



Automatic grape leaf diseases identification via UnitedModel based on multiple convolutional neural networks

Miaomiao Ji^a, Lei Zhang^b, Qiufeng Wu^{c,*}

^a College of Engineering, Northeast Agricultural University, Harbin 150030, China

^b School of Medicine, University of Pittsburgh, Pittsburgh 15260, USA

^c College of Science, Northeast Agricultural University, Harbin 150030, China

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ABSTRACT

Grape diseases are main factors causing serious grapes reduction. So it is urgent to develop an automatic identification method for grape leaf diseases. Deep learning techniques have recently achieved impressive successes in various computer vision problems, which inspires us to apply them to grape diseases identification task. In this paper, a united convolutional neural networks (CNNs) architecture based on an integrated method is proposed. The proposed CNNs architecture, i.e., UnitedModel is designed to distinguish leaves with common grape diseases i.e., black rot, esca and isariopsis leaf spot from healthy leaves. The combination of multiple CNNs enables the proposed UnitedModel to extract complementary discriminative features. Thus the representative ability of UnitedModel has been enhanced. The UnitedModel has been evaluated on the hold-out PlantVillage dataset and has been compared with several state-of-the-art CNN models. The experimental results have shown that UnitedModel achieves the best performance on various evaluation metrics. The UnitedModel achieves an average validation accuracy of 99.17% and a test accuracy of 98.57%, which can serve as a decision support tool to help farmers identify grape diseases.

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1. Introduction

Grapes, as one of the most commonly cultivated economical fruit crops throughout the world, are widely used in the production of wine, brandy or nonfermented drinks and are eaten fresh or dried as raisins [1]. However, grapes are vulnerable to various different types of diseases, such as black rot,

esca, isariopsis leaf spot, etc. It is estimated that losses caused by grape diseases in Georgia, USA in 2015 were approximately \$1.62 million. Around \$0.5 million was spent on diseases control and the rest was the loss caused by the diseases [2]. Thus, early detection of grape diseases can potentially cut losses and control costs and consequently can improve the quality of products.

For decades, the diseases identification is mostly performed by human. The process of recognition and diagnosis is subjective, error-prone, costly and time-consuming. In addition, new diseases can occur in places where they were

* Corresponding author.

E-mail address: qfwu@neau.edu.cn (Q. Wu).

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previously unidentified and, inherently, where there is no local expertise to combat them [3]. As a result, an automatic identification method for grape disease identification is in urgent demand.

The development of sophisticated instruments and fast computational techniques have paved the way for real-time scanning and automatic detection of anomalies in a crop [4]. Although traditional machine learning methods have gained some valuable experience in identification and diagnosis of crop diseases, they are limited to following the pipelined procedures of image segmentation (such as clustering method [5], threshold method [6], etc.), feature extraction (such as shape, texture, color features, etc. [7]), and pattern recognition (such as k-nearest neighbor method (KNN) [8], support vector machine (SVM) [1], back propagation neural network (BPNN) [9], etc.). It is difficult to select and extract the optimal visible pathological features and thus highly skilled engineers and experienced experts are demanded, which is not only to a considerable extent subjective but also leads to a great waste of manpower and financial resources. In contrast, deep learning techniques can automatically learn the hierarchical feature of pathologies and do not need to manually design the feature extraction and classifier. Deep learning method has so excellent generalization ability and robustness that it excels in many areas: signal processing [10], pedestrian detection [11], face recognition [12], road crack detection [13], biomedical image analysis [14], etc. In addition, deep learning techniques have also achieved impressive results in the field of agriculture and benefit more smallholders and horticultural workers, including diagnosis of crop diseases [15], recognition of weeds [16], selection of fine seeds [17], pest identification [18], fruit counting [19], research on land cover [20] etc, which has contributed to dealing with image classification of areas of interest. Furthermore, some applications focused on predicting future parameters, such as crop yield [21], weather conditions [22] and soil moisture content in the field [23]. Inspired by the great success of CNN-based methods in image classification, we propose an integrated model, denoted UnitedModel, for automatic grape leaf disease identification.

The rest of this paper is organized as follows. Section 2 starts with an overview of related works. Section 3 introduces dataset as well as data preprocessing and covers details of the proposed UnitedModel. In Section 4, we conduct all the experiments, discuss the limitation of the proposed UnitedModel and prospect the future work. In Section 5, we conclude this paper.

