



# Stacking ensemble model of deep learning for plant disease recognition

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## Abstract

Diverse plant diseases have a major impact on the yield of food crops, and if plant diseases are not recognized in time, they may spread widely and directly cause losses to crop yield. In this work, we studied the deep learning techniques and created a convolutional ensemble network to improve the capability of the model for identifying minute plant lesion features. Using the method of ensemble learning, we aggregated three lightweight CNNs including SE-MobileNet, Mobile-DANet, and MobileNet V2 to form a new network called Es-MbNet to recognize plant disease types. The transfer learning and two-stage training strategy were adopted in model training, and the first phase implemented the initialization of network weights. The second phase re-trained the network using the target dataset by injecting the weights trained in the first phase, thereby gaining the optimum parameters of the model. The proposed method attained a 99.37% average accuracy on the local dataset. To verify the robustness of the model, it was also tested on the open-source PlantVillage dataset and reached an average accuracy of 99.61%. Experimental findings prove the validity and deliver superior performance of the proposed method compared to other state-of-the-arts. Our data and codes are provided at <https://github.com/xtu502/Ensemble-learning-for-crop-disease-detection>.

**Keywords** Plant disease recognition · Ensemble learning · CNN · Lightweight · Image classification

## 1 Introduction

The 2020 World Population Data Sheet declares that the population of the world is expected to increase to over 9 billion by 2050 (<https://interactives.prb.org/2020-wpds/>), which requires increasing crop yields and minimizing plant damage by timely recognition of plant diseases. As a result,

recent studies on plant disease recognition that involve food security have attracted a lot of attention. The diverse plant diseases have great threats to food production, and serious disease types can even cause no harvest entirely. In particular, the major food crops such as rice and maize, which occupy important positions from the production perspective, are consumed as staple foods by over half of the world population, but they are quite susceptible to various diseases too. In the past several years, the degree of damage caused by plant diseases is rapidly growing at an alarming rate due to primary changes in methods adopted for crop cultivation and the influence of harmful organisms. Early recognition and diagnosis acts a pivotal part in suppressing the outbreak of plant diseases (Atoum et al. 2016). It can effectively reduce the losses caused by various plant diseases and has the dual effects of increasing crop yields while avoiding the excessive usage of biocides. However, to date, the most used approach for plant disease recognition still relies on the visual observations of plant disease experts or experienced growers in many areas, explicitly in developing countries. This approach requires experts to monitor continuously, which is prohibitively labor-intensive, expensive,

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and unfeasible for many farms (Chug et al. 2022; Ding and Taylor 2016). Additionally, it is not always possible to meet plant disease experts at any time. In most cases, farmers must go long distances to access plant protection experts for plant disease problems, which makes consultation time-consuming and expensive. Other than that, this approach cannot be transplanted in a broad range. Hence, there are realistic importance and a great need to construct a useful, simple, quick, and reliable method to automatically recognize diverse plant diseases.

In the last few decades, a new manner for identifying plant diseases is being provided with the advancement of pattern recognition and machine learning (ML) techniques. A specific classifier that categorizes the plant images into diseased or healthy types is usually employed in the identification of plant diseases. For instance, Kaur et al. (2018) introduced a support vector machine (SVM) classifier to recognize 3 varieties of soybean leaf diseases comprised of downy mildew, frog eye, and septoria leaf blight; their average accuracy approximately reached 90.00%. After performing the extraction of Scale invariant feature transform (SIFT) features, Mohan et al. (2016) used the classifiers including k-nearest neighbour (k-NN) and SVM to identify three types of paddy diseases, and they realized the recognition accuracy of 93.33% with k-NN while 91.10% with SVM. Kumari et al. (2019) utilized an artificial neural network (ANN) method to identify cotton and tomato diseases; they attained an average accuracy of 92.5%. Chouhan et al. (2018) trained an ANN model called BRBFNN, which was based on the radial function, to identify tomato and cotton crop diseases, and they realized an average accuracy of 86.21%, etc. Despite promising results introduced in the literature, the aforementioned methods primarily rely on the manual feature extraction of the preprocessed corpus, which has a certain subjectivity and consumes a large amount of work, especially, when the image dataset is large-scale. In recent years, a novel ML technique named deep learning (DL), explicitly convolutional neural network (CNN), which can overcome the above-mentioned challenges and automatically extract image features (Chen et al. 2021a, b, c), has been developed to become a preferred method owing to the competitive performance (Tuncer 2021; Qi et al. 2021). Jayagopal et al. (2022) trained a CNN model to recognize leaf-borne infestation and they achieved the best accuracy of 95%. Sethy et al. (2020) introduced a network structure, which used CNN to extract features and SVM for classification. In the experiment of 5,932 samples, they identified 4 classes of rice plant diseases including tungro, bacterial blight, brown spot, and blast, and the combination of SVM and ResNet50 performed better with a 98.38% *FI-score*. Coulibaly et al. (2019) reported a deep CNN-based approach and transfer learning to identify the mildew disease of pearl millet. They identified 6 mildew diseases as well as healthy

types on a dataset of 500 natural rice crop images and realized an accuracy of 95.00%. By using 500 natural rice plant images, Lu et al. (2017) proposed a deep CNN model to recognize 10 typical rice plant diseases, and they attained a 95.48% accuracy. In another research, Gandhi et al. (2018) used generative adversarial networks (GAN) to enrich the local images, and the MobileNet along with Inception V3 models were employed to identify plant diseases. For their experiments on the PlantVillage dataset (Hughes and Salathé 2015), their models attained the accuracy of 92% and 88.6%, respectively. Based on the ResNet50, Wenchao and Zhi (2022) introduced the focal loss function and proposed a new model, namely G-ResNet50, to recognize four types of Strawberry leaf diseases. They achieved an average recognition accuracy of 98.67%. Mohanty et al. (2016) trained a CNN model on the PlantVillage dataset to recognize plant disease types comprised of 26 plant diseases and 14 species, and their model realized a 99.35% accuracy, etc. Although very useful results were attained in the aforementioned literature, the difference and diversity of the images used in the research are limited because most materials are photographed in laboratory environments rather than in natural on-field scenarios. In practice, images should be taken under a wide range so that they contain diverse symptom features of plant diseases (Barbedo 2018). Next, various crop diseases can appear on any part of the plant, whether it is stems, leaves, fruits, or roots. Additionally, the deep learning models used above are primarily the classical deep CNN models with a large volume, which are not easy to be deployed into embedded systems. Despite the limitations, previous research has successfully demonstrated the capability of deep CNNs (DCNNs) to identify various plant diseases. In this study, using the approaches of convolutional ensemble learning, three lightweight CNNs including SE-MobileNet, Mobile-DANet, and MobileNet V2 were employed as the backbone extractor to generate a new convolutional ensemble network called Es-MbNet, where three logistic regressions were designed as the base-classifiers and the Softmax were explored as the meta-classifiers depending upon a two-level stacking strategy. The first-level classifier produces output values for training data that are highly differentiated and have good predictive ability, and the second-level classifier learns from the first-level classifier to improve the accuracy and stability of model prediction. Furthermore, the transfer learning and two-stage training strategy were adopted in model training. The first stage performed the initialization of the network weights, and the second stage fine-tuned the network weights using the target dataset. In brief, the major contributions of this study can be recapitulated below.

