Bulletin of Electrical Engineering and Informatics
Vol. 14, No. 1, February 2025, pp. 268∼275
ISSN: 2302-9285, DOI: 10.11591/eei.v14i1.7269

Fusing Xception and ResNet50 features for robust grape leaf disease classification

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Article Info

Article history:

Received Jul 28, 2023
Revised Aug 27, 2024
Accepted Sep 4, 2024

Keywords:

Bilinear pooling
Convolutional neural networks
Disease classification model
Identification of grape diseases
ResNet50
Xception

ABSTRACT

Grapes are one of the most widely cultivated fruits worldwide, and their economic and nutritional value makes them a significant crop in agriculture. However, grape plants are vulnerable to various diseases that can have detrimental effects on crop yield and quality. Accurate and timely identification of grape leaf diseases is crucial for efficient disease control and ensuring sustainable viticulture practices. In this study, we present a disease classification model specifically designed for grape leaves. The model incorporates bilinear pooling, utilizing the intermediate features extracted from two powerful convolutional neural network (CNN) models, Xception, and ResNet50. The outer product operation is applied to the extracted features, enabling the capture of intricate interactions and relationships between the features. The accurate classification of grape leaf diseases provided by our model offers significant benefits for grape farmers, vineyard owners, and agricultural researchers. It facilitates early disease detection, enabling proactive disease management strategies. Additionally, it assists in optimizing crop health, minimizing yield losses, and ensuring sustainable grape production.

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1. INTRODUCTION

Plant diseases can have a significant impact on agricultural yields, leading to reduced crop productivity and economic losses for agricultural producers [1]-[6]. Early recognition and timely intervention in managing these diseases is vital to mitigate their negative effects and maximize crop benefits. Early identification and intervention approaches play a vital role in mitigating disease epidemics and ensuring sustainable crop production. By promptly identifying and addressing plant diseases, farmers can implement appropriate control measures, such as applying fungicides strategically or implementing crop rotations, to minimize yield losses and ensure the safety of their crops [7], [8]. Additionally, early disease recognition can also aid in the prevention of disease spread to neighboring plants, preserving the overall health of agricultural systems. The use of traditional methods for plant disease diagnosis has been recognized as challenging and inefficient in many agricultural settings. Traditional methods often rely on visual indicators and hands-on inspections, making it difficult to accurately identify diseases, especially in their early stages. Depending only on visible signs can be unreliable, as different diseases may exhibit similar symptoms, leading to misdiagnosis and inappropriate treatments. Moreover, these conventional approaches may not be suitable for detecting pathogens that are not visibly evident on plant surfaces, further complicating the diagnostic process. Recognizing these limitations, there has been a growing emphasis on adopting modern, technology-driven approaches such as state-of-the-art image-based recognition technologies and AI-based approaches for more accurate and efficient plant disease diagnosis and management. Techniques in deep learning (DL) and machine learning (ML) have been broadly applied to image recognition tasks in numerous areas. In the medical field [9]-[12]. In autonomous driving systems [13]-[16]. In the field of agriculture [17]-[21]. Particularly in the automation of plant disease identification [22]-[27].

With respect to implementing DL for grape vine leaf infection identification, several studies have been conducted. Research by Andrushia *et al.* [28] focuses on detecting diseases in grape leaves by employing convolutional capsule networks. The proposed method achieves a remarkable accuracy of 99.12% in effectively identifying and classifying various diseases affecting grape leaves. Research by Çakmak [29] proposes the use of the EfficientNet B0 DL model for classifying leaves of grapevines and compares it with other well-known DL architectures. The model is trained using transfer learning and fine-tuning on a dataset containing 3000 images of grapevine leaf types. Results show that the suggested EfficientNet B0 architecture outperforms classical convolutional neural network (CNN) and state-of-the-art VGG19, MobileNet V2, Inception V3, and ResNet152 models, reaching an outstanding accuracy of in leaf classification. Research by Koklu *et al.* [30] examines using DL techniques for grapevine leaf classification. The most successful approach involves extracting features from MobileNetv2's Logits layer, reducing them with the Chi-Squares method, and utilizing the cubic squared support vector machine (SVM) kernel, resulting in impressive classification accuracy. Research by Adeel *et al.* [31] introduce a new framework for early-stage recognition and categorization of grape diseases, integrating DL-based feature extraction from pre-trained models (AlexNet and ResNet101) with a proposed Yager Entropy along with Kurtosis (YEaK) technique for feature selection. The approach utilizes a parallel fusion method and least squared support vector machine (LS-SVM) for classification.