2. Related works

Machine learning techniques were applied widely in plant disease classification in the early stage. Li et al. [24] proposed a method based on K-means clustering segmentation of the grape disease images and a SVM classifier was designed based on thirty-one effective selected features to identify grape downy mildew disease and grape powdery mildew disease with testing recognition rates of 90% and 93.33%, respectively. Significant progress has been made in the use of image processing approaches to detect various diseases in crops.

Athanikar and Badar [9] applied Neural Network to categorize the potato leaf image as either healthy or diseased. Their results showed that BPNN could effectively detect the disease spots and could classify the particular disease type with an accuracy of 92%. The deployment of deep CNNs has especially led to a breakthrough in plant disease classification, which can find very high variance of pathological symptoms in visual appearance, even high intra-class dissimilarity and low inter-class similarity that may be only noticed by the botanists [25]. Lee et al. [26] proposed a CNN approach to identify leaf images and reported an average accuracy of 99.7% on a dataset covering 44 species, but the scale of datasets was very small. Zhang et al. [27] used GoogLeNet to address the detection of cherry leaf powdery mildew disease and obtained an accuracy of 99.6%. Their results also demonstrated transfer learning can boost the performances of deep learning model in crop disease identification. Mohanty et al. [15] fine-tuned deep learning models pre-trained on ImageNet to identify 14 crop species and 26 diseases. The models were evaluated on a publicly available dataset including 54,306 images of diseased and healthy plant leaves collected under controlled conditions. They achieved the best accuracy of 99.35% on a hold-out test dataset.

Although the basic CNN frameworks, such as AlexNet [28], VGGNet [29], GoogLeNet [30], DenseNet [31] and ResNet [32] have been demonstrated effective and widely used in crop diseases classification, most previous works had troubling boosting up the classification accuracy rate to some extent. As a matter of fact, a single model can't meet the further requests in terms of precision. In large machine learning competitions, the best results were usually achieved by the integration of multiple models rather than by a single model. For instance, the well-known Inception-ResNet-v2 [33] was born out of the fusion of two excellent deep CNNs, as the name suggests. Inspired by network in network concept [34], we think that integration is the most straightforward and effective way when the basic models are significantly different. We propose the UnitedModel in this study. The UnitedModel is a integration of the powerful and popular deep learning architectures of GoogLeNet and ResNet. We also take advantage of transfer learning to boost accuracy as well as reduce the training time.

3. Materials and methods

3.1. Dataset and preprocessing

Our dataset comes from an open access repository named PlantVillage which focuses on plant health [35]. The dataset used for evaluating the proposed method is composed of healthy (171 images) and symptom images including black rot (pathogen: *Guignardia bidwellii*, 476 images), esca (pathogen: *Phaeomoniella* spp, 552 images) and isariopsis leaf spot (pathogen: *Pseudocercospora vitis*, 420 images) (see Table 1). The identification of grape diseases is based on its leaf, not flower, fruit or stem. For one thing, the flower and fruit of grape only appear in a limited time while the leaf presents most of the year. For another thing, the stem of grape can hardly present the symptoms of the diseases timely, while

Table 1 – Introduction of grape leaf dataset.

Label	Category	Number	Data augmentation	No data augmentation		Leaf symptoms	Illustration
			Training samples	Validation samples	Test samples		
1	Black rot	476	288	72	116	Appear small, brown circular lesions	See Fig. 1 first row
2	Esca	552	288	72	192	Appear dark red or yellow stipes	See Fig. 1 second row
3	Isariopsis leaf spot	420	288	72	60	Appear many small rounded, polygonal or irregular brown spots	See Fig. 1 third row
4	Health	171	96	24	51	–	See Fig. 1 fourth row
Total samples		1619	960	240	419	–	–

**Fig. 1 – The grape leaf images after data augmentation.**

the leaf is generally sensitive to the state of plants, whose shape, texture and color usually contains richer information.

The raw images are divided into training dataset and test dataset. 360 Symptom and 120 healthy images are selected for training and the rest images are used for testing. To prevent over-fitting, the training dataset is further split into training (80%) and validation data (20%). Thus the training dataset is 960 samples in total, validation dataset is 240 samples in total and test dataset is 419 samples in total [36]. The original images in the PlantVillage dataset are RGB images of arbitrary size. Data preprocessing is necessary and all the images are resized to the expected input size of the respective networks, i.e. 224×224 for VGGNet, DenseNet and ResNet, and 229×229 for GoogLeNet. Model optimization and prediction are both performed on these rescaled images. To avoid over-fitting and to boost the generalizability of the CNNs, data augmentation techniques which include rotating, flipping, shearing, zooming and colour changing are randomly performed in training phase as shown in Fig. 1.