- We have collected a plant disease dataset of major food crops like rice and maize. It contains approximately 1000 images captured from real field wild conditions,

and each image has been assigned to a specific category. This dataset is expected to facilitate further research on plant disease recognition.

- A two-level stacking-based convolutional ensemble learning model, namely Es-MbNet, is proposed for the recognition of crop diseases. In the proposed Es-MbNet, three lightweight CNNs were used as the feature extractors and the corresponding three logistic regression models were designed as the base-classifiers. The Softmax was finally explored as the meta-classifiers based on the stacking strategy.
- The two-stage transfer learning was executed in model training. This progressive strategy helps the model discover the coarse features of crop disease images first, and then transform its attention to delicate details gradually, without the need for learning all scale features of the images meantime.

The rest of this writing is organized as follows. Section 2 presents the details of the acquired images followed by an introduction of related work. This section primarily discusses the proposed method for crop disease recognition. Section 3 brings the experimental analyses; extensive experiments are conducted and assessed through comparative analysis. Finally, Sect. 4 concludes the paper and advises on future work.

## 2 Materials and methods

### 2.1 Acquired images

In the experiments of plant disease recognition, we have obtained around 1000 plant disease images containing 466

maize and 500 rice plant disease samples, which are both captured in an on-field cultivation farm environment from the innovation base of ZeHuo Digital Technology Co., Ltd. The plant disease type of each image is known in advance referring to the expertise of the domain experts. It is noteworthy that all the plant disease images are provided in JPG format and have complicated backdrop conditions. For example, some images were photographed with the background of other plant leaves or clutter field grasses, and in other images, the background conditions are the on-field soils of diverse colors. Also, the photographers' fingers are included in the context of the images sometimes. Besides, the lighting strengths were uneven because of the varied weather conditions at the different photographing time. After acquiring the raw images, we used Photoshop software to uniformly adjusted the size of these photographs to  $256 \times 256$  pixels. The rice plant diseases mainly consist of rice blast, brown spot, leaf smut, leaf scald, stackburn, white tip, straighthead, and stem rot. The maize diseases contain crazy top, gibberella ear rot, maize eyespot, Goss's bacterial wilt, gray leaf spot, common smut, and phaeosphaeria spot. Figure 1 displays the sample images of those plant disease types.

Moreover, the publicly accessible datasets, such as the PlantVillage dataset, AI Challenger dataset (<https://www.kaggle.com/jinbao/ai-challenger-pdr2018>), and Sethy et al. (2020) dataset, are also used in our experiments. Among them, PlantVillage is an open-source plant image repository used for the algorithm test of identifying and classifying diverse plant diseases. It includes 54,306 plant leaf images comprised of 12 healthy plants and 26 disease types in 14 species, and all the images are raw colored photographs of plant leaves captured under controlled backdrop conditions. All the sample images have been adjusted to a fixed size of

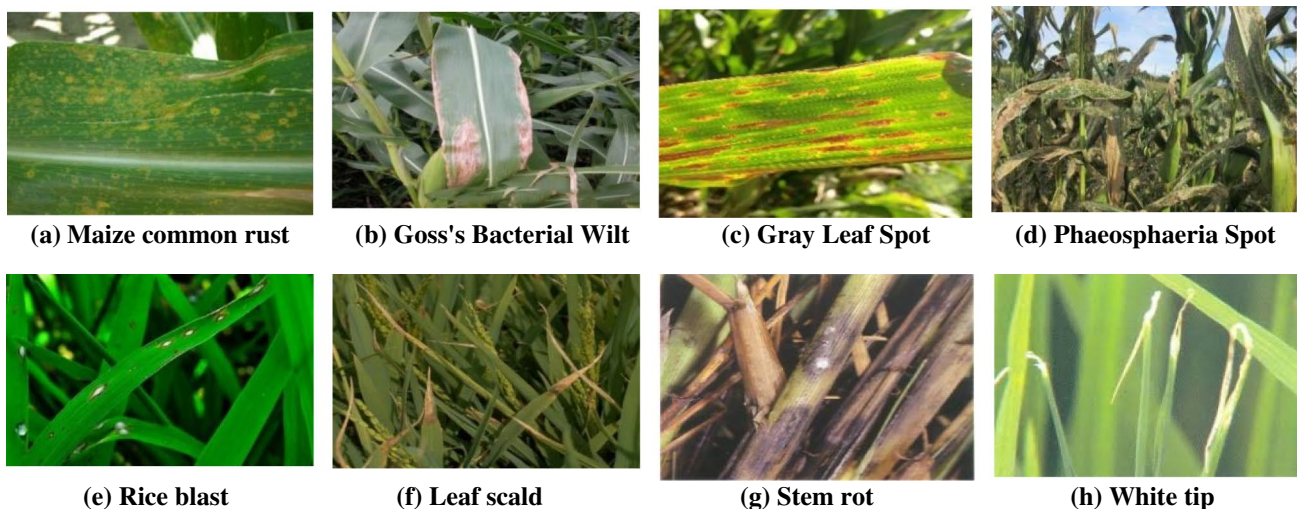


Fig. 1 Examples of plant disease images

256 × 256 pixels to fit the model. The partial data of the AI Challenger dataset is derived from the PlantVillage, and 4 types of potato plant disease images, including early blight fungus general, early blight fungus serious, late blight fungus general, and late blight fungus serious, as well as the healthy category are selected in our experiments. The Sethy et al. dataset is a paddy leaf image dataset, in which 5,932 paddy leaf images are collected under a natural field environment. Figure 2 presents the partial sample images of the public paddy and potato datasets, and the detailed sample numbers and categories are summarized in Table 1.

