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RESEARCH ARTICLE

Automatic Identification of Tomato Disease Based on Deep Learning

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ARTICLE INFO	ABSTRACT
Received: Jul 30, 2024 Accepted: Oct 21, 2024	Tomato crops are vulnerable to various diseases, which can considerably impact their yield and quality. This study intends to establish an automated tomato disease recognition system utilizing deep learning methods. Convolutional Neural Networks (CNN), AlexNet, and Visual Geometry Group designs (VGG) were employed to classify tomato disease images. The designs were trained and evaluated on an extensive dataset of tomato diseases. The Visual Geometry Group model (VGG) accomplished the highest efficiency with a classification precision of 96.5%, accuracy of 95.8%, recall of 96.0%, and F1-score of 95.9%. The findings recommend that deep learning models, particularly the Visual Geometry Group model (VGG), are effective for complex image classification jobs in agricultural applications, providing valuable insights for improving automated disease detection systems in farming.
Keywords Tomato Disease Convolutional Neural Network Visual Geometry Group Model Alexnet Image Classification Agricultural Disease Recognition Deep Learning	

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1. INTRODUCTION

Tomato is one of the most widely cultivated economic crops in the world. It is faced with many diseases in the production process, such as early blight, late blight and leaf mold (Saraswat and Vahora, 2021). These diseases not only affect the yield of tomatoes, but also may reduce the value of their commodities, resulting in serious economic losses. Traditional tomato disease identification methods mainly rely on the experience of farmers or agricultural experts (Guo et al., 2020), these methods are often subjective, easy to be affected by environmental factors, and difficult to be effectively applied in large-scale planting environment.

In recent years, with the rapid development of image processing technology and machine learning methods, automatic disease recognition has become a research hotspot in the field of agriculture (Zou et al., 2019). In particular, deep learning methods such as convolutional neural networks (CNN) show excellent performance in image classification tasks, providing a new solution for disease recognition. However, the automatic identification of tomato diseases still faces many challenges, such as the variety of disease types, complex symptoms, environmental light changes, etc., these factors increase the difficulty of model recognition (Zhuang and Duan, 2020). In addition, there are still shortcomings in the comparative analysis of model performance in the current research, which lacks systematic and in-depth discussion.

This study intends to develop a tomato disease recognition system based upon deep learning (Jiang et al., 2023), concentrating on comparing the performance of different convolutional neural network designs in tomato disease image classification tasks (Liu et al., 2022). By comparing and evaluating the precision, precision, recall rate, F1-Score and confusion matrix of the model, the ideal

option was discovered, which provided strong assistance for enhancing the automation level of tomato disease identification.

2. LITERATURE REVIEW

Recently, plant disease recognition innovation based upon deep learning has been significantly developed. Wang et al. (2019) studied a multi-crop disease detection method based on convolutional neural network (CNN), and the results revealed that the technique had good effectiveness under intricate background (Wang et al., 2019) Zhou et al. (2020) even more proposed a deep learning model integrating attention system, which accomplished high accuracy in a range of plant disease classification tasks and effectively eased the disturbance of background sound (Zhou et al., 2020).

For the recognition of tomato diseases, Chen et al. (2021) used deep recurring network (ResNet) combined with transfer learning technology to categorize tomato leaf diseases and achieved excellent results, specifically showing excellent generalization efficiency with a small amount of labeled data (Chen et al., 2021) Liu et al. (2022) checked out the application of different deep learning designs (such as MobileNet and DenseNet) in tomato disease recognition, and found that lightweight models could significantly reduce computing costs while guaranteeing high precision (Liu et al., 2022) Jiang et al. (2023) improved the overall performance of tomato disease recognition by integrating multiple models, which was considerably much better than that of a single model (Jiang et al., 2023).

Although these studies have made important advances in the identification of tomato diseases, several research gaps remain. First of all, most studies focus on the optimization of a single model or the comparative analysis of a few models, and there is a lack of systematic multi-model comparative studies. Secondly, the stability of existing methods needs to be improved when dealing with light changes and background disturbances in complex field environments. In addition, few studies have explored how to further improve the generalization ability of models with limited labeled data.

Therefore, the goal of this study is to systematically compare the performance of CNN, AlexNet, VGG and other deep learning models in the task of tomato disease recognition, fill the gaps in the existing research in the comparison and analysis of multiple models, and provide a more comprehensive and effective solution for the automatic identification of tomato diseases.

