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Rice disease and pest identification integrating albert pre-trained language model and improved BILSTM[1]

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ABSTRACT - To solve the low recognition accuracy and slow recognition efficiency in traditional rice disease and pest recognition technology, this study adopts a bidirectional encoder representation pre-training model from a transformer for preliminary recognition of rice diseases and pests. At the same time, a bidirectional long short-term memory network is introduced for further recognition, and the model is optimized using conditional random fields to design a fusion algorithm for rice disease and pest recognition. The outcomes denoted that when the learning rate was 0.0001, the loss of the fusion algorithm was 0.04, indicating its high accuracy. In the identification of 6 types of rice diseases and pests, the average training time of the fusion algorithm was 31.4 seconds, the central processing unit occupancy rate was 94.3%, and the memory occupancy rate was 66.4%, proving that the algorithm had high efficiency in disease and pest identification. On the PlantVillage dataset, the accuracy of the fusion algorithm was 94.3%, higher than other algorithms, indicating its good recognition performance. The fusion algorithm effectively improves the rice disease and pest identification accuracy and efficiency, providing strong technical support for preventing and controlling other agricultural diseases and pests.

Key words: Rice; Diseases and pests; Pre-trained model; Bi-LSTM; Recognition.

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INTRODUCTION

As the growth of the global population, people's demand for food is increasing. Rice, as one of the critical sources of food in the world, is susceptible to various diseases and pests (DPs) during the cultivation, leading to a decrease in rice yield and quality (Arinichev *et al*., 2021). Therefore, the prevention and control of rice DPs has become a hot topic of research for relevant professionals. In recent years, deep learning (DL) technology has continued to advance and has been maturely utilized in agricultural fields such as DPs detection (Vasantha, Kiranmai & Krishna, 2021). Natural language processing (NLP) targets to enable computers to understand, process, and generate human language, and has made significant progress (Sharma, Kumar & Deka, 2022). In NLP technology, Bidirectional Encoder Representation from Transformers (BERT) has been widely used in NLP tasks such as question answering, etc (Muppala and Guruviah 2021). A Lite Bidirectional Encoder Representation from Transformers (ALBERT) is an optimized model of BERT. Compared with BERT, its number of parameters is greatly reduced, which significantly improves the speed of model training and prediction without sacrificing performance (Chen *et al*., 2022). Therefore, ALBERT is more suitable for computing environments with limited resources. In this context, the study first uses the ALBERT model for feature recognition of DPs, and then improves the Bidirectional Long Short Term Memory (BiLSTM) network using the Conditional Random Fields (CRF) algorithm to determine the types of pests and diseases. The innovation of the research lies in using CRF to optimize BiLSTM, integrating the optimized BiLSTM with ALBERT model into a new model, and applying this model to the identification of rice DPs, improving the accuracy and efficiency of rice DPs identification.

This article mainly contains four parts. The first part is a review of the current research conditions of rice DPs identification technology. The second part is the design of a rice DP identification technology that integrates ALBERT and improved BiLSTM. Firstly, a rice DP identification method based on ALBERT is implemented, and then BiLSTM is introduced on the basis of ALBERT and improved. The third part is the experimental result analysis of rice DP identification technology integrating ALBERT and improved BiLSTM. The first section is the effectiveness analysis of the designed identification model, and the second section is the practical application effect analysis of the designed identification model. The last part summarizes the entire text and represents the deficiencies of the research.

