

Article

Rice Disease Classification Using a Stacked Ensemble of Deep Convolutional Neural Networks

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Abstract: Rice is a staple food for almost half of the world's population, and the stability and sustainability of rice production plays a decisive role in food security. Diseases are a major cause of loss in rice crops. The timely discovery and control of diseases are important in reducing the use of pesticides, protecting the agricultural eco-environment, and improving the yield and quality of rice crops. Deep convolutional neural networks (DCNNs) have achieved great success in disease image classification. However, most models have complex network structures that frequently cause problems, such as redundant network parameters, low training efficiency, and high computational costs. To address this issue and improve the accuracy of rice disease classification, a lightweight deep convolutional neural network (DCNN) ensemble method for rice disease classification is proposed. First, a new lightweight DCNN model (called CG-EfficientNet), which is based on an attention mechanism and EfficientNet, was designed as the base learner. Second, CG-EfficientNet models with different optimization algorithms and network parameters were trained on rice disease datasets to generate seven different CG-EfficientNets, and a resampling strategy was used to enhance the diversity of the individual models. Then, the sequential least squares programming algorithm was used to calculate the weight of each base model. Finally, logistic regression was used as the meta-classifier for stacking. To verify the effectiveness, classification experiments were performed on five classes of rice tissue images: rice bacterial blight, rice kernel smut, rice false smut, rice brown spot, and healthy leaves. The accuracy of the proposed method was 96.10%, which is higher than the results of the classic CNN models VGG16, InceptionV3, ResNet101, and DenseNet201 and four integration methods. The experimental results show that the proposed method is not only capable of accurately identifying rice diseases but is also computationally efficient.

Keywords: rice diseases; sustainable agriculture; stacking; EfficientNet; ensemble learning; lightweight



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1. Introduction

Rice is one of the most widely cultivated food crops in the world [1]. As the main primary food in the diet of the world's population, rice accounts for about 36% of global consumption demand [2]. In China, the area of rice cultivation accounts for about 20% of the world's rice cultivation area, and its production accounts for about 40% of total rice production worldwide [3]. Thus, the stability and sustainability of rice production plays a decisive role in food security. However, the yield and quality of rice have always been

affected by disease [4–6]. As the global climate changes, such damage is becoming increasingly serious and extending to previously unaffected regions [7,8]. Spraying chemical pesticides is currently the most effective method to control diseases [6]. The extensive use of chemical pesticides causes serious environmental pollution and pesticide residues that are a threat to people's health.

Nowadays, with the improvement in living standards and the increase in environmental protection awareness, the demand for reducing pesticide pollution, environmental protection, and ecologically sustainable development is increasing. Clearly, the precise prevention and control of diseases are important ways to reduce the use of chemical pesticides and ensure the sustainability of rice production. Above all, the accurate and rapid identification of diseases is a fundamental step for early disease monitoring, diagnostics, and prevention. For example, using disease identification results, farmers can use the appropriate dose of pesticides to prevent and control that disease.

Traditionally, the classification of rice diseases is performed manually, and diseases are assessed by specialists who perform naked-eye observations according to their experience and knowledge [9]. The process is laborious, time-consuming, and has low recognition accuracy. To overcome these drawbacks, various image-based classification methods using machine learning have been widely applied to classify plant diseases [10,11].

These conventional machine-learning methods [12] include support vector machines (SVMs), multilayer perceptrons, k -means, k -nearest neighbors, and artificial neural networks. Phadikar et al. [13] built a rule-based classifier with extracted features such as color, shape, and the position of the infected portion to classify different rice diseases. Xiao et al. [14] presented a rice blast recognition method based on principal component analysis and a backpropagation (BP) neural network. Their experimental results show that its average recognition rate is 95.83%. Abdullah et al. [15] presented a complete, portable, and real-time device for predicting rice diseases. Prajapati et al. [16] classified rice images as one of three rice diseases using an SVM and extracted features such as color, shape, and texture. Kang et al. [17] extracted 14 color, shape, and texture features as the input values of a BP neural network to identify lesion regions. Sethy [18] reviewed studies based on image segmentation, feature extraction, feature selection and classification published in 2007–2018 with a focus on the development of the state of the art. Although classical image-based classification methods have achieved impressive results in terms of accuracy, this accuracy depends largely on manually designed features to express the characteristics of rice diseases. Because feature design is a difficult process, the accuracy and generalization of classification are poor in new application scenarios.