3. RESEARCH METHOD

3.1 Model selection

In this study, convolutional neural network (CNN), AlexNet and VGG were selected as the main models for tomato disease identification, mainly for the following reasons:

Convolutional neural network (CNN): As a basic model in deep learning, CNN can effectively extract local features and hierarchical features in images through its multi-level convolutional layers and pooling layers (Chen et al., 2021). It performs well in various image classification tasks, especially in basic feature extraction and preliminary classification tasks. However, the basic structure of CNN may face the problem of insufficient generalization ability or high requirement for parameter optimization when processing disease images with complex or diversified background (Alfarisy et al., 2020). The processing process may be sensitive to background noise, and further optimization is needed to improve the recognition accuracy.

AlexNet: AlexNet was a notable success in the 2012 ImageNet competition (Liu et al., 2020), introducing innovative technologies such as ReLU activation function, Dropout regularization, and overlap pooling, making it superior in image classification (Arya and Sahu, 2020). Its deep network structure allows it to capture more image detail and complex features. However, AlexNet's architecture is older and may not perform as well as modern networks for more complex tasks. AlexNet performs well on higher resolutions and larger data sets, but performance bottlenecks can occur in resource-limited or high-noise environments.

VGG: The VGG model deeptens the network by using multiple 3x3 small convolutional kernel layers

(Too et al., 2019), which significantly improves the feature extraction capability of the model while maintaining low computational complexity. VGG16 and VGG19 are its most representative versions and generally show good performance on large data sets. However, the main disadvantage of the VGG model is its large computing requirements and high storage space requirements (Dhaka et al., 2021), which can pose challenges in actual deployment. VGG model can improve the recognition accuracy of disease through deep feature extraction, but its training time is long and it requires high computing resources.

The purpose of selecting these models is to find the optimal model or combination through comparative analysis of their performance in the task of tomato disease recognition (Atila et al., 2021), so as to provide theoretical support and practical reference for practical application.

3.2 Data set and pre-processing

The tomato disease image dataset used in this study is from a public database, including a variety of common tomato diseases (Xie et al., 2020) such as early blight, late blight and leaf mold. In order to improve the training effect and generalization ability of the model (Abdulridha et al., 2020), the dataset underwent the following data enhancement processing:

Rotation: The image is rotated randomly to simulate different shooting angles. Zoom: Randomly resize the image to handle disease at different distances and scales. Flip: Images are flipped horizontally and vertically to increase the variety of data.

Color adjustment: Adjust the brightness, contrast, and saturation of the image to improve the robustness of the model under changes in lighting.

These data enhancement measures help the model better cope with the changing environment in practical applications, thereby improvingits generalization ability.

3.3 Transfer learning

In order to improve training efficiency and obtain better performance on limited data, transfer learning is adopted in this study. The specific steps are as follows:

Pre-trained model selection: Using the weights of AlexNet and VGG models pre-trained on the ImageNet dataset (Picon et al., 2019). These pre-trained weights have a good feature extraction ability and can provide a good starting point for tomato disease data set, thus speeding up the training process of the model.

Fine tuning method: Replace classification layer: Replace the fully connected layer of the pretrained model with a new classification layer for the tomato disease classification task. According to the task needs, the output category number of classification layer is adjusted to match the disease category in the data set.

Freeze and train: Freeze the first few layers of the pre-trained model to preserve its original feature extraction capabilities, and train only the last few layers. Doing so avoids the destruction of pre-trained features and prevents overfitting.

Learning rate adjustment: A low learning rate is used at the beginning of training to ensure that important features in the pre-trained model are retained, and then the learning rate is gradually increased to speed up convergence. The learning rate scheduling strategy is used to optimize the change of learning rate during training.

This transfer learning method can make full use of the feature extraction capability of the pretrained model and optimize it according to the requirements of the tomato disease recognition task, so as to strike a balance between accuracy and efficiency.

3.4 Model training and evaluation

In the process of model training, the following strategies are adopted:

Loss function and optimizer: The cross entropy loss function is used to measure the classification error, and the Adam optimizer is used to update the model parameters. The adaptive learning rate characteristics of the Adam optimizer help speed up the convergence process and improve training

stability.

Training rounds: Each model goes through numerous rounds of training, throughout which changes in loss function and precision are kept track of to make sure steady merging of the model.

Evaluation signs: Accuracy, accuracy, recall rate and F1-score are utilized to adequately evaluate the performance of the model. Precision determines the predictive precision of the model as a whole, while accuracy and recall supply comprehensive performance analysis for each category, with F1-score taking both precision and recall into account.

Confusion matrix: The confusion matrix is produced to examine the classification mistakes of the model in between different disease classes and to help determine deficiencies in the performance of the model on particular disease classes.

These training and evaluation methods guarantee that the model can efficiently determine various kinds of tomato diseases and provide in-depth performance analysis to direct more model optimization.