This study looked into the effects of grape leaf diseases on crop yield and quality, acknowledging the significant economic and nutritional value of grapes in agriculture. While previous studies investigated various aspects of grape diseases, they often lacked explicit focus on the timely recognition and categorization of grape diseases of these diseases, which is crucial for efficient disease control. In response to this gap, our study presents a novel disease classification model tailored specifically for grape leaves. Our model captures intricate interactions and relationships, enabling accurate disease classification. The implications of our model extend to grape farmers, vineyards, and agricultural researchers, providing them with the means for early disease detection and proactive management strategies.

Emphasizing the importance of preventative disease control, agricultural experts and researchers continually work to develop state-of-the-art technologies and methods for early disease detection, contributing to the resilience and productivity of global agricultural production systems. The purpose of this paper is to present a concise and scientifically grounded disease classification model for grape leaves. Leveraging the Xception and ResNet50 architectures, the model incorporates bilinear pooling to capture feature interactions. By performing the outer product operation on the intermediate features, the model accurately identifies and classifies diseases affecting grape leaves. Extensive experiments demonstrate a remarkable test accuracy of 99.94%, affirming the model's effectiveness.

2. METHOD

2.1. Dataset

In this research, we employed a dataset of 9,027 photos obtained from [32]. This dataset, referred to as the grape disease dataset, includes four categories. Sample photos from the dataset is illustrated in Figure 1 and the dataset's distribution is illustrated in Figure 2. Before training and evaluating the model, the photos undergo a preprocessing stage, where they are resized to 224×224 pixels and processed with a method for image preprocessing. The dataset is subsequently partitioned into subsets: 5,416 photos for training, 1,806 photos for validation, and 1,805 photos for testing.

2.2. Model evaluation metrics

In this research, several evaluation metrics were employed to gauge the performance of the DL models, including accuracy, F1-score, precision, and recall. Accuracy was used to measure the overall performance, whereas precision and recall assessed the model's capability to accurately identify positive cases. The F1-score offered a balanced view by integrating both precision and recall, which allowed for a more nuanced evaluation of the model's effectiveness. By utilizing these diverse metrics, a comprehensive understanding of the model's performance was achieved.

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \tag{1}$$

$$Precision = \frac{TP}{TP + FP} \tag{2}$$

$$Recall = \frac{TP}{TP + FN} \tag{3}$$

$$F_1 - Score = \frac{Precision * Recall}{Precision + Recall} \tag{4}$$

In this, TP stands for true positive, TN represents true negative, FP denotes false positive, and FN refers to false negative.