Recently, deep-learning methods [19,20], which are efficient techniques for feature representation learning, have been rapidly developed and successfully applied in many fields [21,22]. The accuracy and generalization of image recognition has been greatly improved by employing DCNNs. Rice disease classification is also an area in which DCNNs have performed better than classical machine-learning techniques [23–26]. To achieve artificial intelligence-assisted rapid and accurate rice disease classification detection, Wang et al. [6] proposed the ADSNN-BO model, which achieved a test accuracy of 94.65%. To enhance the diagnostic accuracy of traditional CNNs in small-sample rice disease image sets, Lu et al. [27] proposed the ACNN-TL model, which is based on a CNN structure combined with atrous convolution and transfer learning. Pan et al. [28] proposed a two-stage method called RiceNet, which includes YoloX and a Siamese network, to identify four important rice diseases. Stephen et al. [29] discussed four CNN architectures for classifying and identifying healthy and diseased leaves such as brown spot, hispa, and leaf blast. Yang et al. [30] proposed the rE-GoogLeNet CNN model to accurately identify rice leaf diseases in the natural environment. To improve the network structure and increase accuracy, Bi and

Wang [31] proposed a double-branch DCNN model with a convolutional block attention module. Their results show that the accuracies of the classic models VGG-16, ResNet-50, ResNet50 + CBAM, MobileNet-V2, GoogLeNet, EfficientNet-B1, and Inception-V2 are lower than the accuracy of their model (98.73%). In the study of Ahad et al. [32], a rice disease classification comparison of six CNN-based deep-learning architectures was conducted using a database of the nine most common rice diseases in Bangladesh. Although deep-learning-based methods have achieved remarkable results in image identification, there are still some limitations. It is difficult to select appropriate network structures, parameters, and algorithms, and optimizing recognition performance requires long training times in practice. In addition, the high computational cost and greater network depths hinder DCNN applications in practice, making them especially unsuitable as embedded models in resource-constrained devices.

Exploring lightweight CNN models that can achieve the best accuracy with a minimal computational budget is a valuable research direction [33,34]. As lightweight networks have developed, they have also been widely used in the task of rice disease identification. Many excellent methods have been proposed and achieved good recognition results [35–37]. Representative algorithms include MobileNet, ShuffleNet, GhostNet, and EfficientNet. Chen et al. [4] used a MobileNet-V2 pre-trained on ImageNet as the backbone network and added an attention mechanism to learn the importance of inter-channel relationship and spatial points for input features. Their model achieved an average identification accuracy of 99.67% on a public dataset. To realize the lightweight identification of rice diseases, Yuan et al. [38] used the ECA attention mechanism to improve the MobileNetV3Small model. Their experimental results showed that the recognition accuracy rate reached 97.47% while reducing the number of parameters by 26.69%. Zhou et al. [39] proposed an improved ShuffleNet V2 model (GE-ShuffleNet) to increase the accuracy of rice disease classification. The experimental results showed that the identification accuracy of their model is higher than that of ShuffleNetV2, MobileNetV2, AlexNet, Swim Transformer, EfficientNetV2, VGG16, GhostNet, and ResNet50. To address the problems of extensive computation and high storage cost of DCNNs, Chi et al. [40] proposed a lightweight image recognition model called L-GhostNet, which is based on an improved GhostNet. Padhi et al. [41] presented a paddy disease classification model using the EfficientNetB4 architecture and trained on the publicly available Paddy Doctor Dataset, which achieved a test accuracy of 96.91%. Yang et al. [42] developed a rice disease recognition algorithm using YOLOv8n and achieved an average recognition accuracy of 93.9%. Bhuyan et al. [43] proposed a novel stacked parallel CNN (called SE_SPnet) using squeeze-and-excitation (SE) for classifying rice leaf diseases.

Unlike classification approaches that use a single fixed model, ensemble learning uses a set of learners and applies rules to integrate the learning results to obtain better performance than a single learner [44–46]. The effectiveness of ensemble learning has been widely demonstrated in a variety of applications [47–50]. Therefore, in this study, the advantages of lightweight DCNNs were combined with those of ensemble learning, and a method was developed for rice disease classification. The experimental results demonstrate the accuracy and robustness of the proposed method. This work provides a reference for the accurate identification of rice diseases and reduction of the unnecessary use of pesticides.

The main contributions of this study are as follows: (1) The use of randomly generated multiple single classifiers with a simple structure (CG-EfficientNet) as the base learners can avoid the need to select optimal single-network model parameters and design appropriate network structures. (2) The sequential least squares programming (SLSQP) algorithm was used to calculate the weight of each base model to consider the differences between learners, which are ignored in the traditional stacking method.

The rest of this article is organized as follows. Section 2 describes the datasets of collected images. The theoretical background, including the architecture of EfficientNet and stacking ensemble strategy, is detailed in Section 3 along with a description of the proposed method. The experimental results are presented in Section 4. A discussion of the weaknesses and strengths of the proposed model along with future work is given in Section 5. Finally, the study's conclusions are summarized in Section 6.