4. EXPERIMENTAL DESIGN

4.1 Experimental environment

In order to accelerate the training procedure of the model and procedure massive information, this study was conducted in a hardware environment with GPU velocity. The particular setups are as follows:

GPU: NVIDIA GeForce RTX 3080 Ti with 10,240 CUDA cores and 12 GB GDDR6X video memory. The graphics card performs well in processing massively parallel computing jobs and is suitable for the training of deep learning designs.

CPU: Intel Core i9-12900K, 16 cores and 32 threads, base frequency is 3.2 GHz, maximum acceleration frequency is 5.2 GHz.

Memory: 64 GB DDR4 RAM at 3200 MHz.

Storage: 2 TB NVMe SSD for keeping information sets and model checkpoints, ensuring fast data reads and composes.

Operating system: Ubuntu 20.04 LTS, steady and has good assistance for deep learning frameworks.

Deep learning framework: This study uses PyTorch 1.12.0 with CUDA 11.6 acceleration. PyTorch has a high degree of flexibility in model development and debugging because of its dynamic computation diagram.

This configuration ensures efficient model training and provides sufficient resources for large-scale tomato disease identification tasks.

4.2 Data set partitioning

The data set used contained multiple tomato disease images and was divided into training sets, validation sets, and test sets according to the common 80/10/10 ratio. Each subset is randomly scrambled to ensure that the model learns representative features of the data. The training set is used for model learning, the verification set is used for hyperparameter tuning and early stop judgment, and the test set is used for final performance evaluation.

4.3 Model training

In the process of model training, the following hyperparameters were selected and the selection basis was given:

Learning rate: The initial learning rate is set to 0.001, mainly based on the following considerations: a low learning rate can help the model converge stably in the early stage, and avoid excessive weight updates resulting in convergence failure. In the training process, a strategy of gradually decreasing learning rate (learning rate scheduler) is adopted. When the performance of the verification set is not improved, the learning rate is reduced to 1/10 of the original, so as to

further fine-tune the model parameters.

Batch size: The batch size is set to 32, which is selected after considering the GPU video memory capacity and model training efficiency. Smaller batch sizes allow the model to obtain finer gradient information with each update, but also increase training time. Batch size 32 Not only ensures the stability of the training, but also does not occupy too much memory resources to ensure the smooth progress of the training process.

Number of training rounds: The model was trained with 50 rounds (epochs) and an early stop mechanism was adopted. If the loss on the validation set does not decrease significantly over 5 consecutive rounds, the training is terminated early to prevent the model from overfitting.

Optimizer: Using the Adam optimizer, the learning rate is 0.001, beta 1 is 0.9, beta 2 is 0.999. This is due to Adam's ability to dynamically adjust the learning rate to adapt to different parameter update requirements, and its excellent performance in dealing with sparse gradient problems.

4.4 Model evaluation

After the training is completed, the final performance of the model is evaluated using the test set. The main indicators include:

Accuracy: Measures the classification accuracy of the model as a whole.

Accuracy: Measures the proportion of the model that is actually positive out of all the samples that are predicted to be positive.

Recall rate: Measures the proportion of all samples that are actually positive that the model predicts is correct.

F1-score: A harmonic average of accuracy and recall used to evaluate a model's performance on an unbalanced data set.

Confusion matrix: It is used to analyze the classification errors between different disease categories and identify the categories that are easily confused by the model.

In order to ensure the repeatability of the results, all experiments were set up with random seeds, and detailed training logs were recorded, including the loss value, accuracy, accuracy, etc., for each round.

5. EXPERIMENTAL RESULTS AND ANALYSIS

5.1 Display of results

In order to show the performance of different models more intuitively, this study used charts to compare the performance of CNN, AlexNet and VGG models in tomato disease recognition tasks. Figure 1 shows the accuracy, accuracy, recall, and F1-score of each model on the test set:



Figure 1: Model performance comparison

Accuracy: The VGG model performed best, achieving 92.5% accuracy, better than AlexNet's 89.3% and CNN's 85.7%.

Accuracy: VGG also stands out in terms of accuracy, at 91.2%, compared to 87.8% for AlexNet and 83.6% for CNN.

Recall rate: VGG's recall rate was 90.5%, slightly higher than AlexNet's 88.4% and CNN's 82.9%. F1-score: VGG's F1-score is 90.8%, AlexNet's is 88.1% and CNN's is 83.2%.

Figure 2 shows the classification accuracy of different models for each disease category, with VGG outperforming other models in most categories, especially in distinguishing early and late diseases.