In crop production, DP identification can help farmers accurately determine the type and degree of DPs, and take targeted prevention and control measures to improve crop yield. As the advancement of NLP technology and DL algorithms, many researchers have attempted to apply these technologies to the crop DPs identification, and have achieved certain results. Poornampliya *et al*. (2022) raised an artificial intelligence-based rice recognition method to more quickly identify crop DPs. The method used image processing technology and DL models to detect crop DPs, and the outcomes denoted that the recognition efficiency of this method was relatively high. Rathore and Prasad (2020) raised a DP recognition method with sequence convolutional neural network (CNN) to raise the detection speed and accuracy of crop pests and diseases. The outcomes denoted that this method's prediction accuracy reached 99.61%. Upadhyay and Kumar (2022) designed a detection method for rice DPs with the size, shape, and color recognition of disease spots in leaf images to find a proper method for diagnosing rice DPs. The method used global thresholding technology to binarize the images and trained a fully connected CNN. The outcomes denoted that the accuracy of the method on the dataset was as high as 99.7%. Puspitasari *et al*. (2023) designed an expert diagnostic system based on naive Bayes network to accurately diagnose the DPs of black rice crops. The system used naive Bayes to obtain the percentage information of rice that may be affected by pests. The outcomes denoted that the diagnostic accuracy of this method was 80%, which could effectively diagnose pests on black rice crops. Chithambarathanu and Jeyakumar (2023) designed a crop DP identification technology based on DL methods for effective crop DP management and control. The technology connected intelligent mobile devices with crop related diseases through deep CNNs. The outcomes denoted that using this technology for disease driving improved crop yields.

Tholkapiyan *et al*. (2023) raised a rice disease recognition model based on hybrid DL technology to achieve automatic detection of crop DPs. The model combined meta heuristic optimization algorithm and DL to evaluate the types of rice diseases. The outcomes denoted that the method had high detection accuracy. Iqbal *et al*. (2023) raised a disease detection system that combines image processing and VGG19 to reduce the losses of rice after suffering from pests and diseases. VGG19 was used as a classifier to classify diseases and extract features using image processing techniques. The outcomes denoted that the accuracy of DP detection in this method reached 97.94%, which was better than other models. Tyagi *et al*. (2024) developed a lightweight DP detection system based on CNNs with mobile application integration for accurate detection of rice leaf diseases. It could effectively extract regions of interest from rice disease images and classify the images using a lightly weighted CNN. The outcomes denoted that the accuracy, precision, recall, and F1 score of the system were superior to those of traditional models.

Nugroho *et al*. (2024) designed a rice DP expert system based on deterministic graphical strategy to effectively diagnose rice pillar infections. The system tested multiple rice sowing sites in a certain region and evaluated the accuracy level using post tests. The outcomes denoted that the confidence level of the accuracy level was 100%, indicating a high detection accuracy. Rajpoot, Tiwari & Jalal (2023) raised an early automatic detection method for rice leaf diseases with a hybrid DL and machine learning approach to address the issue of slow recognition speed in traditional rice DP identification methods. The method utilized regional CNNs and VGG 16 transfer learning to extract features, and used random forest algorithm for classification. The outcomes denoted that the average accuracy of this method for rice disease classification was 97.3%, and the effect was good.

In summary, scholars have obtained significant results in the field of crop DP identification. Nevertheless, these technologies still face low computational efficiency and high model complexity. In view of this, the study is based on the ALBERT model and introduces BiLSTM for optimization. At the same time, the CRF algorithm is utilized to raise the accuracy of the BiLSTM model, aiming to achieve precise prevention and control of rice DPs, improve rice output, and provide scientific basis for maintaining food security.

MATERIALS AND METHODS

This part mainly elaborates on the implementation of rice DP recognition technology that integrates ALBERT and improved BiLSTM. The first section is the implementation of a rice DP recognition method designed based on the ALBERT model, and the second section is the design process of integrating the improved BiLSTM into the ALBERT model.

*Identification technology of rice diseases and pests based on ALBER*T

Accurate identification of different DPs is greatly significant for the healthy growth of rice in the prevention and control of rice DPs. In traditional DP recognition, methods based on dictionaries and rules, statistical machine learning, Recurrent Neural Network (RNN), Long Short-Term Memory (LSTM), etc. are often used. However, these methods also have disadvantages such as high requirements for feature selection, dependence on corpora, and low recognition accuracy (Simkhada and Thapa, 2022). Therefore, to address the issues in identifying rice DPs, the ALBERT model is introduced in the study. ALBERT is a lightweight version of BERT, with four fifths of the number of parameters. It embeds vector parameterized factorization, achieves cross layer parameter sharing, removes dropout, and proposes inter sentence coherence loss to model inter sentence coherence, achieving better results with a smaller model. The backbone network of the ALBERT architecture is a Transformer-Encoder structure with a non-linear GELU activation function, similar to BERT. The ALBERT model technology roadmap is denoted in Figure 1.

