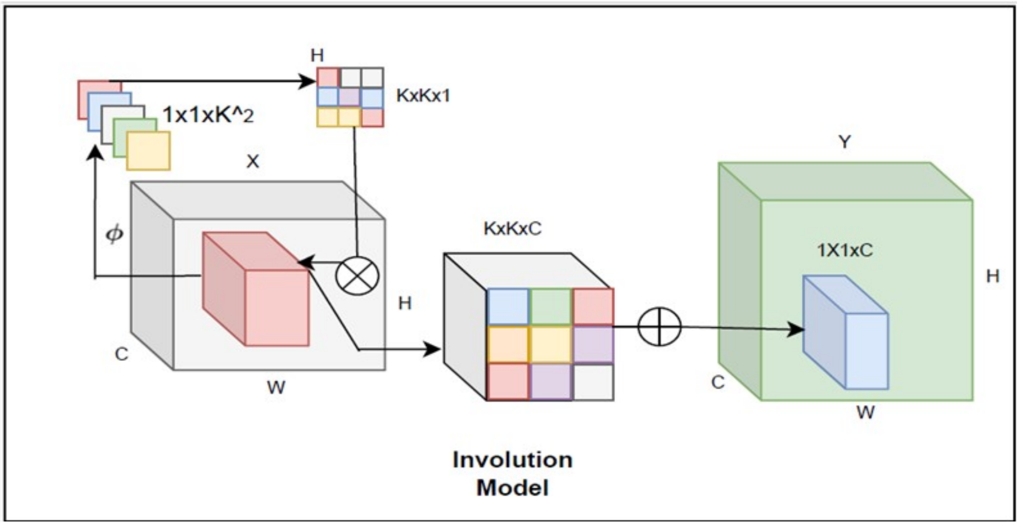

Figure 4. Involution Model for Automated Leaf Disease Detection

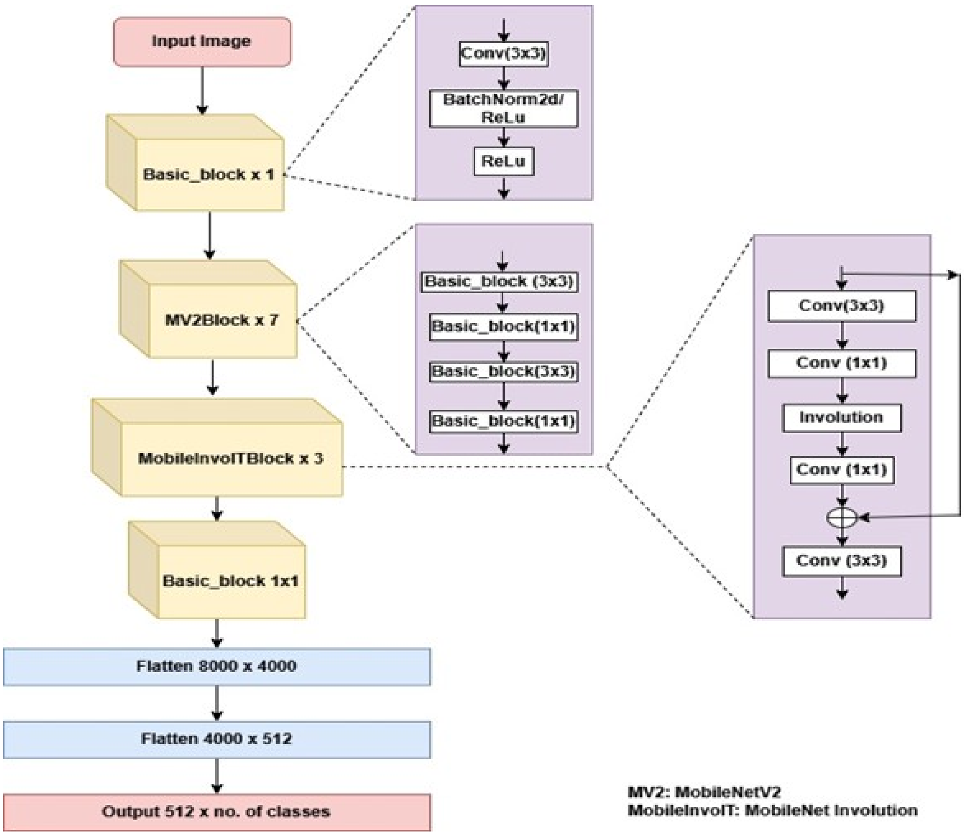

Figure 5. Proposed Model of the Involution Neural Network

The self-attention mechanism extracts important features in the input image (Chen *et al.,* 2021), improving its ability for object classification and detection. The attention mechanism computes an attention map over image pixels that assigns weights to the pixels or regions based on the relevance to the task. The mechanism then aggregates the features from different regions to emphasize the most important portions. It uses a transformer (Yang *et al.,* 2019)-like mechanism to capture long-range dependencies and process global information. However, transformer mechanisms have built-in concepts of spatial information. Therefore, positional encoding is used in the model to obtain information about location features in the image. In this way, both low-level and high-level visual features that can effectively detect changes in color and texture are captured. The shape of the leaves or other parts of the plant was used to identify the disease. The MobileNet Involution block is further followed by another basic block and two