Considering that the number of healthy samples in our work is relatively small with 171 samples in total, the proportion between healthy samples and diseased samples is set to 1: 3 while the *class_weight* ratio of them is set to 3: 1. By this way, the loss function can be adjusted in the training process and healthy samples can obtain more attention.

3.2. Identification model of grape leaf diseases

In this paper, the grape leaf diseases identification can be formulated as a multi-class classification problem. The classification process of this work can be described as follows (Fig. 2). Assuming a mapping function from grape leaf images to corresponding predicted labels (i.e. “Label”, “Label2”, “Label3” and “Label4”) $f: X \rightarrow Y$. Then the grape leaf training dataset is denoted as $(x_1, y_1), (x_2, y_2), \dots, (x_n, y_n)$. The training dataset is the input of the CNN model A. During training, the weights of A are updated continuously to minimize the average loss function which is defined as:

$$J(\omega) = -\frac{1}{n} \sum_{i=1}^n y_i \log(h_{\omega}(x_i)) \quad (1)$$

where x is the training sample, n is the number of input data, y_i is the true label and $h_{\omega}(x_i)$ is the predicted label of the CNN model A given current weights ω . Then, the end-to-end optimization can be performed using the stochastic gradient descent (SGD) method. The gradient of the loss function can be computed with the following equation:

$$\omega_{t+1} = \mu\omega_t - \alpha \nabla J(\omega_t) \quad (2)$$

where μ is the momentum weight for the current weights ω_t and α is the learning rate. Noted that the iterative operation

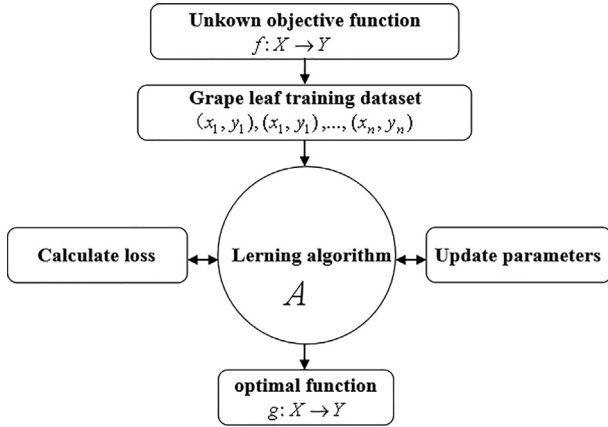


Fig. 2 – The mathematical model of grape leaf disease identification.

of ω is limited in added layers because all parameters in convolutional layers are set to the pre-trained network weights and fixed. After a series of epochs, an optimal function $g: X \rightarrow Y$ is obtained, which is the final hypothesis. Then we can input the test dataset into A and get the corresponding predicted labels.

3.3. Architecture of UnitedModel

The UnitedModel proposed for grape leaf disease identification is based on two popular deep learning architectures i.e., GoogLeNet and ResNet. GoogLeNet, the winner of ILSVRC 2014, was precisely aimed to reduce the computational cost and complexity. The whole architecture of GoogLeNet is stacked by inception modules that combine multi-scale feature extraction and dimension reduction layers based on the Hebbian principle and embedding learning. In our work,

InceptionV3 is selected as one component of the UnitedModel. ResNet won the first place in ILSVRC 2015 and COCO 2015 classification challenge with error rate of 3.57%, which introduced residual units for addressing the degradation problem of CNNs. ResNet is stacked by many residual units. Given the size of the dataset used in this work, ResNet50 becomes our first choice to be another basic network of the UnitedModel, which also has high performance in classification tasks. Given sufficient data, the most straightforward way of improving the performance of CNNs is increasing their parameters. In this study, GoogLeNet increases its width: the number of units at each layer while ResNet increases the depth: the number of network layer. The integration is most effective when the basic models are significantly different because their combination will enable the integrated network to capture more distinguishing feature information, thereby improving identification accuracy.