## 2.2 Related work

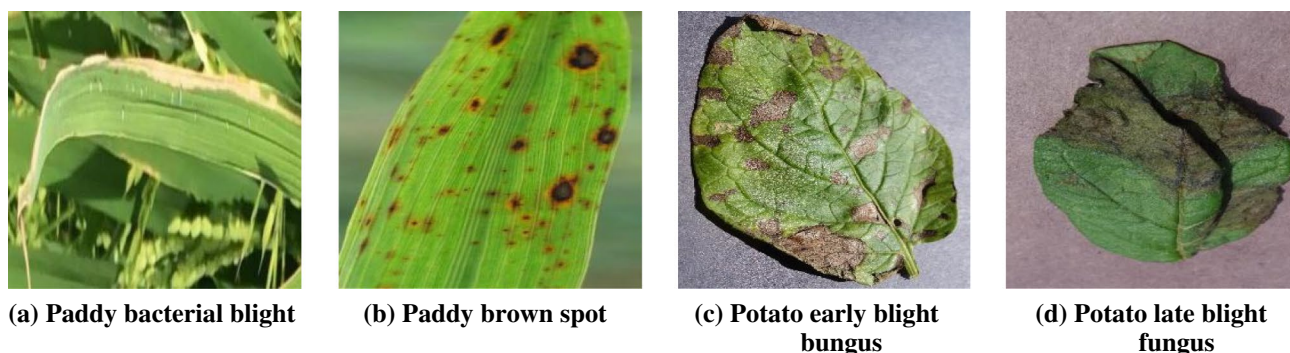
### 2.2.1 Mobile-DANet

To our knowledge, DenseNet (Huang et al. 2017) reveals the latest state-of-the-art with excellent feature extraction capability because the feature layers receive all the features from its preceding layers and its feature maps are output to all later layers. In many image recognition fields, DenseNet has attained impressive performance. Nevertheless, such dense connections also increase the amount of calculation and consume more memory. Besides, each layer connects feature maps gained from the previous layers without considering

the channel relationship characteristics, which does not involve the inter-dependencies between channels. Therefore, on the basis of this, Chen et al. (2021a, b, c) proposed a new network architecture named Mobile-DANet which compressed the size of the model using depthwise separable convolutions (DWSC) (Sifre 2014) in place of the standard convolution layers. Further, a hybrid attention mechanism including channel-wise and spatial attention modules was incorporated into the network to learn the importance of inter-channel relationships and space-wise points for the input features, thereby improving the accuracy of model classification. Their experimental findings demonstrate the effectiveness and feasibility of the proposed method. Hence, the Mobile-DANet was used in our network.

### 2.2.2 SE-MobileNet

Due to plenty of parameters and great volume for the classical deep CNN models, it is hard for them to be practically applied in mobile portable devices. As a consequence, the research and application of lightweight networks has gained significant attention in the past years. MobileNet is a type of lightweight network architecture depending upon DWSC and has shown promising capability in addressing both large-scale and small-scale problems (Sifre 2014; Li et al.



**Fig. 2** The sample images of paddy and potato datasets

**Table 1** The details of the public paddy and potato datasets

Species	Plant disease type	Number of sample images	Number of training and validation	Number of testing
Paddy	Bacterial blight	1584	1384	200
	Blast	1440	1240	200
	Brown spot	1600	1400	200
	Tungro	1308	1108	200
Potato	Healthy	1634	1430	204
	Early blight fungus general	232	203	29
	Early blight fungus serious	583	510	73
	Late blight fungus general	510	446	64
	Late blight fungus serious	287	251	36



2019). However, as mentioned earlier, the inter-dependencies between channels are not considered in the classical MobileNet architecture, which does not involve the channel relationship characteristics. Therefore, the SE block incorporated MobileNet, namely SE-MobileNet, was introduced in reference (Chen et al. 2021a, b, c), where the existing MobileNet was optimized by embedding the SE block into the pre-trained model. Concretely, the top layers of classical MobileNet were truncated and the SE block was added behind the pre-trained MobileNet, which was followed by an additional convolutional layer of  $3 \times 3 \times 512$  for high-dimensional feature extraction. Then, the completely linked (CL) layer was replaced by a global pooling layer, which was followed by a new CL ReLU layer with 1024 neurons. At last, a CL Softmax layer with the actual number of categories was used as the top layer of the modified network for the classification. Thus, SE-MobileNet is also used as the feature extractor of our proposed network.

## 2.3 Proposed approach

### 2.3.1 Es-MbNet model

As mentioned previously, SE-MobileNet is memory efficient. It achieves considerable accuracy compared with other deep CNNs, while saving more overhead. The volume of SE-MobileNet is only half of the deep convolution neural network Densenet-121 and about 1/30 of VGGNet-19. On the other hand, using the deep separable convolution in place of the traditional convolution, Mobile-DANet compresses the model volume and realizes the maximum reuse of input features by incorporating the channel-wise and spatial attention mechanism and preserving the structure of transition layers in DenseNet. Additionally, in the mainstream lightweight networks, MobileNet V2 (Sandler et al. 2018) is relatively small and has fewer parameters. Derived from the MobileNet V1, the inverted residual connections and linear bottleneck architecture are introduced in MobileNet V2, which primarily aims to solve the problem of vanishing gradient and achieves some improvement over MobileNet V1. Therefore, based on the three lightweight CNN models, this study integrates the SE-MobileNet, Mobile-DANet, and MobileNet V2 to form a new convolutional ensemble network, which we termed Es-MbNet, to enhance the stability and robustness of the model for plant disease recognition.

In general, there are three main ensemble learning strategies, such as Bagging, Boosting, and Stacking. Among them, the Stacking strategy can be used to represent Bagging and Boosting methods, and it also has better classification performance (Doan 2017). Therefore, in this study, we adopted the Stacking strategy and a two-level stacking architecture was utilized in the proposed method. Where the first-level classifier produces output values for training

data that are highly differentiated and have good predictive ability, and the second-level classifier learns further from the first-level classifier to enhance the accuracy and stability of model prediction. Three logistic regressions are designed as the base-classifiers in Es-MbNet and the Softmax is explored as the meta-classifier by applying the idea of stacking strategy. Algorithm 1 depicts the specific procedure of stacking-based ensemble learning. More specifically, the detailed processes of the proposed method are presented below.

1. Use three network models to extract the features from the training images and construct a migrated feature training set:  $D = \{D_1, D_2, D_3\}$ , where  $D_k = \{(x_{k,1}, y_{k,1}), (x_{k,2}, y_{k,2}), \dots, (x_{k,N}, y_{k,N})\}$ ,  $(x_{k,i}, y_{k,i})$  denotes the features extracted by image  $i$  using the CNN model  $k$  and the corresponding category information,  $k \in \{1, 2, 3\}$ ,  $y_{k,i} \in \{1, 2, \dots, C\}$ ,  $C$  indicates the number of image classes and  $N$  is the total number of training samples.
2. Construct a base classifier  $H = \{H_1, H_2, H_3\}$  composed of three logistic regression models, and train a logistic regression model using each of the three features in the migration feature training set.
3. The probability feature space is constructed and a meta-classifier  $L$  comprised of *Softmax* classification function is trained. For arbitrary data  $x_{k,1} \in D_k$ , the classifier  $H_k$  is used to predict and obtain the probability distribution  $P_{i,k} = [p_{i,k}^1, p_{i,k}^2, \dots, p_{i,k}^M]$ , where  $p_{i,k}^j$  denotes the probability that sample  $i$  is predicted by the classifier  $H_k$  to the category  $j$ . The dataset  $D_H = \{(x'_1, y_1), (x'_2, y_2), \dots, (x'_N, y_N)\}$ ,  $x'_i = [P_{i,1}, P_{i,2}, P_{i,3}]$  is then constructed depending on the probability distribution, and it is used for training the classifier  $L$ . Figure 3 depicts the architecture of the proposed Es-MbNet.