flattening layers. The Softmax classifier is used at the output layer. The size of the output layer depends on the number of diseases in the training set. The output layer assigns the disease/health label to the input image.

Results and Discussion

The experiments were carried out on the PlantVillage dataset for 8 different crops and 23 health classes. The implementation is performed in Python using TensorFlow and Keras libraries. All the experiments were conducted on a Linux-based machine equipped with dual Xeon processors, 128 GB of RAM, and an 8 GB graphics card. The involutional models are trained using a stochastic gradient descent optimizer for 40 epochs, with a fixed learning rate of 0.01 and a batch size of 32. The results are compared with those of four well-known pretrained CNN models, namely, InceptionResNetV2 (IRV2), InceptionV3 (IV3), VGG16, and VGG19. The models are evaluated in terms of naive-accuracy (NA) and kappa coefficient (κ) parameters. The accuracy and loss graphs for the proposed model are shown in Figure 6.

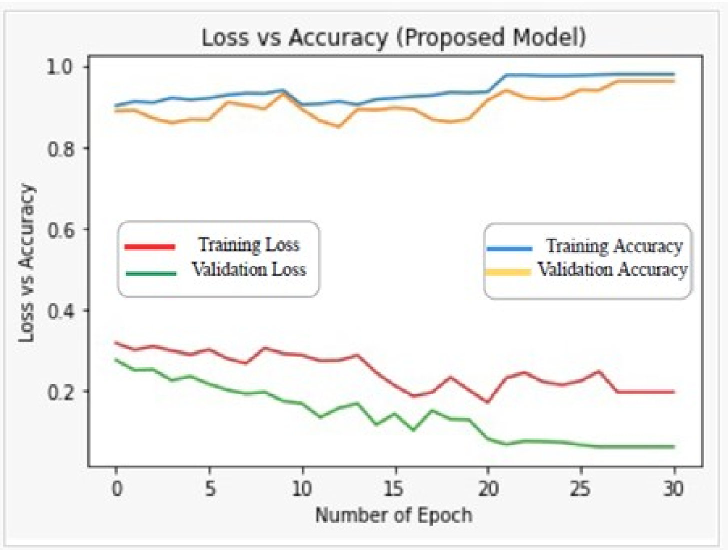

Figure 6. Loss Vs Accuracy Graph of the Proposed Model

Both graphs illustrate that the proposed model is well fit for the problem under consideration.