2. Rice Image Datasets

The images used in this study were obtained in two ways. Some images were captured in the open field environment of the Agriculture Research Demonstration Bases of the Chongqing Academy of Agricultural Sciences and Southwest University, Chongqing, China. Digital cameras (for example, a Nikon D810 with a wide-angle lens which was manufactured by Nikon Corporation, and purchased in Beijing, China.) were used to obtain the images of lesions at a short distance (20–50 cm) directly perpendicular to the surface of the rice. When collecting images, the camera was set to automatically adjust the focal length and aperture, automatic white balance was selected, and the flash was turned off. The images were collected under sunny daylight conditions—direct sunlight, wind, and rain were avoided—and the light was as diffuse as possible. Other images were collected from public datasets on the Internet. All disease images were selected and labeled manually under the guidance of plant pathologists, and the image resolution was at least 224×224 pixels.

A total of 3380 images of four common rice diseases (667 rice bacterial blight, 735 rice false smut, 603 rice kernel smut, and 754 rice brown spot images) and 621 normal leaf images were used to test the effectiveness of the proposed method. The dataset was randomly split into training, validation, and test sets using a 6:2:2 ratio. Representative rice images used in this study are shown in Figure 1.

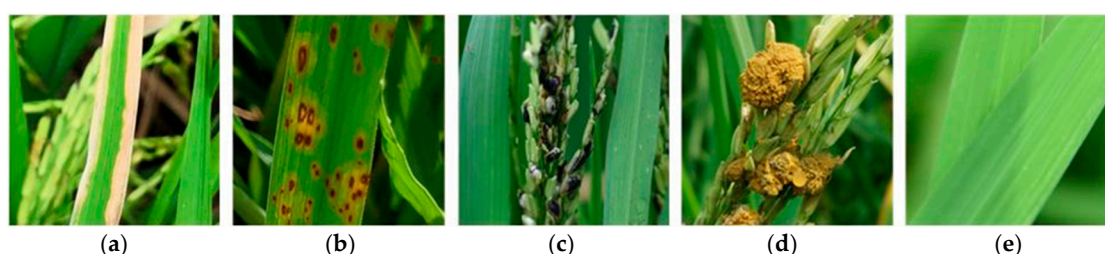


Figure 1. Representative rice images used in this study. (a) Rice bacterial blight, (b) rice brown spot, (c) rice kernel smut, (d) rice false smut, and (e) healthy leaves.

3. Methods

To improve the accuracy and stability of rice disease classification, the following lightweight deep CNN ensemble method for rice disease classification is proposed. First, a new lightweight deep CNN model called CG-EfficientNet, which is based on an attention mechanism and EfficientNet, was designed as the base learner. Second, CG-EfficientNet models with different optimization algorithms and network parameters were trained on rice disease datasets to generate seven different CG-EfficientNet models, and a resampling strategy was used to enhance the diversity of the individual models. Then, the SLSQP algorithm was used to calculate the weight of each base model. Finally, logistic regression was used as the meta-classifier for stacking. The framework of our method is depicted in Figure 2.

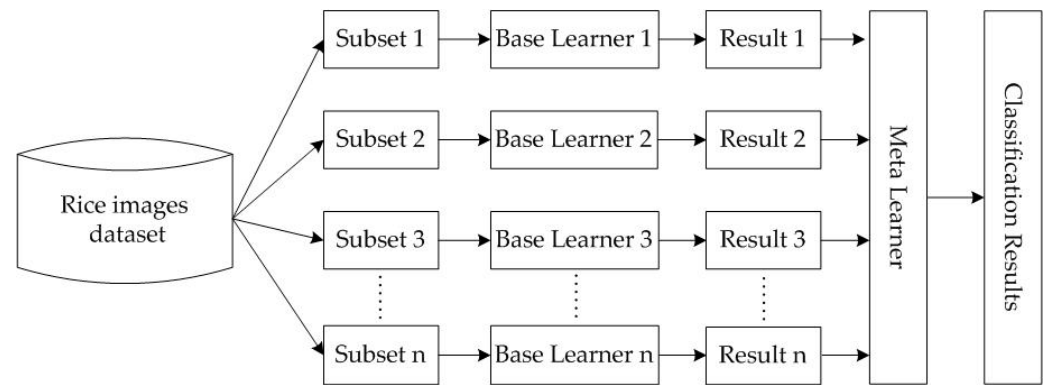


Figure 2. Framework of the proposed method.