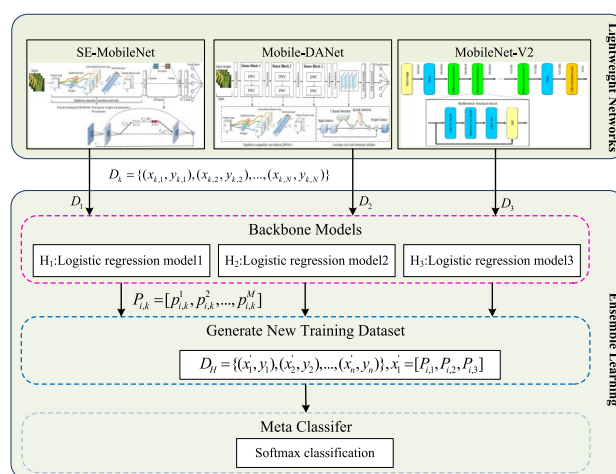


Fig. 3 The proposed Es-MbNet architecture

**Algorithm 1:** Stacking ensemble learning

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**Input:** Training dataset  $D$   
 First-level classifier is composed of several classifiers:  $H = \{H_1, H_2, \dots, H_m\}$ , where  $m$  is the number of classifiers.  
 Secondary classifier  $L$

**Begin**

- 1: Train each sub-classifier in  $H$  using dataset  $D$
- 2:     for  $t=1, 2, \dots, m$  do
- 3:         Train  $H_t$  using  $D$
- 4:     end for
- 5: Generate a new dataset  $D_H$  based on classifier  $H$  and training set  $D$
- 6:      $D_H = \phi$
- 7:     for  $i=1, 2, \dots, N$  do
- 8:         for  $t=1, 2, \dots, m$  do
- 9:              $z_{it} = H_t(x_i)$ ;
- 10:         end for
- 11:          $D_H = D_H \cup ((z_{i1}, z_{i2}, \dots, z_{im}), y_i)$
- 12:     end for
- 13: Train the secondary classifier  $L$  using the newly generated dataset  $D_H$ .

**Output:** The final class prediction results.  $P, P = L(x'), (x', y) \in D$

**End.**

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Furthermore, the network heads of these three backbone extractors were discarded and the global average pooling (GAP) layers were embedded behind these lightweight network models, which were used to take care of the resolution of various input images. One block comprised of the dropout, batch normalization, and completely associated Sigmoid layer with regularization items is added in each network. In the dropout layer, we adopted a dropout factor of 0.5, and a batch normalization layer was utilized to enhance the robustness of the network and suppress the over-fitting risk to a certain extent. To prevent the over-fitting, the  $L1$  regularization term was applied in this dense layer with a fixed value of  $1 \times 10^{-4}$ , and the Adam (adaptive moment estimation) (Kingma and Ba 2014) was employed as the inner optimizer with a  $1 \times 10^{-3}$  learning rate. Next, the binary cross-entropy was employed as the loss function for the pre-trained backbone networks, and the logistic regression classifier was added to each network for the classification. Then, a fully connected (FC) Softmax layer with the practical number of categories was used as the classification layer of the convolutional ensemble network, and particularly, the optimized focal loss function was applied to process the multi-classification problems. Last but not least, inspired by the performance of Grad\_CAM (gradient-weighted class activation mapping) (Selvaraju et al. 2017), the visualization technique was used to position the defect areas of crop disease images, and the plant disease activation map (PDAM) was formed using a weighted sum of the activation maps of last convolutional layer with the weights learned in the last FC Softmax layer, where the significant regions of the images that caused the classification results made by the CNN were presented.

### 2.3.2 Training procedure and loss function

The transfer learning and two-stage training strategy were adopted in our model training. In the first stage, the parameters were initialized and an adaptation was implemented for the networks, where the original top layers of the backbone networks were substituted by new Sigmoid classification layers, and all the bottom convolution layers were kept frozen, while the newly extended layers were trained using the target dataset. Adam solver was used to update the weights. In the second stage, the network was re-trained (fine-tuned) using the target dataset by injecting the weights learned in the first stage, and all the weights were updated by the SGD optimizer in this stage. The first-level classifiers of the ensemble model used the binary cross-entropy as the loss function, and a logistic regression classifier was added to each network for classification. The formula of the loss function is expressed by

$$L = -\frac{1}{N} \sum_{i=1}^N y_i \log(p(y_i)) + (1 - y_i) \cdot \log(1 - p(y_i)), \quad (1)$$

where  $y$  denotes the label (1 indicates the positive sample, and 0 is the negative sample), and  $p(y)$  is the prediction probability of the positive sample for all  $N$  samples. The second-level classifiers used the FC Softmax layer with the actual category numbers as the classification layer of the network, and the boost focal loss ( $\gamma = 2$ ) function was used as the loss function of classification for plant disease recognition. The hyper-parameters of the model are the minimum batch size of 64, the learning rate of  $1 \times 10^{-3}$ , the momentum of 0.9, and other parameters are set referring to Sethy et al. (2020) work. Algorithm 2 summarizes the detailed procedures of model training.

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**Algorithm 2:** The detailed illustration of the model training.

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**Input:**

Training sample set  $T = \{s_1, s_2, \dots, s_N\}$ . Where  $i=1, 2, \dots, N, s \in R^N$ .

**Begin**

- 1: The convolutional ensemble network was created and an adaptation was implemented for the network.
- 2: Using transfer learning, the network was trained on the objective dataset, and the Adam solver was used to update the weights, as shown below.
 
$$\theta_{k+1} = \theta_k - lr * \hat{b}_k / (\sqrt{\hat{s}_k} + \varepsilon)$$
 where  $\theta$  symbolizes the weight matrix,  $k$  indexes the categories,  $\hat{b}_k$  and  $\hat{s}_k$  signify the bias-corrected first and second moments, respectively.
- 3: Through injecting the weights inferred in Step 2, the whole network is re-trained (fine-tuned) using the objective dataset with the optimizer of SGD, as written by
 
$$\theta_{k+1} = \theta_k - lr * (\partial L(w) / \partial w)$$
 where  $L(\cdot)$  denotes the loss function.
- 4: The three base classifiers of logistic regressions models apply the Binary Cross-entropy function as the loss function, as defined by Eq. (1).
- 5: The Focal Loss (FL) function is enhanced and employed in the Softmax Meta-classification layer, as computed by
 
$$FL = - \sum_k \omega_k (1 - p(k|x))^{y_k} \log(p(k))$$

$$y_k = \begin{cases} 1, & k = \text{true\_type} \\ 0, & k \neq \text{true\_type} \end{cases}$$
 where  $C$  is the total number of types,  $\omega_k$  represents the weighting factor, and  $p(k)$  indicates the predicted distribution.
- 6: Continuously update the weight parameters  $\theta \leftarrow \theta - \alpha \nabla_{\theta} L_{train}(\theta)$  using  $T$  sample set.