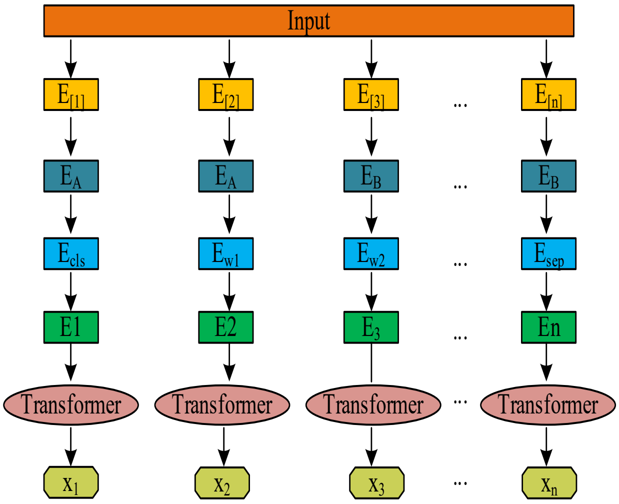
In the ALBERT model, its basic unit is the Transformer, which contains multiple layers of stacked encoders, each of which has a feedforward neural network and a multi-head attention (MHA). In the training of the encoder, the first input is the dataset. Due to the temporal nature of the dataset, it needs to be vectorized and specific positional encoding needs to be added. The transformation formula for the dataset is denoted in equation (1).

$$X = E\left(X_0\right) + p, X \in R^{B\times S\times D} \qquad (1)$$

In equation (1), X means the matrix vector of the dataset. E means the linear transformation function. X_0 means the initial dataset, P means positional encoding. R represents real numbers. B represents batch size. S represents sentence length. D represents vector dimension. Then calculate MHA, which is composed of multiple single head attention combinations. Only single-head attention needs to be calculated, and the calculation is denoted in equation (2).

$$\begin{cases} X_A = soft\max\left(\dfrac{Q\times K^T}{\sqrt{d_K}}\right)\times V \\ Q = X\times W_Q \\ K = X\times W_K \\ V = X\times W_V \end{cases} \qquad (2)$$

Figure 1- ALBERT model technology roadmap



In equation (2), X_A represents single-head attention. $\mathrm{softmax}(\cdot)$ represents activation function. Q, K, and V mean query vector, key vector, and value vector, respectively. T represents transpose. W_Q, W_K, and W_V represent weight matrices. MHA can divide the input text into multiple parts and perform independent attention calculations on each part. Each head generates an attention weight vector to indicate which parts of the text it is paying attention to. Finally, these weight vectors are combined into a vector to represent the overall meaning of the text, helping people better understand the complex relationships and semantic information in the text. The implementation of MHA is denoted in Figure 2.

Then it performs residual connections and normalizes them. In deep neural networks, there are often issues such as information decay, etc., which increase the difficulty of training and reduce model performance (Shahriar *et al.*, 2020). Therefore, a technology is needed to address this issue. Residual connection is a more convenient path constructed by passing the input signal directly to the subsequent layers of the network through skip connections. It normalizes the input and output of different Transformer layers through normalization operation, and uses residual connection operation to superimpose the normalized input and output, thus achieving multi-layer stacking. To achieve global parameter sharing of MHA module feedforward neural network, it is necessary to perform linear transformation on attention and activate it through an activation function. The calculation method is denoted in equation (3).