3.1. EfficientNet

EfficientNet is a novel lightweight CNN proposed by Tan et al. in 2019 [51]. EfficientNet has attracted extensive attention because it can balance the model's depth, width, and image resolution through composite coefficients. Previously, when training a deep-learning model, the most common methods for improving model accuracy were to expand the width of the network, increase the depth of the network, and enhance the resolution of the input image. The network width, depth, and resolution were not fully balanced. Thus, EfficientNet combines three scaling methods to optimize performance. It achieves this balance by considering the following constraints:

$$\begin{aligned}
 \text{depth: } d &= \alpha^\phi \\
 \text{width: } w &= \beta^\phi \\
 \text{resolution: } r &= \gamma^\phi \\
 \text{s.t. } \alpha \cdot \beta^2 \cdot \gamma^2 &\approx 2 \\
 \alpha \geq 1, \beta &\geq 1, \gamma \geq 1
 \end{aligned} \tag{1}$$

where α , β , and γ are the scaling coefficients of each dimension that can be determined by a grid search, and ϕ is the compound coefficient. By changing the value of ϕ , EfficientNet-B0 can be scaled up to obtain models EfficientNet-B1 to EfficientNet-B7.

Based on a comprehensive consideration of the accuracy and number of parameters of all the models in the EfficientNet series, in this study, EfficientNet-B0 was adopted as the baseline network for further improvement. Table 1 presents the detailed information of each layer of EfficientNet-B0.

Table 1. EfficientNet-B0 network structure.

Stage	Operator	Resolution	# Channels	# Layers
1	Conv 3×3	224×224	32	1
2	MBConv1, $k3 \times 3$	112×112	16	1
3	MBConv6, $k3 \times 3$	112×112	24	2
4	MBConv6, $k5 \times 5$	56×56	40	2
5	MBConv6, $k3 \times 3$	28×28	80	3
6	MBConv6, $k5 \times 5$	14×14	112	3
7	MBConv6, $k5 \times 5$	14×14	192	4
8	MBConv6, $k3 \times 3$	7×7	320	1
9	Conv 1×1 & Pooling & FC	7×7	1280	1

3.2. CG-EfficientNet

To maintain high accuracy while making the identification model more lightweight, EfficientNet was modified in our work to obtain CG-EfficientNet. In this new model, the

convolutional block attention module (CBAM) was used as the lightweight attention module to replace the mobile inverted bottleneck convolution (MBConv) module of the main module in EfficientNet-B0. In addition, a ghost module was used to modify the convolution layer of the network and hence reduce the number of parameters and computation time of the network.

CBAM is a lightweight attention module that can be used in DCNNs to improve the performance of image recognition by focusing on important information and ignoring irrelevant information [52]. It is composed of a channel attention module and spatial attention module. When the network passes intermediate feature maps through the CBAM attention module, it adaptively adjust the weights based on the image content to focus on important channels and spatial positions, thereby enhancing the model's classification capabilities and performance. In contrast to CBAM, the SE attention mechanism in EfficientNet lacks a spatial attention mechanism. Therefore, when using EfficientNet to recognize rice disease, only the channel features are considered to determine which features are useful, and the different spatial features, which play an important role in rice disease recognition, are lost. This affects the recognition performance of the rice disease recognition model to a certain extent. To address this issue, the SE attention mechanism embedded in EfficientNet is replaced by the lightweight CBAM in our work.

The ghost module is a model compression method. It can substantially reduce the number of network parameters and the amount of computation while ensuring model accuracy is retained [53]. The ghost module can be integrated into any CNN architecture. Traditional CNNs often generate a large number of redundant and similar feature maps during feature extraction, which typically require a large number of network parameters and floating-point operations (FLOPs), resulting in a significant consumption of computational resources. However, the ghost module applies a series of linear transformations to generate these redundant feature maps, reducing the amount of computation caused by some convolution operations. Because of this, to reduce the computational complexity of generating feature maps using the EfficientNet model, we replaced the first convolutional layer in the EfficientNet model with a ghost module in our designed recognition model.

Integrating the ghost module and CBAM into EfficientNet-B0, the architecture of CG-EfficientNet is shown in Figure 3. This figure also shows the mobile inverted bottleneck convolution (MBConv).

Compared with the EfficientNet-B0 model, the following two aspects of CG-EfficientNet have been improved. (1) The ghost module is used to optimize the first convolution layer of EfficientNet-B0 to reduce the number of parameters and computation time of the network, as shown in Figure 3a. This module replaces standard convolution calculations with lightweight linear calculations to generate redundant feature maps. The process does not change the size of the output feature map, but the numbers of computations and parameters are much smaller than those of standard convolution, and the calculation speed is faster. (2) The CBAM was used to replace the SE attention mechanism within the MBConv module in EfficientNet-B0. The structures of the new MBConv module are shown in Figure 3b,c. The CBAM captures the channel-wise key information considered by the original SE module as well as the position information on the spatial axis. As a result, the recognition network pays attention to the relevant areas of rice disease spots without losing the relevant position information.