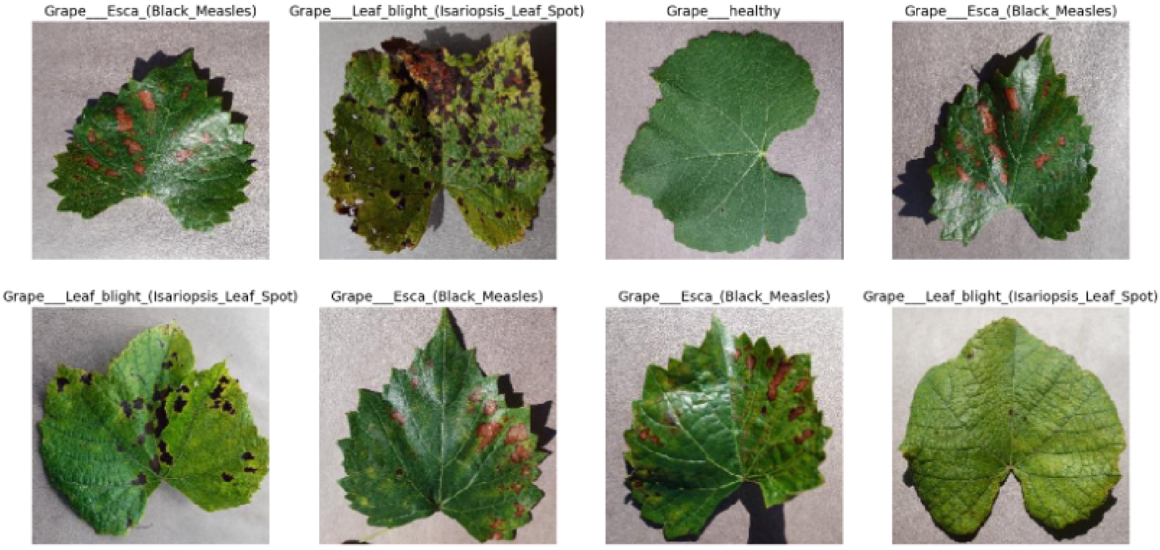


Figure 1. Instances of grape diseases in the grape disease dataset

Figure 2. A dataset distribution

2.3. The proposed model architecture

This research paper presents a new method for precise classification of grape diseases. The approach combines the Xception [33] and ResNet50 [34] models, which are pre-trained CNNs, along with bilinear pooling. The recommended model comprises two parallel CNNs based on Xception and ResNet50, respectively, which individually analyze grape images. The bilinear pooling technique is employed to capture complex interactions among various regions within the images. The ultimate goal of the model is to correctly classify pictures into four distinct classes related to grape diseases. The model proposed for classifying grape diseases is shown in Figure 3 with the following layers: i) input layer: this layer represents the input to the model, which expects an image with dimensions 224×224 and 3 color channels (RGB); ii) Xception layer: this is a CNN layer based on the Xception architecture. It takes the input photo and produces a feature map with dimensions 7×7 and 2048 channels; iii) ResNet50 layer: this is another CNN layer based on the ResNet50 design. It also takes the input photo and produces a feature map with dimensions 7×7 and 2048 channels; iv) bilinear pooling layer: this layer performs bilinear pooling, which combines the feature maps from the previous two layers into a single feature vector. It reduces the spatial dimensions to 1×1 while retaining the 2048 channels; v) flatten layer: this layer flattens the output of the bilinear pooling layer into a 1D vector of size 2048; vi) batch normalization layer: this layer applies batch normalization to the flattened vector to normalize the activations and improve training efficiency; vii) dense layer: a fully connected layer with 256 neurons that takes the normalized feature vector and performs linear transformations; viii) dropout layer: a dropout layer is inserted following the dense layer. It helps to prevent overfitting; and ix) final output layer: the dense layer is considered the final output layer, another fully connected layer with 4 neurons, representing the output classes. The model has a total of 44,982,956 parameters, out of which 44,871,212 are trainable, and 111,744 are non-trainable. Figure 4 offers a detailed overview of significant aspects, encompassing the model's architecture layers, output shapes, the trainable params, and the overall parameter count assessed for each layer in the model.