**Output:**

Obtain the optimum model parameters  $\theta_{best}$ .

**End.**

### 3 Experimental analysis

We have primarily used Python 3.6 to perform the experiments apart from some image processing operations executed by the Photoshop and Matlab software. Where OpenCV-python3, Tensorflow, and Keras libraries are utilized for algorithm running. The hardware configuration includes the Intel® Xeon(R) E5-2620V4 CPU, 64G memory, and GeForce RTX 2080 TI GPU.

#### 3.1 Experiments on the open database

Using the method proposed in Sect. 2.3, we performed the model training and test on the PlantVillage dataset. Except that some raw images were drawn from the database as the test set to evaluate the model, the ratio of the samples randomly assigned to the training set to those in the validation set was 4:1, and the choice of the division ratio referred to the work of Mohanty et al. (2016). In particular, to further investigate the performance of the proposed method, we considered the well-known CNNs, such as VGGNet (Simonyan and Zisserman 2014), Inception V3 (Szegedy et al. 2016), ResNet (He et al. 2016), DenseNet, InceptionResNet (Szegedy et al. 2017), and others, to compare models. Through transfer learning, these baseline CNN models were built and the weights of the bottom convolutional layers were

initialized by injecting the weights pre-trained on ImageNet (Russakovsky et al. 2015). The completely associated layers of all the network heads that are used for the classification were substituted by new FC Softmax layers with the actual number of classes, and the parameter training optimizer was Adam, with a 64 mini-batch size, 100 epochs, and a  $1 \times 10^{-3}$  learning rate. By doing this, we accomplished the training of these CNN models and multiple experiments were carried out on the publicly accessible dataset.

An exhaustive analysis was implemented on the results output by these CNN models, and we measured the performance of the plant disease recognition model using the metrics like *Accuracy*, *Recall*, and *F1-Score*, which were separately calculated as follows.

$$Accuracy = \frac{TP + TN}{TN + TP + FN + FP}, \quad (2)$$

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

$$F1-Score = \frac{2TP}{2TP + FN + FP}, \quad (4)$$

where TP (true positive) means the number of correctly identified crop images in each class, TN (true negative) indicates the sum of accurately identified crop samples in

**Table 2** The results trained on the PlantVillage repository

Models	20 epochs of iteration training			100 epochs of iteration training				Time (h)
	Training accuracy %	Validation accuracy %	Training losses	Training accuracy %	Validation accuracy %	Training losses	Validation losses	
VGGNet-19	94.15	92.55	0.6578	95.53	91.74	0.8492	0.6003	02:11:08
Inception V3	99.83	98.00	0.0727	99.96	98.69	0.9996	0.6016	03:17:23
ResNet-50	99.52	97.60	0.0183	99.99	98.21	0.0004	0.0924	01:51:14
DenseNet-121	99.95	98.91	0.0430	100.00	99.13	0.0058	0.4343	04:44:51
InceptionResNetV2	99.68	97.98	0.1260	99.98	98.26	0.0164	0.9977	07:46:55
MobileNet V2	97.09	97.00	0.1092	99.80	98.48	0.0163	0.0464	02:47:35
Mobile-DANet	97.35	97.41	1.0758	97.84	98.69	0.8980	0.5617	04:53:32
SE-MobileNet	97.62	97.43	1.1801	99.72	98.57	0.9972	1.0074	02:52:23
Es-MbNet	97.12	98.96	0.9786	98.37	98.96	0.6108	0.5808	00:24:28

all other types except for the related ones, FP (false positive) denotes the number of samples that don't belong to the category but mistakenly classified as this one, and FN (false negative) is the number of inaccurately identified samples. Table 2 displays the training and validation accuracy of the different methods.

As seen in Table 2, the proposed Es-MbNet has achieved a superior performance gain compared to other state-of-the-art methods. After training for 20 and 100 epochs, the training *Accuracy* of the model has separately reached 97.12% and 98.37%, and especially, the validation accuracy of the proposed method has attained the top value of 98.96% in all the compared methods except for DenseNet-121, which is a deep CNNs with a relatively large volume. Because of the dense connection, DenseNet-121 requires more storage and computational resource to train the model, e.g., it took more than 4 h for DenseNet-121 to complete the entire 100 epochs of iteration training, while the time-consuming of Es-MbNet is around 24 min. In contrast, the proposed Es-MbNet achieves the best trade-off between classification accuracy

and model efficiency. The crucial explanation behind the solid performance of the proposed method is that the Es-MbNet integrated the merits of multiple networks through the stacking-based convolutional ensemble learning, which enhances the feature extraction of plant lesion symptoms. In addition, the transfer learning and two-stage training strategy make the network acquire the optimal weight parameters, which helps the model obtain satisfying results. Last but not least, the time-consuming of the proposed method is even less than that of either skeleton model used in the Es-MbNet, which is because that the three simple classifiers, the logistic regressions instead of Softmax classifiers are designed as the base-classifiers in the completely associated layers of the Es-MbNet, reducing the computational complexity and the number of model parameters. Conversely, owing to the single network, other CNNs did not achieve the best results through the parameters of the networks were initialized by loading the models pre-trained on ImageNet instead of inferring from scratch. As a consequence, the model trained by the proposed method was further used to

**Table 3** The recognition results and measure metrics analysis

ID	Plant types	Number of recognized samples	Number of correct samples	<i>Accuracy</i> (%)	<i>Recall</i> (%)	<i>F1-Score</i> (%)
1	Apple_healthy	129	127	99.80	99.84	99.22
2	Apple_scab	126	126	99.80	100.00	99.21
3	Maize_healthy	70	70	99.23	100.00	94.59
4	Maize_cercospora	40	32	99.23	80.00	88.88
5	Grape_healthy	84	84	99.61	100.00	98.24
6	Grape_black_rot	236	233	99.71	98.72	99.36
7	Tomato_healthy	118	117	99.42	99.15	97.50
8	Tomato_blight	112	109	99.61	97.32	98.19
9	Potato_healthy	30	27	99.71	90.00	94.73
10	Potato_blight	100	100	99.90	100.00	99.50
–	Average	–	–	99.61	98.08	98.08