3.3. Stacking Ensemble Method

Stacking is a meta-learning method [47]. Stacked models can achieve higher classification accuracy and robustness than single models. In this study, a feature-weighted stacking ensemble method is proposed. It includes two main parts: construction of the base learners

and construction of the integration strategy. The structure of the proposed model is shown in Figure 4.

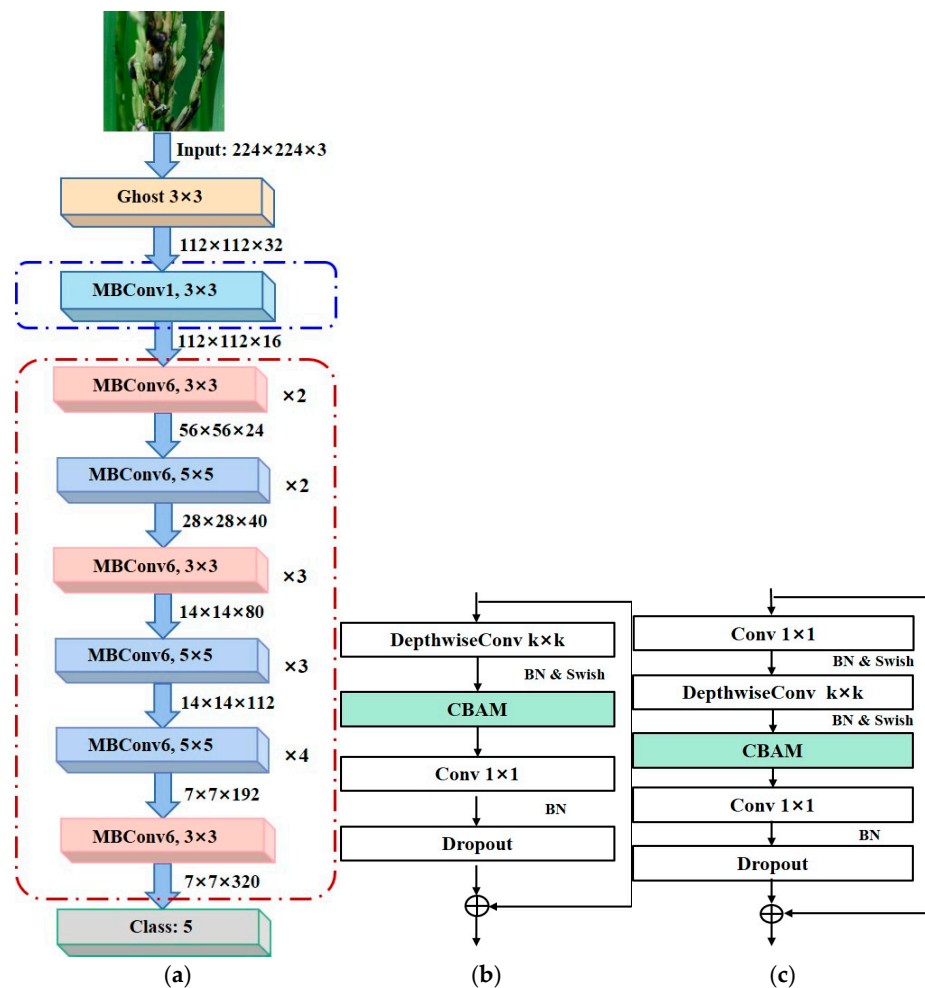


Figure 3. Architecture of CG-EfficientNet. (a) Overall structure, (b) MBConv1, and (c) MBConv6.