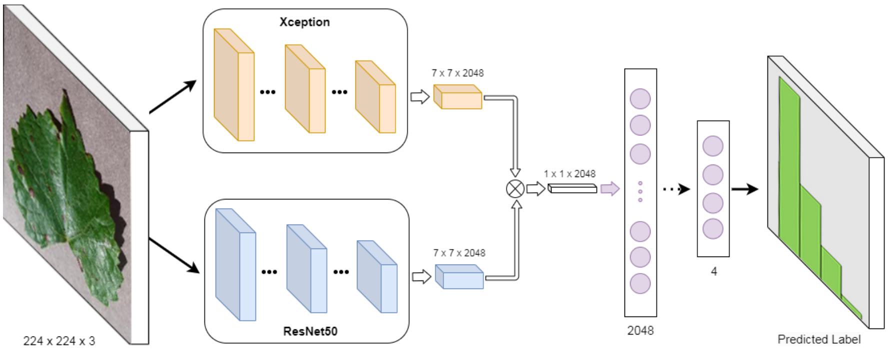
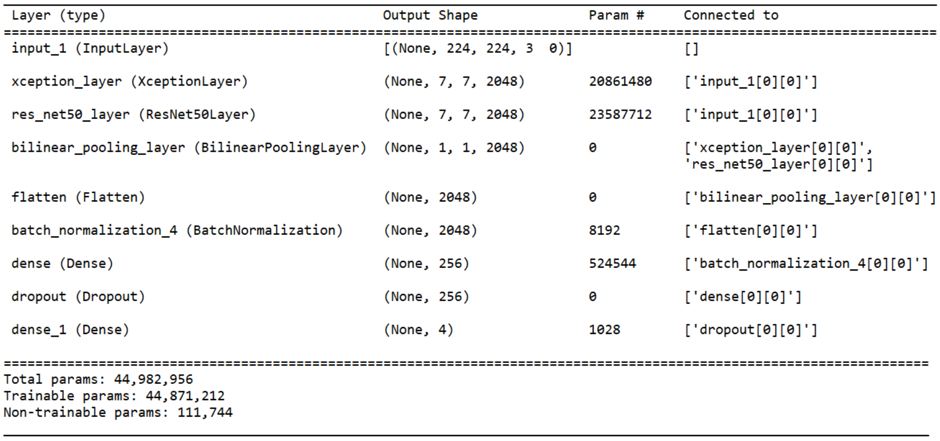


Figure 3. Proposed model for grape disease classification



```
 Layer (type)                                Output Shape            Param #     Connected to
==========================================================================================================
 input_1 (InputLayer)                        [(None, 224, 224, 3  0)]             []

 xception_layer (XceptionLayer)              (None, 7, 7, 2048)      20861480    ['input_1[0][0]']

 res_net50_layer (ResNet50Layer)             (None, 7, 7, 2048)      23587712    ['input_1[0][0]']

 bilinear_pooling_layer (BilinearPoolingLayer)  (None, 1, 1, 2048)   0           ['xception_layer[0][0]',
                                                                                  'res_net50_layer[0][0]']

 flatten (Flatten)                           (None, 2048)            0           ['bilinear_pooling_layer[0][0]']

 batch_normalization_4 (BatchNormalization)  (None, 2048)            8192        ['flatten[0][0]']

 dense (Dense)                               (None, 256)             524544      ['batch_normalization_4[0][0]']

 dropout (Dropout)                           (None, 256)             0           ['dense[0][0]']

 dense_1 (Dense)                             (None, 4)               1028        ['dropout[0][0]']

==========================================================================================================
Total params: 44,982,956
Trainable params: 44,871,212
Non-trainable params: 111,744
```