An illustration for the workflow of the proposed method is shown in Fig. 3. Given a testing image, the well-trained UnitedModel extracts two different feature sets by using GoogLeNet and ResNet and then performs the prediction based on the combined feature sets. In Fig. 4, we show the detailed structure of the UnitedModel. Considering that our dataset is relatively small, direct training from scratch on the dataset of grape leaf diseases will result in over-fitting. And thus transfer learning is adopted. The training phase is as follows: Firstly, the input image is resized to the expected input size of the respective networks and propagated forward to each basic single model, i.e. InceptionV3 and ResNet50. The feature maps are extracted by multi-type convolution filters arranged in InceptionV3 and ResNet50. And then through global average pooling (GAP), the feature maps extracted from convolution layers will be output in the form of two-dimensional matrix and then merged operation concatenation (Fig. 3). After that, a dropout layer, a fully connected layer, an another dropout layer, a classification layer (Fig. 4) are added. Within

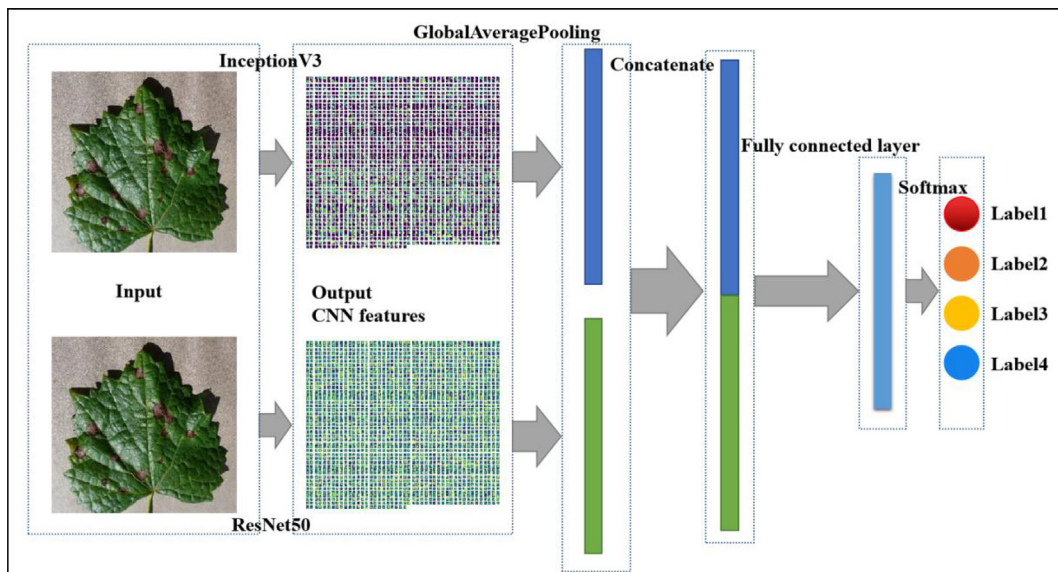


Fig. 3 – An illustration for the workflow of the proposed method.

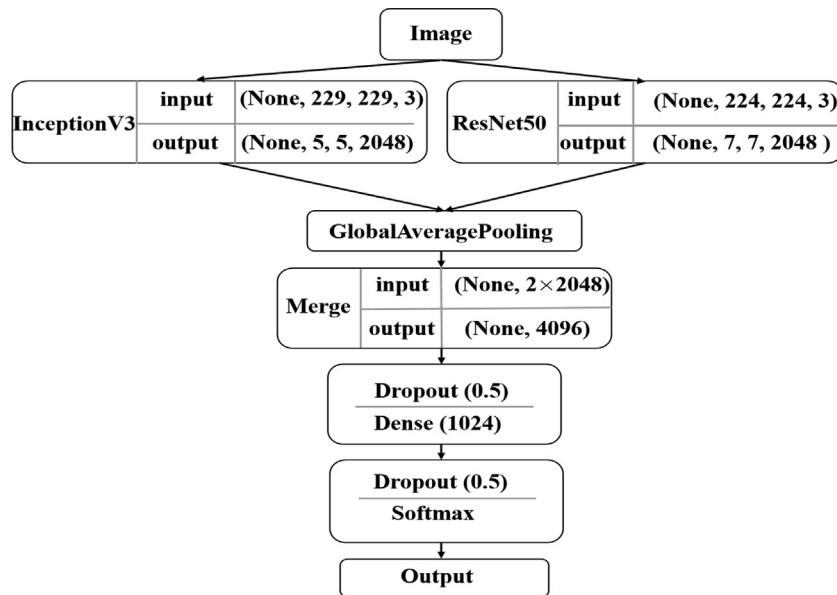


Fig. 4 – Structure of UnitedModel.