$$X_H = \mathrm{ReLU}(\mathrm{Linear}(\mathrm{Linear}(X_A))) \tag{3}$$

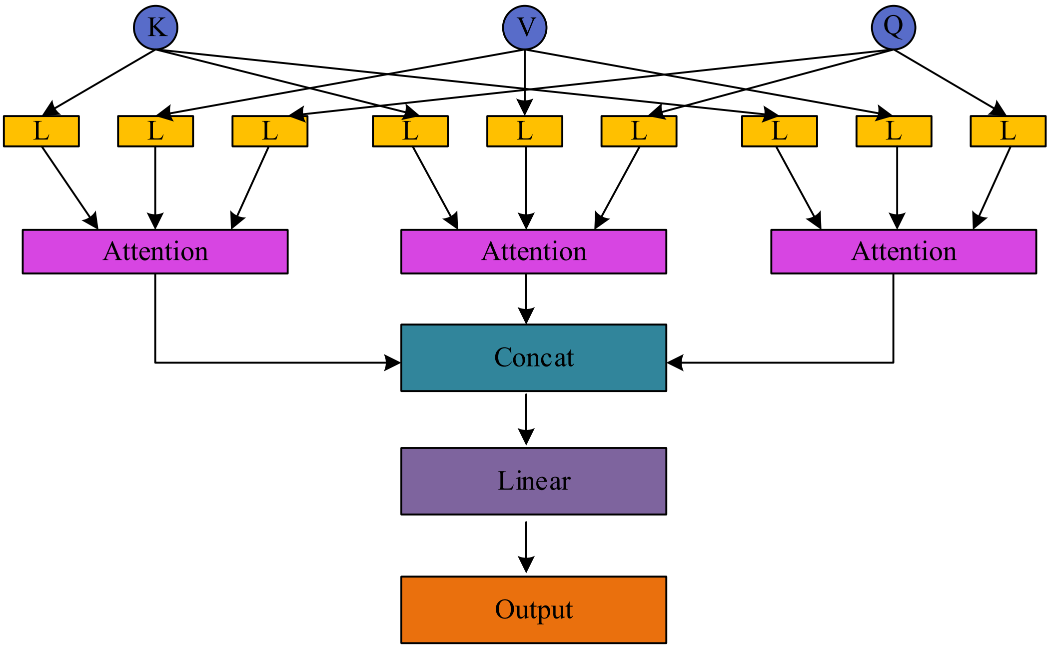
In equation (3), X_H represents shared MHA. $\mathrm{ReLU}(\cdot)$ represents linear rectification activation function. $\mathrm{Linear}(\cdot)$ represents linear transformation function. Lastly, the network is trained, and the training process is optimized using Adaptive Moment Estimation (Adam). The calculation method is denoted in equation (4).

$$L = -\left[y \log \hat{y} + (1-y)\log(1-\hat{y})\right] \tag{4}$$

In equation (4), L means cross entropy loss, y represents true output, and $\hat{y}$ represents predicted output. The process of identifying rice pests and diseases based on the ALBERT model is shown in Figure 3.

In Figure 3, it first inputs the text data of rice DPs, uses annotation tools to annotate and check for errors. Then it inputs the text data into the ALBERT model, and utilizes the BERT model to identify the features of different pests and diseases. Then, based on the entity label matching template, it compares and confirms the existence of pests and diseases. If the pests and diseases exist, it indicates accurate identification. Then, they are saved according to the category of pests and diseases, and the identification is complete. If the pest does not exist, the identification is incorrect. The pest does not belong to rice and will not be saved. The identification is complete.

Figure 2 - Multi-head attention implementation process



Disease and pest identification algorithm integrating ALBERT and improved BiLSTM

Although the DP recognition technology based on the ALBERT model can effectively identify rice DPs, in the training of the MHA layer of the ALBERT model, it cannot capture the relative positions between different features well, resulting in missing position information and inaccurate output results (Khan *et al.*, 2023). Therefore, the study introduces BiLSTM to further capture the information between rice DP feature sequences to ensure their orderliness, and predicts the categories of different DPs through CRF algorithm to better handle the dependency relationship between adjacent labels and improve the effectiveness of the model. BiLSTM is a DL model commonly utilized to process time series data with good predictive effectiveness. The roadmap for implementing BiLSTM is denoted in Figure 4.