Figure 4. The model's layers for grape disease classification

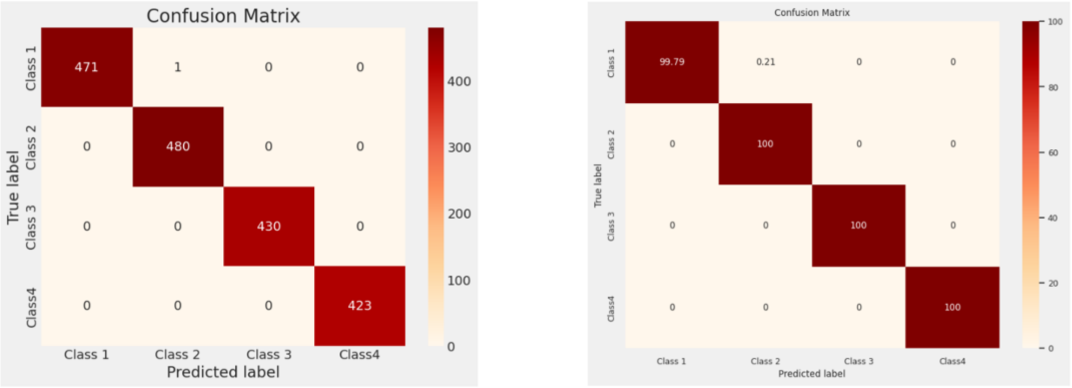
3. RESULTS AND DISCUSSION

3.1. Environmental configurations

The experimental outcomes were generated by performing the tests on the Kaggle environment. The system utilized for these experiments featured 13 GB of RAM and a P100 GPU with 16 GB of memory. The models underwent training for 30 epochs in total, with batch size set to 32 applied throughout the training phase. In the proposed model, a strategy for scheduling the learning rate (LR) [35] was incorporated into the training phase, the LR is adjusted by reducing it by a factor of 0.5 after every two training epochs. This allows the model to make necessary changes in case the training accuracy does not improve. To avoid the problem of overfitting, the model uses regularization methods [36], which help in preventing the model from becoming too specific to the training data and improve its overall performance. These measures are essential, especially in real-world applications, where achieving the best possible performance is crucial.

3.2. Evaluation overall

The accuracy of the proposed model reaching 99.94% on the test set is remarkable and indicates an remarkable level of performance. This suggests that the model can accurately categorize almost every instance within the test data, with only a negligible percentage of misclassifications. This high degree of accuracy strongly suggests that the model can generalize effectively and make accurate predictions on new, unseen data. The confusion matrix, showcasing the results of the proposed model, is presented in Figure 5. Figure 5(a) shows the number of estimates for each class, where the diagonal elements represent the correctly predicted instances for each class, and the off-diagonal elements show misclassifications. Figure 5(b) presents the proportion of predictions in percentage form, providing a clearer visualization of the model's accuracy across the four classes. According to the confusion matrix results, the proposed model demonstrates a remarkable level of accuracy, maintaining strong consistency with the true labels.



(a) (b)

Figure 5. Confusion matrix of the suggested model: (a) displays the number of estimates and (b) the proportion of predictions

Table 1 presents a comprehensive analysis of the metrics for evaluation for each grapevine disease category. This classification report serves as a summary of the model's efficiency in classification tasks. It encompasses metrics such as precision, recall, and F1-score for each class label. The report is instrumental in assessing how accurately the model classifies instances across different classes, with higher scores reflecting superior performance. In this result, the model reached perfect scores in all categories, highlighting its exceptional accuracy in classification. Furthermore, Figure 6 provides an overview of performance metrics, including loss and accuracy, assessed during both the training and validation phases of the model.

Table 1. The classification report results for the model

Class	Precision	Recall	F1-Score	Support
Grape_Black_rot	1.00	1.00	1.00	472
Grape_Esca_(Black_Measles)	1.00	1.00	1.00	480
Grape_Leaf_blight_(Isariopsis_Leaf_Spot)	1.00	1.00	1.00	430
Grape_healthy	1.00	1.00	1.00	423