the classification step, each neuron in fully-connected layers provides a full connection to all learned feature maps. Accordingly, the united two-dimensional feature matrix combines freely with each other, generating different feature maps and thus improving the flexibility and characterization ability of the model [37]. Since the abundant training parameters and complex structures in the proposed UnitedModel easily cause over-fitting, dropout layers are used with rate 0.5. The softmax classifier is used as the final classification layer to obtain the classification results.

3.4. Experimental environment

The proposed model is built using the open source Keras framework on top of TensorFlow. All experiments are conducted on a system with the specifications in Table 2.

The original architectures of VGGNet, GoogLeNet, DenseNet and ResNet are trained as the control experiments of UnitedModel to explore whether the integrated approach can improve the performance in the grape diseases identification task and where the improvement is significant. To enable a fair comparison between the results of all the experimental configurations, all the hyper-parameters are standardized. The SGD algorithm is used to learn the best set of weights and biases of the neural networks that minimize the loss function. While learning, the SGD algorithm works by randomly choosing a small number of training inputs referred to as batch size which is set to 16. The learning rate is set to 0.001. It is the rate at which a function moves through the search space. A small learning rate leads to more precise results but it requires more training time. The momentum is an additional factor to determine how fast the SGD algorithm converges on the optimum point. It is set to 0.9. Early stopping mechanism is used to deal with the problem of over-fitting and speed up the training process. The training ends when

Table 2 – Experimental environment.

Hardware	Software
CPU: Intel Core i7-6700HQ	Windows10
RAM: 8 GB DDR4	CUDA9.0+CuDNN7.0
GPU: NVIDIA GEFORCE GTX 960M	Keras, Tensorflow

the network does not significantly improve its validation performance after 3 epochs.

3.5. Evaluation metrics

The evaluation of the different experimental configurations is based on a train-validation-test scheme. The actual training is carried-out on the training dataset while the validation dataset is used to avoid over-fitting. The performance of each model is assessed on the test dataset. Precision, recall and average F1-score are used as evaluation metrics. Experimental results are reported across all our experimental configurations. Due to its increased sensitivity to imbalances among the classes, the overall accuracy is also computed [38]. The precision, recall and F1-score are expressed in the following:

$$precision_c = \frac{TP_c}{TP_c + FP_c} \quad (3)$$

$$recall_c = \frac{TP_c}{TP_c + FN_c} \quad (4)$$

$$F1 - score = \frac{2}{4} \sum_{c=1}^4 \frac{recall_c * precision_c}{recall_c + precision_c} \quad (5)$$

where TP is true positive, FP is false positive, FN is false negative, c is the class of grape diseases and healthy type is included. For a more detailed comparison at different operating points, confusion matrix analysis for VGGNet, GoogLeNet, DenseNet, ResNet and UnitedModel is also performed.