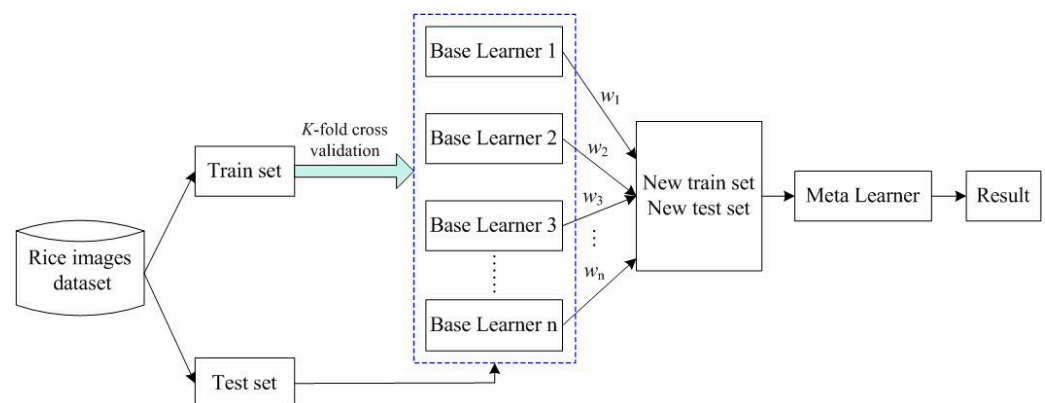


Figure 4. Structure of the stacking ensemble algorithm.

3.3.1. Construction of the Base Learners

In a typical implementation of stacking, the base learners should be as diverse as possible. Generally, the individual learners are created using different training sets, parameters, and learning algorithms. In this study, we used different training sets generated by random re-sampling and different parameters to generate seven different CG-EfficientNets. Table 2 presents the parameter settings for the CG-EfficientNets.

Table 2. Parameter settings for the CG-EfficientNets.

Single Classifier	Optimizer	Learning Rate	Batch Size
CG-EfficientNet1	Adam	0.001	32
CG-EfficientNet2	Adamax	0.002	16
CG-EfficientNet3	SGD	0.001	64
CG-EfficientNet4	RMSProp	0.002	32
CG-EfficientNet5	AdaGrad	0.001	16
CG-EfficientNet6	Nadam	0.002	64
CG-EfficientNet7	Adadelta	0.001	32

To improve the accuracy and generalization ability of the integrated model, k -fold cross validation was performed on the collected data. Because of the randomness of the training and test sets, the same model may yield different performance on different datasets, and k -fold cross validation can reduce this randomness and improve the stability and reliability of classification models by dividing the dataset into different training and test sets multiple times. In this article, we set the value of k to 10. To improve the accuracy and generalization ability of the integrated model, k -fold cross validation was performed on the collected data. Because of the randomness of the training and test sets, the same model may yield different performance on different datasets, and k -fold cross validation can reduce this randomness and improve the stability and reliability of classification models by dividing the dataset into different training and test sets multiple times. In this article, we set the value of k to 10.

In the proposed method, adopting multiple randomly generated single classifiers with a simple structure and initial parameters as the base learners avoids the problems of selecting optimal single-network model parameters and designing the appropriate network structures. Thus, the selection of initial parameters for single classifiers can be based on existing research in the literature and experience.

3.3.2. Construction of the Integration Strategy

In the traditional stacking ensemble method, the classifications of multiple base learners are combined using methods that weight all models equally, such as hard voting or simple averaging. In practice, a different weight could be used for each learner, as some learners might be superior to others and thus should be more heavily weighted [43,54]. To address this problem, a feature-weighted stacking ensemble integrated method based on SLSQP is proposed. In this method, the cross-entropy loss function is adopted to evaluate the classification performance of all base classifiers on the validation set. Then, the SLSQP is used to optimize and minimize this function and to calculate the weight of each base model. Thus, a new weighted feature set is generated as metadata. Finally, the logistic regression that combines the outputs of the base classifiers is learned.

SLSQP is a gradient-based method for solving nonlinear optimization problems with constraints and was proposed by Kraft in 1988 [55]. A constrained nonlinear optimization problem can be described as follows.

$$\min_{x \in R^n} L(x) \quad (2)$$

In this study, the cross-entropy loss was used as the objective function $L(x)$, calculated as

$$L(x) = -\frac{1}{N} \sum_{i=1}^N \sum_{c=1}^M y_{ic}(x) \log[p_{ic}(x)] \quad (3)$$

where N is the sample size, M is the number of categories, y is the sign function ($y = 0$ or 1), and $p_{ic}(x)$ is the probability that the input instance x belongs to category c .

SLSQP solves the optimization problem iteratively for a local minimum, starting with a solution x^0 as an initial guess. The solution $x^{\ell+1}$ is obtained from x^ℓ by

$$x^{\ell+1} = x^\ell + \alpha^\ell d^\ell \quad (4)$$

where d^ℓ is the search direction and α^ℓ is the iteration length within the ℓ -th iteration.

The feature-weighted stacking ensemble algorithm proceeds as follows.