**Table 4** Comparison to the results of recent literature on the PlantVillage repository

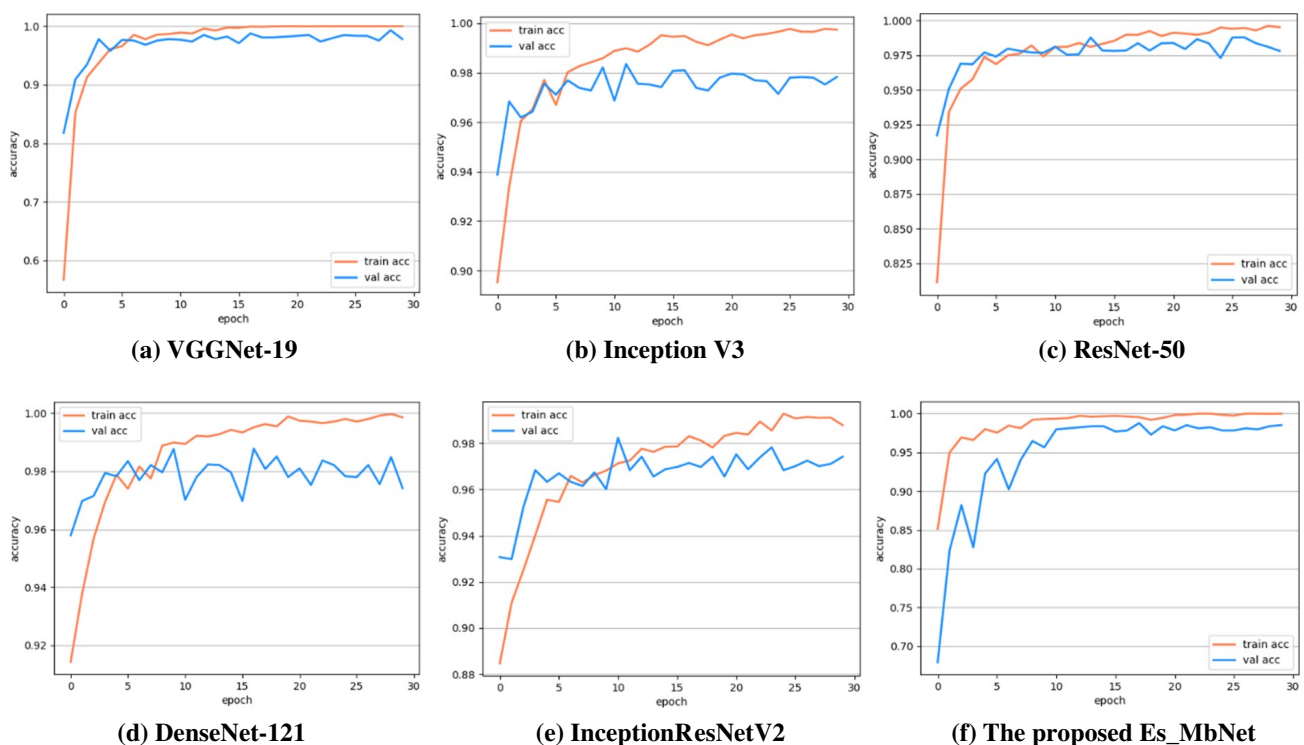
References	Years	CNN models	No. of types	Accuracy (%)
Tm et al. (2018)	2018	LeNet	10	94.95
Elhassouny et al. (2019)	2019	Smart CNN	10	90.30
Geetharamani and Pandian (2019)	2019	Nine-layer deep CNN	39	96.46
Karthik et al. (2020)	2020	Attention-based Residual CNN	4	98.00
Tuncer (2021)	2021	Cost-optimized hybrid CNN	30	99.00
Zeng et al. (2022)	2022	GMA-Net	38	99.43
Hassan and Maji (2022)	2022	Inception based CNN	17	99.39
Proposed approach (2022)	2022	Es-MbNet	38	99.61

recognize plant diseases on new unseen images, and referring to the work introduced by Hari et al. (2019), the partial crop species like maize, tomato, grape, apple, and potato were chosen to perform the test of plant disease identification. Table 3 represents the recognition results and related metrics measurement.

It can be visualized from Table 3 that most of the samples in each class have been accurately recognized by the proposed method and an average *Accuracy* reaches 99.61%, which reveals that the Es-MbNet model has an outstanding capability to recognize plant diseases under controlled backdrop conditions. Moreover, apart from recognizing the normal or diseased crops, the Es-MbNet also distinguishes the specific types of plant diseases, and both the average *Recall* and *F1-Score* achieve 99.08%, respectively. On

another front, the experimental findings on the PlantVillage dataset obtained by some previous research have also been summarized in Table 4. The details such as the references, years, used models, the number of classifications, and the highest accuracy are all included in this table. The comparison of the proposed approach with other influential methods demonstrates the superiority of our approach for identifying plant diseases under simple backdrop conditions.

Furthermore, a series of experiments were carried out on the public paddy and potato image datasets, and Fig. 4 portrays the training performance of different methods. After training for 30 epochs, the proposed method has attained a validation *Accuracy* of 98.51%, which is the highest accuracy of all the methods, as shown in Fig. 4f. Thereupon, the model trained by the proposed method was further employed

**Fig. 4** The training performance of different methods

**Table 5** The identified results of the proposed method

Species	Plant disease types	Tested samples	Correct samples	Accuracy (%)	Recall (%)	F1-Score (%)
Paddy	Bacterial blight	200	200	100.00	100.00	100.00
	Blast	200	200	100.00	100.00	100.00
	Brown spot	200	200	100.00	100.00	100.00
	Tungro	200	200	100.00	100.00	100.00
Potato	Healthy	204	203	99.91	99.50	99.75
	Early blight fungus general	29	27	99.25	93.10	85.71
	Early blight fungus serious	73	66	99.41	90.41	94.96
	Late blight fungus general	64	55	98.67	85.93	87.30
	Late blight fungus serious	36	32	98.92	88.88	83.11
Average	–	–	–	99.57	98.09	98.09

**Table 6** The recognized results of paddy diseases in literature (Sethy et al. 2020)

Paddy disease types	Bacterial blight	Rice blast	Rice brown spot	Tungro
Bacterial blight	197	3	0	0
Blast	7	193	0	0
Brown spot	0	4	196	0
Tungro	0	0	0	200

**Table 7** The potato disease identification results compared with the literature (Liang et al. 2019)

Potato disease types	Accuracy in literature (Liang et al. 2019) (%)	Accuracy of this study (%)
Healthy	100	99.91
Early blight fungus general	89	99.25
Early blight fungus serious	88	99.41
Late blight fungus general	88	98.67
Late blight fungus serious	92	98.92

to identify the classes of new sample images, and the test results are summarized in Table 5. Plus, Table 6 presents the report in literature (Sethy et al. 2020) for comparison, and Table 7 lists the results compared with the existing work (Liang et al. 2019).