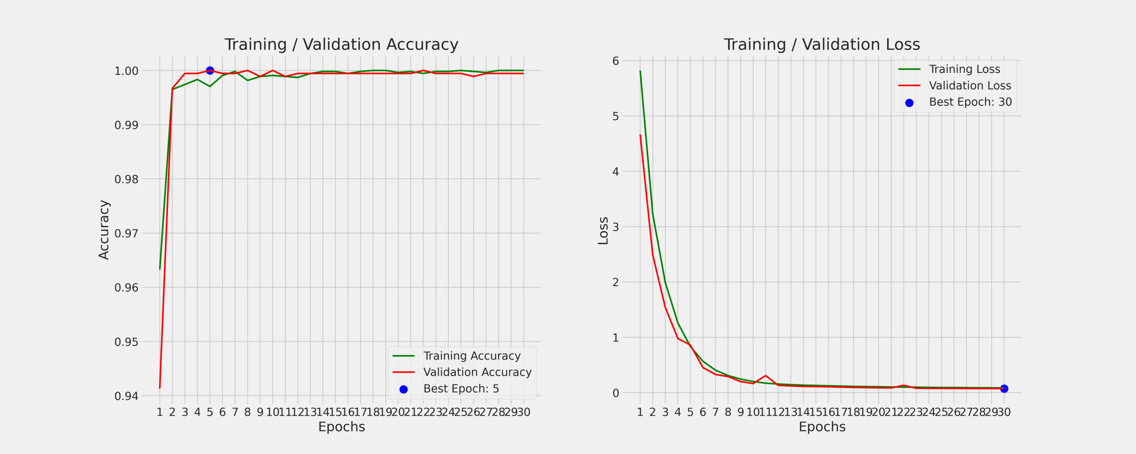


Figure 6. Visualizations of loss and accuracy for the suggested model

Table 2 presents an extensive evaluation of the proposed model in contrast to other cutting-edge approaches addressing comparable issues. The findings demonstrate that the suggested model outperformed all the mentioned techniques in the table, showcasing superior performance. Previous studies, such as those referenced by [36]-[42], utilized various techniques and datasets to address similar challenges. For instance, methods ranged from employing faster DR-IACNN, ShuffleNet V1 and V2, SVM, GrapeNet model, VGG16, UnitedModel, to exception model. Accuracy rates varied across these studies, with reported values ranging from 86.29% to 99.14%. In contrast, our study, utilizing the grape disease dataset and incorporating Xception, ResNet50, and bilinear pooling techniques, achieved a notably higher accuracy rate of 99.94%. This comparison underscores the superior performance of our proposed model, demonstrating its effectiveness in grape leaf disease classification tasks.

Table 2. A comparison between our proposed model and existing methods for similar issues

The study	Dataset	Method of use	Accuracy (%)
[37]	Grape leaf diseases	e faster DR-IACNN mode	99.47
[38]	Grape (Plantvillage dataset)	ShuffleNet V1 and V2	99.14
[39]	Grape (Plantvillage dataset)	SVM	92.00
[40]	Grape (AI challenger 2018 dataset)	GrapeNet model	86.29
[41]	Grape (Myanmar Grapevine Yard)	VGG16	98.40
[42]	Grape (Plantvillage dataset)	UnitedModel	98.57
[43]	Grape (Plant-Village dataset)	Exception model	98.70
This study	Grape disease dataset	Xception, ResNet50, and bilinear pooling	99.94

4. CONCLUSION

In this study, we highlight the importance of early disease management in agriculture. Agricultural experts and researchers continuously work on advanced technologies to detect diseases early, which is crucial for enhancing crop productivity and resilience on a global scale. The main focus of this paper is to present a concise and scientifically grounded disease classification model specifically designed for grape leaves. The model utilizes the powerful Xception and ResNet50 architectures and incorporates bilinear pooling to capture feature interactions. By doing so, the model accurately identifies and classifies diseases affecting grape leaves. Extensive experiments were conducted, and the results were impressive, showing that the model achieved an exceptional test accuracy of 99.94%. This high accuracy confirms the effectiveness of the model in disease classification. Overall, this research contributes to the ongoing efforts to protect crop health and ensure sustainable agriculture practices.

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