- (1) Train each base learner using the training subset and calculate the cross-entropy loss of each base learner on the validation set.
- (2) Optimize the loss function using the SLSQP algorithm and calculate the weight of each base learner. The feature-weighted training set for the meta-learner is constructed by combining the output and weight of each base learner, which have been obtained through k -fold cross validation. For the i th-fold cross validation, the feature weights can be represented as

$$\hat{S}_i = [w_1 S_{i,1}, w_2 S_{i,2}, \dots, w_T S_{i,T}] \quad (5)$$

where T is the number of base learners and $w_1, w_2, \dots, w_T$ denotes the weights of the base learners. Newly constructed meta-learner features are denoted as $\{(Y_i, \hat{S}_i), i = 1, 2, \dots, k\}$, where Y denotes the sample labels from the original training set.

- (3) Learn the logistic regression that combines the outputs of the base classifiers.

In this study, we used the SLSQP algorithm implemented in SciPy 1.0.

4. Results and Analysis

All the experiments were performed using TensorFlow-GPU 2.4.1 in the Python 3.8 programming environment on a computer with an Intel i7-11700K (3.6 GHz) eight-core processor (The processor was manufactured by Intel Corporation, and purchased in Beijing, China.), 32 GB of memory (RAM), NVIDIA GeForce RTX 3080 Ti graphics card, and Windows 10 operating system. The computing package scikit-learn (sklearn) was used. The accuracy, precision, recall, and F1-score were selected to evaluate the performance of our proposed model [2].

4.1. Performance Comparison of the Combined and Individual Classifiers

Seven CG-EfficientNets were generated randomly using the parameter settings in Table 2 and integrated using the weighted logistic regression meta-classifier. The recognition accuracies of each CG-EfficientNet and the integrated model are reported in Table 3.

Table 3. Classification results obtained by the base learners and proposed integrated model.

Model	Accuracy/%	Precision/%	F1_Score/%	Recall/%
CG-EfficientNet1	90.73	91.10	90.43	90.28
CG-EfficientNet2	91.96	88.92	88.73	89.31
CG-EfficientNet3	91.78	91.65	91.73	91.92
CG-EfficientNet4	87.06	87.98	86.15	86.38
CG-EfficientNet5	89.69	88.96	88.81	88.97
CG-EfficientNet6	88.64	89.05	88.52	88.75
CG-EfficientNet7	90.56	90.45	90.46	90.62
Proposed method	96.10	95.68	95.74	95.81

As seen in Table 3, our proposed method had a higher recognition performance than the base learners. The classification accuracy of the proposed method was 96.10%, which is 4.14% and 7.46% better than that of the classification accuracies of the highest and lowest base learner, respectively. Moreover, the precision, F1-score and recall of the

proposed method were all higher than those of the base learners. These results show that the proposed integrated model not only significantly improved the recognition accuracy but its performance was more stable.

4.2. Performance Comparison with Classical CNN Methods

The proposed model was compared with several frequently used CNN models: VGG16, Inception-V3, ResNet-101, and DenseNet201. The results of image classification using different methods are presented in Table 4.

Table 4. Results of image classification using different methods.

Methods	Accuracy/%	Parameters
VGG16	87.24	48, 533, 829
Inception-V3	90.91	23, 906, 085
ResNet-101	91.96	44, 761, 477
DenseNet201	94.58	20, 294, 213
Proposed method	96.10	4, 392, 549

The results in Table 4 reveal that the classification accuracy of our method was 96.10%, representing improvements of 8.86%, 5.19%, 4.14%, and 1.52% over the accuracies of VGG16, Inception-V3, ResNet-101, and DenseNet201, respectively. Moreover, the proposed method has fewer network parameters.

Table 5 presents the classification performance comparison of different ensemble methods. The experimental results show that the proposed method improved the classification accuracy results of the snapshot, voting, averaging, and stacking methods by 2.70%, 1.87%, 1.69%, and 2.21%, respectively. The proposed integrated model had a higher recognition accuracy because an optimal feature set was selected through the weighting. Therefore, the recognition was more targeted and hence more accurate. This is in contrast with the traditional stacking ensemble model, which ignores the differences between learners. As a result, all classifiers were integrated directly, and hence some invalid decisions were fused, which affected the final recognition results. Thus, the traditional stacking ensemble model's classification ability is poor.

Table 5. Classification accuracy comparison of different ensemble methods.

Methods	Accuracy/%
Snapshot	93.40
Voting	94.23
Average	94.41
Stacking	93.89
Proposed method	96.10

4.3. Performance Results on PlantVillage

To evaluate the robustness of our method, comparative experiments were carried out on the public PlantVillage dataset. In the experiments, 6627 samples of tomato leaf images were used. Each was labeled as one of the following 10 classes: early blight, target leaf spot, late blight, leaf mold, septoria leaf spot, mosaic virus, yellow leaf curl virus, spider mites, two-spotted spider mites, or normal leaf.