Accuracy Analysis

The accuracy of the proposed method as well as other tested methods is reported in Table 2 in terms of the NA along with the accuracy variance for all the crops considered here. The proposed method exhibited a good overall accuracy of 99.03%. Additionally, the accuracy is also determined for specific health classes or diseases. This method is able to detect most plant diseases with high accuracy. Only the 'Common Rust' and 'Potato Healthy' classes had observed accuracies under 90%. The variance in overall accuracy is 0.67%, which can be considered acceptable. Table 3 provides the κ values for different methods, leading to similar observations, with the highest value of 0.9867 for the proposed method indicating its ability to identify plant diseases. Compared to the other methods tested here, the proposed method convincingly outperformed the other methods.

Impact of Learning Rate

Hyperparameters strongly influence the accuracy of deep CNN-based methods. The learning rate is one of the most important hyperparameters in deep CNNs. In this experiment, the learning rate is varied to examine its effects on the classification accuracy. In Figure 7, the κ values are plotted against learning rates ranging from 0.0001 to 0.1. The graphs show that when the learning rate is too small or too large, the accuracy is not good. A learning rate of 0.001 is the most accurate, whereas a learning rate of 0.1 is the least accurate. For all the crops, the same trend in accuracy was observed for both training and validation. Consequently, 0.001 is the recommended learning rate for the proposed method.

Table 2. Classification accuracy of eight different crops in terms of naive accuracy (%) with learning error

Class	Proposed	IRV2	IV3	VGG16	VGG19
Scab	98.83 ± 1.11	89.23± 3.17	83.45± 2.10	98.39 ± 1.24	89.17± 3.39
Apple Black Rot	98.21 ± 1.45	97.33± 1.57	99.01± 0.91	97.53 ± 1.03	99.99±0.01
Apple Cedar Rust	99.10 ± 1.77	100.00±0.00	100.00±0.00	100.00±0.00	100.00±0.00
Apple Healthy	99.00 ± 0.43	96.40±1.02	98.17± 0.74	98.19±0.23	99.01 ± 0.53
Powdery mildew	100.00±0.00	100.0±0.00	100.0±0.00	100.0±0.00	99.52±0.47
Cherry Healthy	100.00 ± 0.00	100.00±0.00	100.00±0.00	99.41±0.58	99.41± 0.58
Gray Leaf Spot	98.13 ± 0.73	100.00±0.00	99.55 ± 0.44	99.14±0.60	97.03±1.09
Common Rust	94.37 ± 0.19	93.33±1.85	91.05±2.01	86.63±2.31	84.23 ± 2.44
Corn Healthy	93.02 ± 2.90	74.80± 3.85	76.92 ± 3.89	92.59± 2.91	90.66 ± 3.35
Northern Leaf Blight	97.50 ± 0.71	99.14± 0.60	100.00±0.00	99.58± 0.41	100.00± 0.00
Grape Black Rot	98.66 ± 1.27	98.46± 0.87	96.17±1.25	98.64± 0.77	100.00±0.00
Black Measles	96.21 ± 0.73	85.71±1.95	96.41±1.11	93.53±1.43	75.00 ± 0.76
Grape Healthy	99.00 ± 0.00	100.00±0.00	98.82±1.17	100.00±0.00	94.14 ± 1.64
Grape Leaf Blight	100.00 ± 0.00	100.00±0.00	100.00±0.00	100.00±0.00	100.00±0.00
Peach Bacterial Spot	98.81 ± 0.61	100.00±0.00	100.00±0.00	100.00±0.00	100.00±0.00
Peach Healthy	100.00 ± 0.00	94.73±2.56	100.00±0.00	91.13± 3.19	92.30 ± 3.01
Bell Bacterial Spot	98.39 ± 0.89	89.54± 2.06	90.00± 2.02	95.45± 1.48	94.55 ± 1.59
Pepper Healthy	98.18 ± 0.58	99.27±0.51	99.63± 0.36	96.63 ± 1.04	97.27 ± 0.95
Early Blight	100.00±0.00	95.23±1.47	90.86 ± 1.94	95.65 ± 1.41	100.00± 0.00
Potato Healthy	86.12 ± 5.19	96.15±3.71	100.00±0.00	90.90 ± 6.12	75.00 ± 7.65
Potato Late Blight	99.13 ± 0.96	98.45±0.86	94.24±1.68	94.03±1.67	94.14 ± 1.64
Strawberry Healthy	100.00±0.00	96.80±1.81	100.00±0.00	98.72± 1.27	98.91 ± 1.08
Leaf Scorch	100.00±0.00	100.00±0.00	100.00±0.00	100.00±0.00	100.00±0.00
OA	98.13 ± 1.26	95.27±4.73	99.04±0.95	98.28± 1.71	97.00 ± 3.00