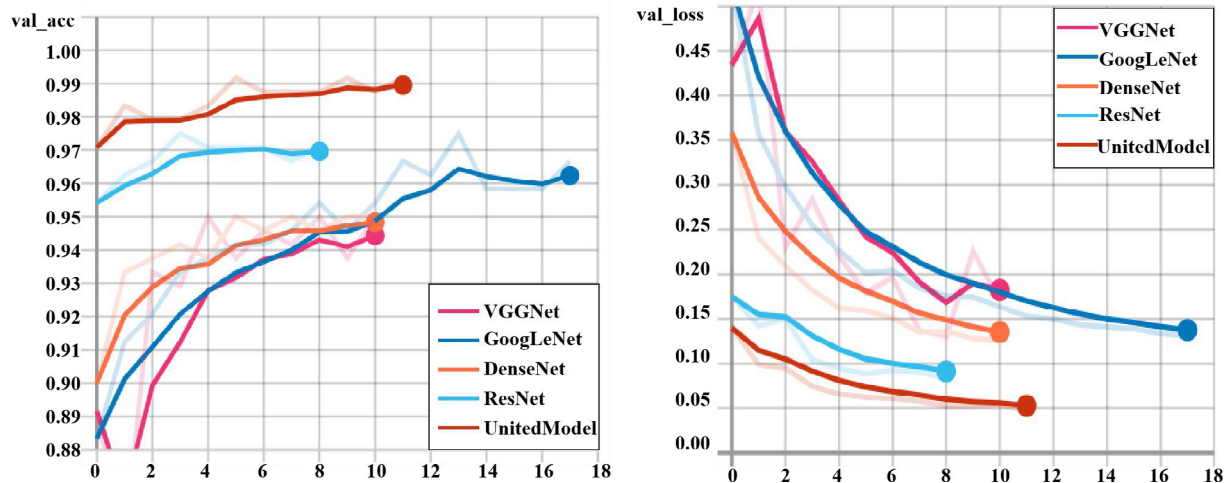


Fig. 5 – Validation accuracy and validation loss of various architectures are compared and the number of epoch is varied in the case of early stopping mechanism. VGGNet, GoogLeNet, DenseNet, ResNet and UnitedModel stop training with the epoch 11, 18, 11, 9 and 12, respectively.

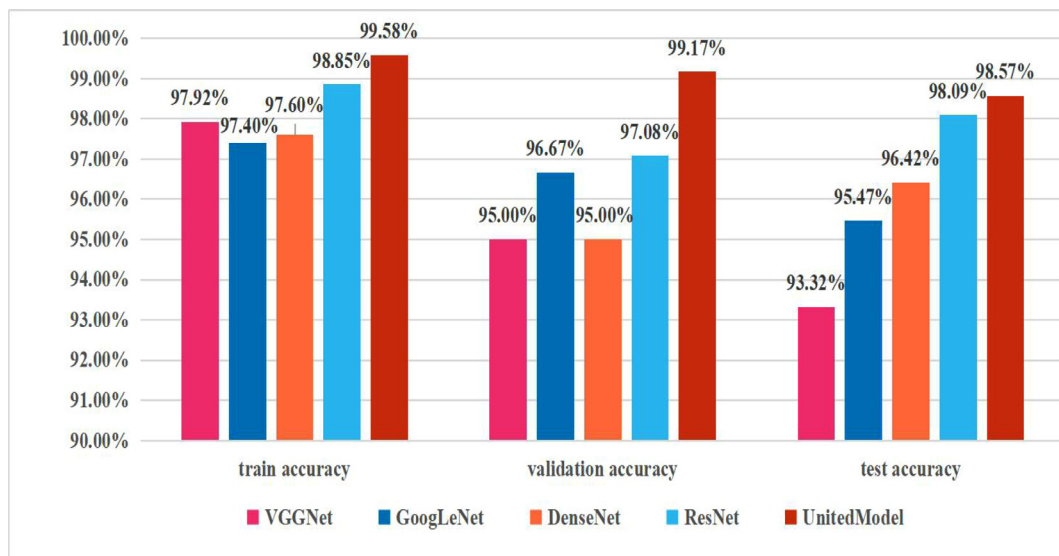


Fig. 6 – Comparison of the average accuracy for the different architectures.

4. Results and discussion

As illustrated in Fig. 5, UnitedModel has a tendency to consistently improve in accuracy with growing number of epochs, with no signs of performance deterioration. On the other hand, loss curve of UnitedModel converges rapidly and has a big gap with other single models in terms of error rate. Consistent with Fig. 6, the performance of GoogLeNet, VGGNet, DenseNet and ResNet is similar and all inferior to UnitedModel.