As seen in Table 5, the tested 200 samples per category for all the paddy disease images have been properly identified by the proposed method, and the recognition *Accuracy* reaches 100%, outperforming the results reported by Sethy et al. (2020) (see Table 6). In addition, for the healthy potato plant, all the 204 samples have been accurately identified by the proposed method except for 1 misidentification, and the *Accuracy* achieves 99.91%. The 27 potato “Early Blight Fungus general” disease samples have been correctly

recognized by the proposed method apart from 2 incorrect identification, and thus the proposed method has gained an *Accuracy* of 99.25%. Among 73 potato “Early Blight Fungus serious” disease images, 66 samples have been accurately identified by the proposed method, and the *Accuracy* rate realizes 99.41%. To sum up, in the 1206 paddy and potato plant images, 1183 samples have been successfully identified by the proposed method and the average *Accuracy* reaches 99.57%. Besides, the average *Recall* and *F1-Score* realize 98.09%, respectively. More than that, from the comparison results between the proposed method and the existing work (Liang et al. 2019) on the identification of potato plant diseases, the proposed Es\_MbNet has also shown strong recognition capability, as shown in Table 7.

### 3.2 Experiments on the local dataset

In like manner, the proposed method was further tested on the local image dataset. To enhance the diversity and difference of local sample images, the data enhancement scheme was utilized to produce new synthetic images for model training, thereby alleviating the risks of over-fitting. The conventional data enhancement techniques paired with the improved DCGAN method were adopted in our data enhancement scheme. In general, the conventional data enhancement techniques including random translation, scale transformation, angle rotation, color jittering, and horizontal or vertical flipping, can generate new images but may destroy the linear relationship of original images too. In comparison, the latest DCGAN can generate diverse images automatically, although the process is more complex than the traditional methods. The classical architecture of DCGAN is designed to produce new images with a size of  $64 \times 64$  pixels since training DCGAN with larger scales is not stable as one module (generator or discriminator) becomes stronger than the other one. But for most of the successful CNNs, the dimensions of input images are assigned a greater value like

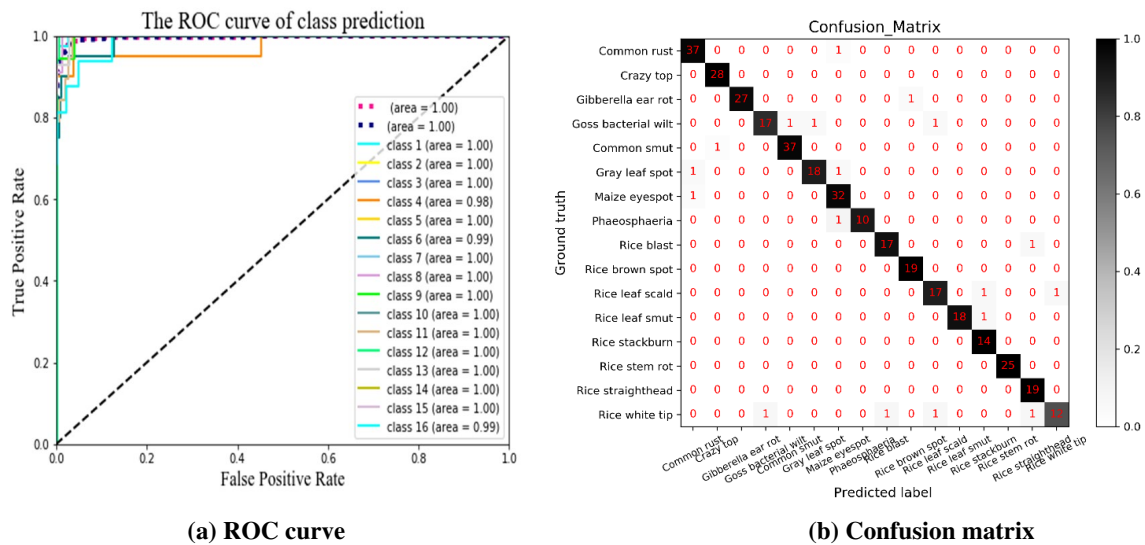


Fig. 5 The identification results on local crop images

Table 8 The measure metrics analysis of identification results

Species	ID	Crop disease types	Number of identified samples	Number of correct samples	Accuracy (%)	Recall (%)	F1-Score (%)
Maize	1	Common rust	38	37	99.16	97.36	96.10
	2	Crazy top	28	28	99.72	100.00	98.24
	3	Gibberella ear Rot	28	27	99.72	96.42	98.18
	4	Goss bacterial Wilt	20	17	98.88	85.00	89.47
	5	Common smut	38	37	99.44	97.36	97.36
	6	Gray leaf spot	20	18	99.16	90.00	92.31
	7	Maize eyespot	33	32	98.88	96.96	94.12
	8	Phaeosphaeria leaf spot	11	10	99.72	90.90	95.24
Rice	9	Rice blast	18	17	99.44	100.00	94.44
	10	Brown spot	19	19	99.72	100.00	97.43
	11	Leaf scald	19	17	98.88	89.47	89.47
	12	Leaf smut	19	18	99.72	94.73	97.29
	13	Rice stackburn	14	14	99.44	100.00	93.33
	14	Rice stem rot	25	25	100.00	100.00	100.00
	15	Rice straighthead	19	19	99.44	100.00	95.00
	16	White tip	16	12	98.60	75.00	82.75
-	Average	-	-	99.37	95.32	95.06	

256 × 256 pixels to improve the performance of the model. Due to this reason, we enhanced the classical DCGAN by modifying the input assignment as 256 × 256 pixels and embedding a convolutional block of 128 × 64 × 3 followed by a 32 × 3 convolutional block in the generator module. Correspondingly, the input size of the discriminator was assigned as 256 × 256 × 3, and then the convolutional block of 32 × 3 followed by a 64 × 128 × 3 convolutional block was also incorporated into the networks. The hyper-parameters of model training were set to the mini-batch size of 16, the

learning rate of  $1 \times 10^{-4}$ , the epochs of  $5 \times 10^5$ , and the Adam solver. By doing this, the new samples were synthesized and greater than 200 images were guaranteed per category.

In addition to preserving a certain number of original images for the model test, the augmented samples were divided into the training and validation sets with the ratio of 4:1 to separately train and determine whether the model was over-fitting. Using the model trained by the proposed method, the new sample images outside modeling were

selected for the test of plant disease identification. Figure 5 shows the ROC curve and confusion matrix of the identification results, and the corresponding evaluation metrics are summarized in Table 8.