Our proposed method was compared with the following classical CNN models: AlexNet, VGG16, Inception-V3, MobileNetV1, ResNet101, and DenseNet201. The parameter settings for these classification models are as follows. All models adopted the training strategy of gradual learning, employed cross-entropy as the loss function, and used Adam to optimize the loss function. The initial learning rate η was set to 10^{-3} . When

the performance of the classification model did not improve over two epochs, the learning rate was decreased by a factor of 0.1. The number of epochs was set to 200, the batch size was set to 32, and the dropout ratio was set to 0.5.

The results of the comparison are presented in Table 6, revealing that our method still achieved good classification performance. This indicates that not only does it have high recognition accuracy but it also has better generalization performance.

Table 6. Classification accuracies of different methods on the PlantVillage dataset.

Model	Accuracy
AlexNet	98.29
VGG16	97.48
Inception-V3	98.91
MobileNetV1	98.74
ResNet101	98.96
DenseNet201	99.06
Proposed method	99.37

5. Discussion

Rice diseases such as rice bacterial blight, rice brown spot, rice false smut, and rice kernel smut occur frequently during rice growth, causing serious losses in rice production. The fast and accurate identification of rice diseases is a prerequisite for controlling them and is an effective way to improve rice yield and quality. In recent years, CNNs have achieved significant developments in rice disease classification. However, they still have some limitations, as discussed in Section 1. To address these issues, the advantages of lightweight CNNs were combined with those of ensemble learning and a lightweight CNN ensemble method was developed for rice disease classification. The experimental results (Tables 4 and 5) demonstrate that the proposed model has better accuracy than single CNN models (VGG16, Inception-V3, ResNet-101, and DenseNet201) and ensemble methods (snapshot, voting, averaging, and stacking).

This algorithm is effective for the following reasons. First, a lightweight CNN model named CG-EfficientNet was designed as the base learner and consisted of an attention mechanism and EfficientNet. Three main improvements were made: the MBConv module of the main module in EfficientNet-B0 was improved, the network convolutional layer was optimized, and the Adam optimization algorithm was used. Thus, the proposed model has a more lightweight network structure, higher classification accuracy, and faster training speed than EfficientNet-B0. Second, the use of randomly generated multiple single classifiers with a simple structure as the base learners (CG-EfficientNet) can avoid the need to select optimal single-network model parameters and design appropriate network structures. Third, the SLSQP algorithm was used to calculate the weight of each base model. The optimal combination of the outputs from the base models was obtained via a meta-learner. Because the results of these base models are weighted according to the difference in the classification accuracy under cross-validation, the proposed weighted stacking ensemble model achieves higher classification accuracy and robustness than single models.

Although our method performs well, it has some limitations that should be improved in future study. The quality of the data is an important factor in the performance of image recognition algorithms. The same recognition algorithm learns different features on datasets of different quality, and hence its recognition performance also varies. Disease datasets are divided into two main categories: private datasets and public datasets. However, most datasets are established for specific practical needs, with limited classes and quantities, and most of them are private. In this work, we collected image samples from different sources,

regions, and seasons to represent a wide range of scenarios so that they provided more of a challenge for the proposed method. These results (Tables 4–6) demonstrate the accuracy and generalization of the proposed method.

In addition, different diseases with similar color characteristics are prone to misclassification. For example, rice false smut is easily misclassified as rice kernel smut. The reason is that both of these diseases occur on the grains of rice; moreover, the dark green color of rice false smut is similar to the black color of rice kernel smut. Thus, the construction of high-quality datasets is crucial. In future research, we will expand and improve the rice disease dataset. The construction of the dataset will be combined with practical usage scenarios, and it will focus on reasonable inter-class and intra-class sample distributions. In addition, we will develop a fast and accurate rice disease identification system that can guide farmers to use pesticides scientifically and reasonably, ensuring the sustainability of rice production.

6. Conclusions

To quickly and accurately identify rice diseases, we proposed a lightweight deep CNN ensemble method. First, a lightweight CNN model based on an attention mechanism and EfficientNet was designed for the base learners. Next, seven different single models were randomly generated and then integrated using a weighted logistic regression meta-classifier. Classification experiments were performed on a dataset of five classes of rice tissue and the PlantVillage dataset. The accuracy of the proposed method was 96.10%. The proposed method was compared with the classical CNN models VGG16, InceptionV3, ResNet101, and DenseNet201 as well as four integration methods, and the results demonstrate the accuracy and effectiveness of the proposed method.

Future work will actively explore lightweight identification models and effective combination methods. In addition, the construction of high-quality datasets will be a focus. We also intend to use these models on different public datasets.

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