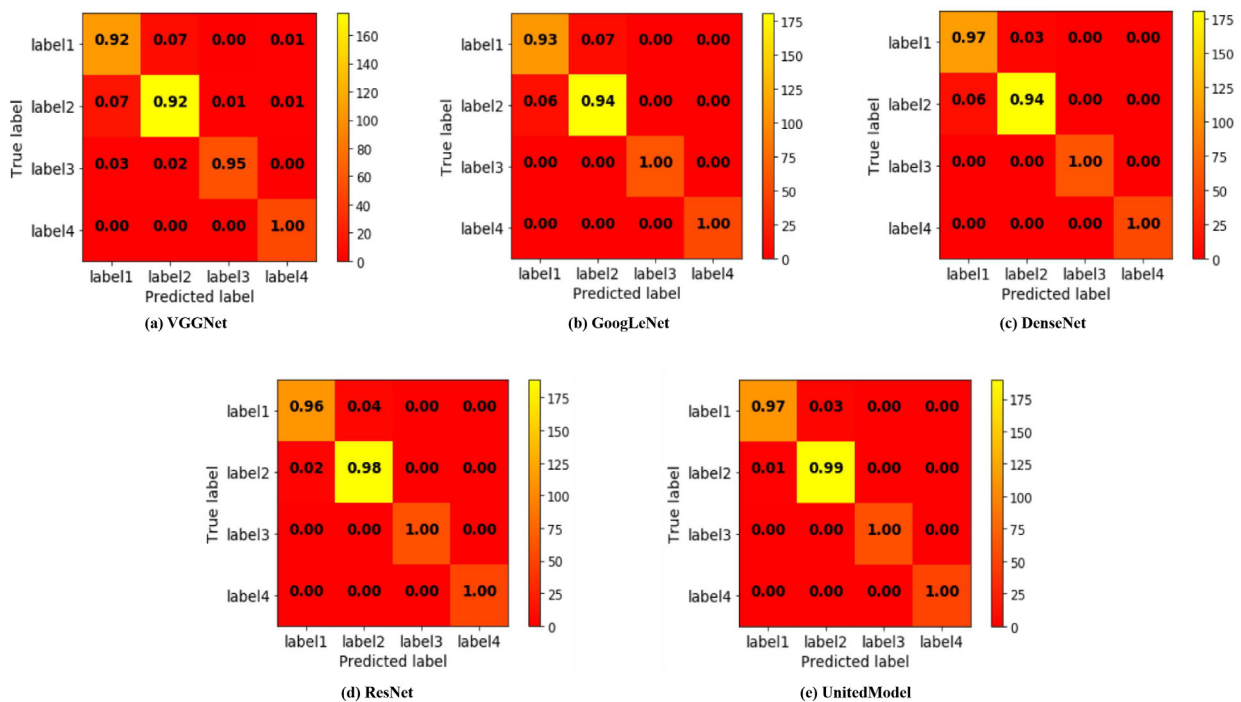
As we can see in Table 3, the average precision (99.05%), recall (98.88%) and F1-score (98.96%) of UnitedModel are the highest among all these models. And scores of VGGNet are the lowest with precision (94.16%), recall (93.32%) and F1-

score (94.40%), which once again proves the superiority of integrated CNNs.

The confusion matrices of different models on test dataset are shown in Fig. 7. The threshold is set to 0.5 and the fraction of accurately predicted images for each class is displayed in detail. The performance of VGGNet is poor. VGGNet tends to distinguish diseased samples as healthy, which is extremely harmful in actual agriculture produce. All the models except VGGNet can distinguish label3 and label4 easily, but label1 and label2 are prone to be misclassified. The large green area of healthy leaves and the golden appearance of leaves infected with isariopsis leaf spot disease make them easier to be distinguished. Meanwhile, the confusion between label1 and label2 is due to their similar pathological features.

Table 3 – Precision, recall and F1-score for the corresponding experimental configurations (best overall performance is displayed in boldface).

Architecture	Criterion	Label Support	Label1 116	Label2 192	Label3 60	Label 4 51	Total/Average 419
VGGNet	Precision		0.8699	0.9514	0.9828	0.9623	0.9416
	Recall		0.9224	0.9167	0.9500	1.0000	0.9332
	F1-score		0.8954	0.9337	0.9661	0.9808	0.9440
GoogLeNet	Precision		0.9076	0.9577	1.0000	1.0000	0.9663
	Recall		0.9310	0.9427	1.0000	1.0000	0.9684
	F1-score		0.9191	0.9501	1.0000	1.0000	0.9673
DenseNet	Precision		0.9642	0.9784	1.0000	1.0000	0.9722
	Recall		0.9655	0.9427	1.0000	1.0000	0.9771
	F1-score		0.9372	0.9602	1.0000	1.0000	0.9744
ResNet	Precision		0.9737	0.9742	1.0000	1.0000	0.9870
	Recall		0.9569	0.9844	1.0000	1.0000	0.9853
	F1-score		0.9652	0.9793	1.0000	1.0000	0.9861
UnitedModel	Precision		0.9825	0.9794	1.0000	1.0000	0.9905
	Recall		0.9655	0.9896	1.0000	1.0000	0.9888
	F1-score		0.9739	0.9845	1.0000	1.0000	0.9896

**Fig. 7 – Confusion matrices for the grape diseases dataset are presented with an overall accuracy associated for individual classes. The confusion matrices are given in terms of percentages, not absolute numbers.**

However, UnitedModel improves the test accuracy of label1 (97%) and label2 (99%). The UnitedModel is a combination of InceptionV3 and ResNet50 and can improve the representative capability by enriching features using multi-network integration method. In this study, we conjecture different CNN models to generate complementary features and we boost the performance by combining the complementary features. In addition, the use of transfer learning makes this process more concise and efficient.