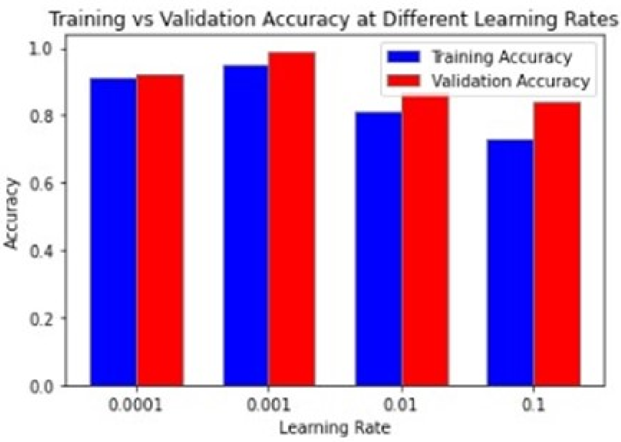

Figure 7. Training Accuracy vs Validation Accuracy Graph at Different Learning Rates

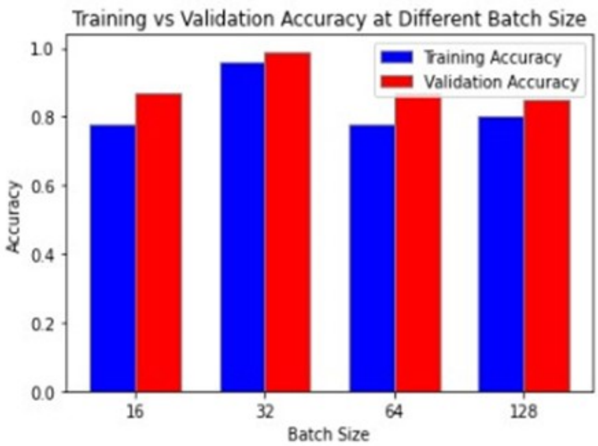

Figure 8. Training Accuracy vs Validation Accuracy Graph for Different Batch Sizes

Table 3. Classification accuracy of eight different crops with learning errors in terms of κ