It can be visualized from Fig. 5a that the identification result of the proposed method shows ideal operating points and the curves of all the categories are generally convex to the left upper corner of the figure. The recognized plant disease types are with a greater true positive rate (TPR) while a smaller false positive rate (FPR), which can also be reflected by the confusion matrix of recognition results in Fig. 5b. Most images in various categories have been accurately recognized by the proposed Es-MbNet method. For instance, except for one misidentification, the other 37 examples were correctly identified in the "common rust" category, and the identification accuracy realizes 99.72%. Likewise, all 28 "Crazy Top" disease samples have been properly recognized by the proposed method, and also, the proposed method has accurately recognized 27 instances of "gibberellin ear rot" in 28 samples, with an accuracy of 99.72%. In summary, a total of 347 instances have been successfully identified in 365 samples, and the average recognition *accuracy* achieves 99.37%. Again, the average *Recall* and *F1-Score* have attained no less than 95.32% and 95.06%, respectively, as shown in Table 8. In another aspect, there are individual identification errors, such as 2 misclassified samples in the category "Leaf scald", and 4 errors in the category "White tip". This is due to that some different disease types like rice

"Leaf scald" and "White tip" have some similarities in their own pathological characteristics, such as whitening, twisting, and withering of leaves. Additionally, the serious clutter field backdrop conditions and irregular illumination intensities, which impact the feature extraction of disease spot images, can lead to the misclassification of crop diseases too. Figure 6 shows the examples of partially recognized results. Among them, the upper samples are the original images, the middle samples are the lesion images presented by the classification activation map (CAM) visualization technology, and the bottom images are the plant disease samples recognized by our method.

As can be observed in Fig. 6, most of the tested sample images have been accurately recognized by the proposed method. Such as Fig. 6a, the practical category of this sample is "Rice Stackburn", which is successfully recognized with a 0.89 probability. Similarly in Fig. 6b, c, these samples are both correctly recognized with a probability greater than 0.99 and 0.74, respectively. In contrast, individual samples such as Fig. 6d are mistakenly categorized because of the extreme clutter field backdrops and non-uniform lighting intensities. Besides, some different crop diseases appearing on the same crop may also influence the identification results. Although individual disease spot images are misclassified, the types of most crop disease samples that have been identified are consistent with their actual types. Furthermore, from the middle defect positioning images exhibited by PDAM in Fig. 6, it can also be observed that most

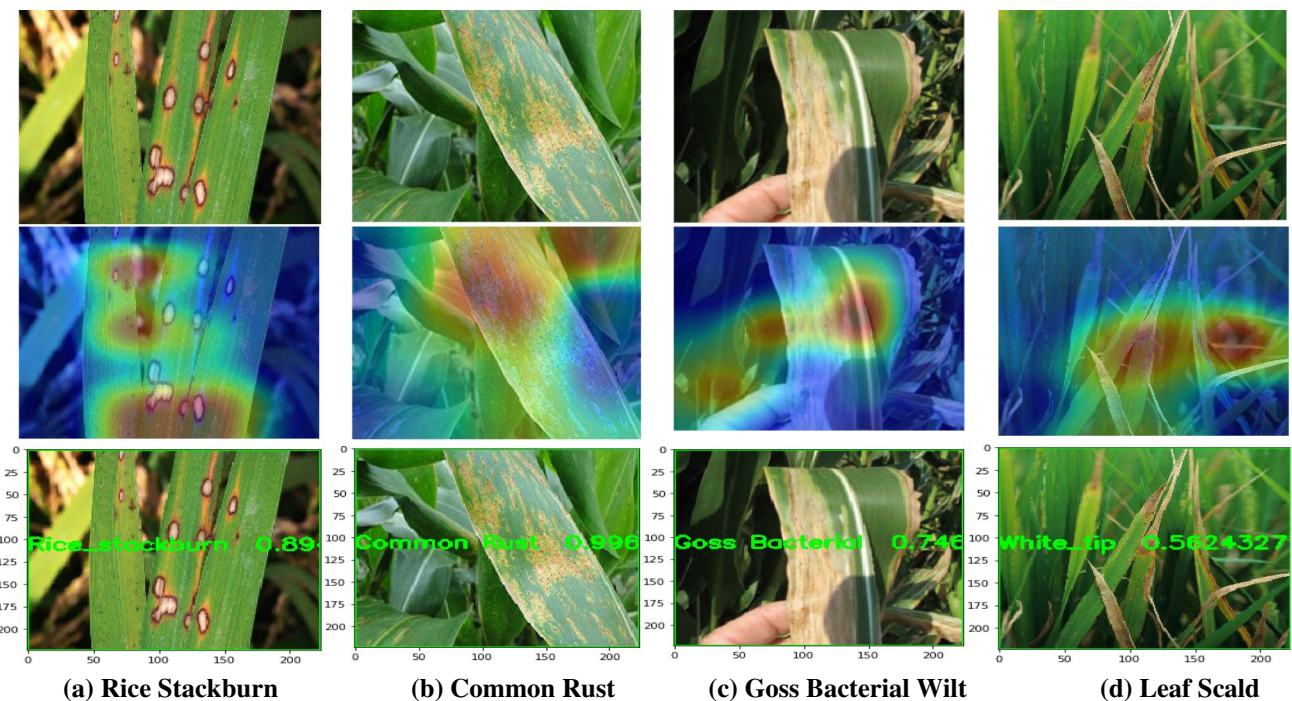


Fig. 6 The examples of identified crop disease images



disease areas have been successfully located by the proposed method. Consequently, based on the results of experimental analysis, we can conclude that the proposed Es-MbNet has a significant ability to recognize diverse crop diseases under natural field wild scenarios and can also be transplanted in other related fields.

## 4 Conclusions

To guarantee a substantial crop yield, the timely and efficient recognition of plant diseases plays a crucial role, and therefore looking for a useful, simple, and fast tool to automatically recognize various plant diseases has a great need and important realistic significance. In this study, a novel convolutional ensemble learning method is proposed to recognize plant disease types. Using a two-level stacking strategy, the three lightweight networks including SE-MobileNet, Mobile-DANet, and MobileNet V2 were employed as the backbone extractor to generate a new convolutional ensemble network, namely Es-MbNet, in which three logistic regressions were designed as the base-classifiers and the Softmax were explored as the meta-classifiers. Further, the transfer learning and two-stage training strategy were adopted in model training, and the first phase only trained the weights on the newly extended layers from scratch while freezing the parameters of the bottom convolutional layers, thereby initializing the network weights. The second phase re-trained the network using the target dataset by injecting the weights trained in the first phases, and thus the optimum weight parameters are gained for the ensemble convolutional network. Experimental findings reveal the proposed method with solid efficacy for plant disease recognition on both the open-source and local datasets. Though competitive performance has been achieved by the proposed method, individual misidentifications still exist in samples with extremely complicated background conditions. In the future, we will collect a wider range of plant disease images under practical on-field wild scenarios to automatically recognize the broad range of plant disease images. Additionally, we want to extend the method to other related fields, such as online fault inspection, computer-aided evaluation, and so on.

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