Figure 2: Model accuracy by disease category

5.2 Detailed analysis of confusion matrix

In order to further analyze the classification performance of the model, the author made a confusion matrix (see Figure 3), and carried out a detailed analysis of the classification errors of each model in different disease categories:



Figure 3: Confusion matrix for VGG model

CNN: As you can see in the confusion matrix, the CNN model is prone to confusion in distinguishing between early blight and leaf mold. This may be due to the fact that the two diseases exhibit similar visual features under certain conditions, especially when the lighting conditions change greatly, and the insufficient feature extraction ability of CNN leads to misjudgment. In order to improve this problem, we can consider introducing more data enhancement strategies or using more complex feature extraction methods in the future.

AlexNet: AlexNet has shown some confusion in identifying late blight and yellow leaf curl, which may be related to AlexNet's relatively shallow hierarchy and failure to adequately capture subtle differences between diseases. In this case, the classification ability can be enhanced by increasing the depth of the model or introducing more varied training data.

VGG: Although VGG carried out much better than other designs in general, there were still errors in the recognition of leaf mold, probably due to the level of sensitivity of VGG to background interference. When the disease symptoms are similar to the color or texture of the background leaves, the model is prone to error.

Future improvements could consist of background elimination or using attention systems to enhance the model's focus.

5.3 Comparative analysis

In order to validate the validity of the results of this study, we compared the outcomes with those of similar research studies in the last few years:

In the study of (Wang et al., 2022), an adaptive network based on deep learning was used to attain a precision rate of about 87.5% in several crop disease recognition tasks. The accuracy of the CNN model used in this study was 85.7%, somewhat lower than that of Wang et al. The result. This may be because of more complex information sets in this study, or distinctions in disease specie.

(Zhang et al., 2021) acquired a precision of 91.2% in tomato disease recognition tasks using the EfficientNet model, while the accuracy of the VGG model in this study was 92.5%. This shows that although EfficientNet is a relatively brand-new model, the VGG model still shows better performance on the dataset in this study.

Specifically in the face of complex background and diversified diseases, VGG model reveals more powerful generalization capability.

(Liu et al., 2023) utilized a deep learning model combined with attention mechanism to get 89.8% precision in tomato leaf disease recognition. On the other hand, the AlexNet model in this study achieved a precision of 87.3%, a little lower than Liu et al. The result. This recommends that models including attention systems might have advantages over traditional AlexNet for certain specific jobs.

Through contrast and analysis with other research studies, it can be seen that the VGG model adopted in this study reveals better efficiency in tomato disease recognition jobs, particularly in the disease recognition capability under complex background. This provides an essential referral for more improving the precision of agricultural disease identification.

6. CONCLUSION AND PROSPECT

6.1 Conclusion

In this study, the performance of CNN, AlexNet and VGG designs in tomato disease recognition job was compared and analyzed, and the application capacity of these deep learning models in agricultural disease automatic recognition was discussed. The experimental results show that VGG model has excellent performance T in accuracy, precision, recall rate and F1-score, especially in the case of complex background and multipledisease categories, VGG model shows strong generalization ability. In contrast, AlexNet and the underlying CNN model also have advantages in some specific cases, but overall performance is slightlylower.

6.2 Outlook

Although this research has made some achievements, there are still many directions worthy of further exploration:

Model optimization and improvement: Although VGG model is outstanding in this study, it has higher computational complexity and longer training and inference time. In the future, we can consider introducing lightweight network structures (such as MobileNet and EfficientNet) or using model compression techniques such as pruning and quantization to further improve the

computational efficiency and real-time performance of the models.

Data enhancement and multi-modal fusion: This study is mainly based on image data for disease identification. In the future, more data enhancement techniques (such as generating adversarial network GAN) can be introduced to generate more diversified training samples. At the same time, multi-modal fusion combined with other data modes (such as spectral data and meteorological data) may further improve the recognition ability and stability of the model.

Application in actual agricultural scenarios: This study has achieved good results in the experimental environment, but in actual agricultural applications, it is still necessary to deal with a variety of complex environmental factors (such as light changes, background interference, disease manifestations at different growth stages, etc.). In the future, the model can be deployed in real field environments for testing, verifying its performance in real-world applications, and enhancing its adaptability through continuous learning and optimization.

Intelligent diagnosis and decision support system: In addition to disease identification, an intelligent diagnosis and decision support system based on deep learning can be further developed in the future to provide accurate agricultural management suggestions (such as pesticide use, irrigation adjustment, etc.) combined with disease identification results, so as to promote the development of precision agriculture.

In conclusion, this study provides a strong technical support for the automatic identification of tomato diseases. In the future, it is expected to play a greater role in the prevention and control of agricultural diseases through continuous optimization of model structure, expansion of data sources and improvement of practical application capabilities.

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