Class	Proposed	IRV2	IV3	VGG16	VGG19
Scab	98.88 ±1.80	85.42 ± 3.33	78.31 ± 3.70	96.88 ± 1.77	85.74 ± 3.26
Apple Black Rot	96.63 ± 1.92	97.93 ± 1.45	99.00 ± 0.99	98.14 ± 1.30	100.00 ± 0.00
Apple Cedar Rust	99.42 ± 1.93	100.00 ± 0.00	100.00 ± 0.00	100.00 ± 0.00	100.00 ± 0.00
Apple Healthy	99.01 ± 0.88	92.53 ± 2.06	96.25 ±1.50	96.29 ± 1.49	98.07 ± 1.10
Powdery mildew	100.00 ± 0.00	100.00 ± 0.00	100.00 ± 0.00	100.00 ± 0.00	98.93±1.05
Cherry Healthy	100.00 ± 0.00	100.00 ± 0.00	100.00 ± 0.00	99.41 ± 0.58	98.93 ±1.05
Gray Leaf Spot	97.27 ± 1.14	100.00 ± 0.00	99.30 ±0.62	98.27 ± 0.85	95.80 ±1.54
Common Rust	89.99 ± 2.91	91.04 ± 2.45	87.97 ± 2.71	82.04 ± 2.96	78.81 ± 3.11
Corn Healthy	91.90 ± 3.01	70.91 ± 4.24	73.35 ± 4.32	91.44 ± 3.33	89.22 ± 3.84
Northern Leaf Blight	97.91 ± 1.03	98.75 ± 0.87	100.00 ± 0.00	99.39 ± 0.60	100.00 ± 0.00
Grape Black Rot	95.01 ± 1.87	97.84 ± 1.23	94.60 ±1.74	98.08 ± 1.09	100.00 ± 0.00
Black Measles	96.16 ± 1.10	78.33 ± 2.74	94.56±1.66	90.19 ± 1.09	73.12 ±3.01
Grape Healthy	100.00 ± 0.00	100.00 ± 0.00	98.68 ±1.30	100.00 ± 0.00	89.05 ±2.01
Grape Leaf Blight	100.00 ± 0.00	100.00 ± 0.00	100.00 ± 0.00	100.00 ± 0.00	100.00 ± 0.00
Peach Bacterial Spot	100.00 ± 0.00	100.00 ± 0.00	99.78 ±0.21	100.00 ± 0.00	100.00 ± 0.00
Peach Healthy	100.00 ± 0.00	94.73 ± 2.56	100.00 ± 0.00	89.44±3.64	92.30± 3.84
Bell Bacterial Spot	97.27 ± 1.84	82.51 ± 3.23	83.27 ± 3.18	92.39 ± 2.41	90.89 ±4.04
Pepper Healthy	96.74 ± 1.43	98.19 ± 1.26	99.09 ± 0.90	91.62 ± 2.51	93.20 ±3.99
Early Blight	100.00 ± 0.00	91.09 ± 2.65	82.92 ± 3.39	91.87 ± 2.57	100.00 ± 0.00
Potato Healthy	85.41 ± 6.17	95.86 ± 4.04	100.00 ± 0.00	90.22 ± 6.55	72.12±4.01
Potato Late Blight	96.16 ± 1.60	91.10 ± 1.64	89.23±3.03	88.83 ± 2.99	89.05 ±3.78
Strawberry Healthy	100.00 ± 0.00	95.50 ± 2.52	100.00 ± 0.00	94.06 ± 2.86	98.46 ±1.00
Leaf Scorch	100.00 ± 0.00	100.00 ± 0.00	100.00 ± 0.00	100.00± 0.00	100.00 ± 0.00
OA	98.04 ± 0.68	97.69 ± 1.32	99.22 ±0.77	96.94 ±1.51	97.35 ±1.00

Impact of Batch Size

Another hyperparameter examined in this experiment is batch size. For various batch sizes, the disease classification accuracy is obtained. In Figure 8, the κ values obtained at various batch sizes are plotted. The figure shows that for moderate batch sizes, the disease classification accuracy is good. For all crops, the batch size that yields the best κ values is 32, and the batch size that yields the worst accuracy is 64. The accuracy is poor for both smaller and larger batch sizes.

Conclusion

In this work, an involution neural network-based method was proposed for plant disease identification using digital images of plant leaves. Initially, the input image is segmented to remove the background details while retaining only the desired part of the leaf. The segmented image is processed through various blocks of the involution neural network model to identify the health class of the leaf. The proposed method can identify diseases in multiple crops. Many existing methods are designed for specific crops only. Compared to those methods, the proposed method is a multicrop disease identification system. The experimental results demonstrated that the proposed method can identify plant diseases with a high accuracy of 99%. It outperformed several other CNN-based methods.

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Conflict of Interest

The authors declare that they have no conflicts of interest.

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