The loss and accuracy curves of the UnitedModel during training phase are presented in Fig. 8. The green and black curves are the loss function values on the training dataset and validation dataset, respectively. The two curves drop rapidly in the first two epochs and start to converge after around 6 epochs. And then, the training loss continues to descend slightly until roughly the final epoch while validation loss is no longer significantly reduced. The red and blue curves represent the training accuracy and validation

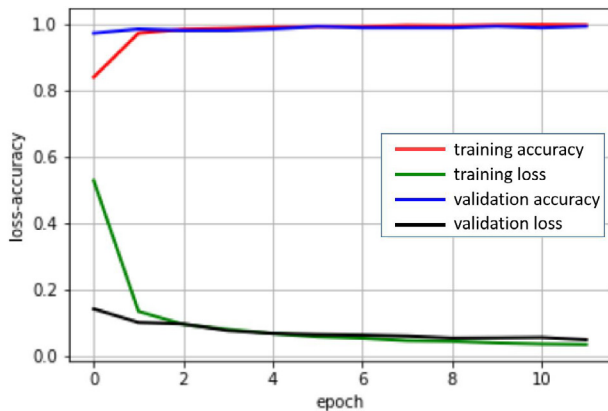


Fig. 8 – The trend of train accuracy, validation accuracy, train loss and validation loss of the UnitedModel.

accuracy, respectively. In Fig. 8, we can observe that after a few epochs they overlap almost completely, showing that UnitedModel gets sufficiently trained.

Experimental results have shown that the proposed UnitedModel integrating InceptionV3 and ResNet50 can achieve promising results for the grape leaf diseases identification task. However, since the training dataset used in our work is composed of samples in a simple background scene, the trained model cannot be applied for real-time diagnosis of grape leaf diseases in the complex background. One direction of future work is to create datasets under un-controlled scenario which can be used for training model to improve the generalizability. Thus the proposed model can be used for the development of mobile systems and devices. Another direction of future work is to compress the model while keeping the same performance. The proposed UnitedModel is a combination of two popular models and is of huge number the parameters. The training of the UnitedModel is great computational cost. It is important to find out an effective pruning mechanism for model compression to reduce computational resources.

5. Conclusions

In this work, we have developed an effective solution to automatic grape diseases identification based on CNNs. We have proposed the UnitedModel which is a united CNNs architecture based on InceptionV3 and ResNet50 and can be used to classify grape images into 4 classes, including 3 different symptom images i.e., black rot, esca, isariopsis leaf spot, and healthy images. UnitedModel takes advantage of the combination of InceptionV3's width and ResNet50's depth and thus can learn more representative features. The representational ability of UnitedModel is strengthened by way of high-level feature fusion, which makes it achieve the best performance in the grape diseases identification task. The experimental results demonstrate that our model can outperform the state-of-the-art basic single CNNs including VGG16, InceptionV3, DenseNet121 and ResNet50. The proposed UnitedModel achieves an average validation accuracy of 99.17% and a test accuracy of 98.57% and thus can serve as a decision

support tool to help farmers identify the grape diseases. We also provide a practical study for dealing with the insufficiency and unbalance of dataset. The methods of data augmentation techniques, early stopping mechanism and dropout are used to improve the generalization ability of model and reduce the risk of over-fitting. In addition, we have proposed an effective multi-network integration method which can be used to integrate more state-of-the-art CNN models and can also be easily extended to other plant disease identification tasks.

Declaration of Competing Interest

We declare that we have no financial and personal relationships with other people or organizations that can inappropriately influence our work, there is no professional or other personal interest of any nature or kind in any product, service and company that could be construed as influencing the position presented in, or the review of, the manuscript entitled "Automatic Grape Leaf Diseases Identification via UnitedModel Based on Multiple Convolutional Neural Networks".

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