In Figure 4, BiLSTM contains two independent LSTMs that process the input feature sequence from two directions. Each LSTM unit includes inputting, forgetting, outputting gates, and cell state, and the calculation methods for each component are indicated in equation (5).

$$\begin{cases} i_t = \sigma\left(w_{xi}\, x_t + w_{hi}\, h_{t-1} + w_{ci}\, c_{t-1} + b_i\right) \\ f_t = \sigma\left(W_{xf}\, x_t + w_{hf}\, h_{t-1} + w_{cf}\, c_{t-1} + b_f\right) \\ C_t = f_t \times c_{t-1} + i_t \times \widetilde{c}_t \\ O_t = \sigma\left(w_{xo}\, x_t + w_{ho}\, h_{t-1} + w_{o}\, c_t + b_0\right) \\ h_t = o_t \times \tanh\left(c_t\right) \end{cases} \tag{5}$$

In equation (5), i_t represents the output gate, t represents the time step, σ represents the sigmoid activation function, x_t refers to the output of the current time step, f_t represents the forget gate, c_t refers to the cell state of the current time step, $\tilde{c}_t$ means the updated cell state, o_t means the output gate, h_t refers to the hidden state update, $\tanh(\cdot)$ means the hyperbolic tangent function, w means the weight matrix, and b represents the bias vector. At each time step of BiLSTM, although the Softmax layer can be used to directly predict the labels for that time step, the predicted labels do not take into account the information of the labels before and after, resulting in poor prediction performance. Therefore, after bidirectionally encoding the text vector sequence trained by the ALBERT model using BiLSTM, the CRF algorithm is introduced to optimize BiLSTM and further predict the feature sequence to obtain the final result. The CRF algorithm is a conditional probability distribution model that outputs random variables given a set of input random variables. It is commonly used to label sequences and considers the interaction between labels. It utilizes a global inference algorithm to optimize the optimization results of the entire sequence. The technical roadmap of CRF algorithm process is shown in Figure 5.

In the CRF algorithm, for two random variables, if one variable holds true and the other variable forms a Markov random field denoted by an undirected graph, and holds true at any node, then the conditional probability distribution is a conditional random field. The specific expression is shown in equation (6).

Figure 3 - Rice DPs identification based on the ALBERT model

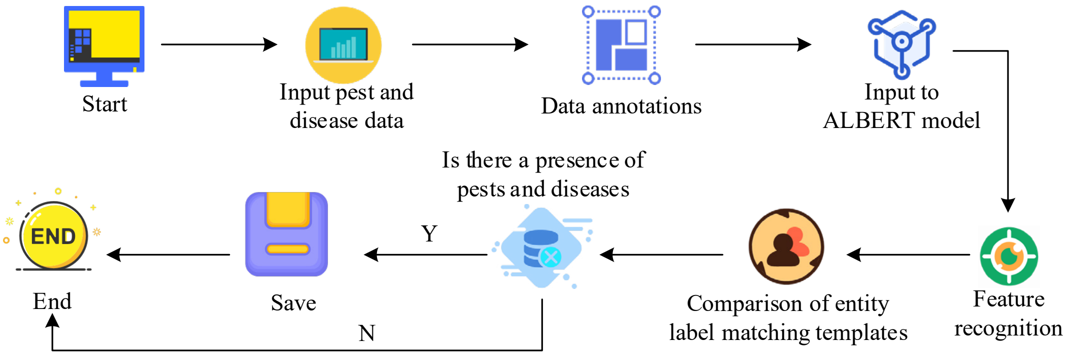


Figure 4- BiLSTM implementation roadmap

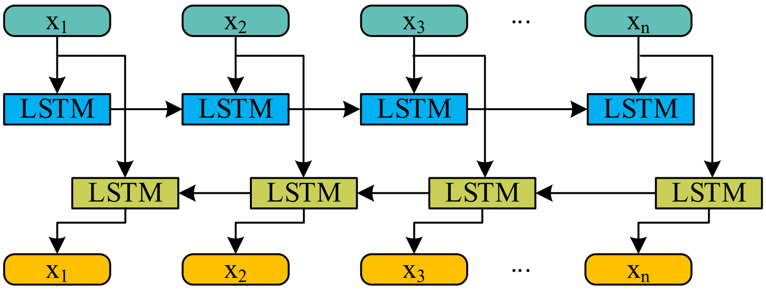


Figure 5 - BiLSTM implementation roadmap

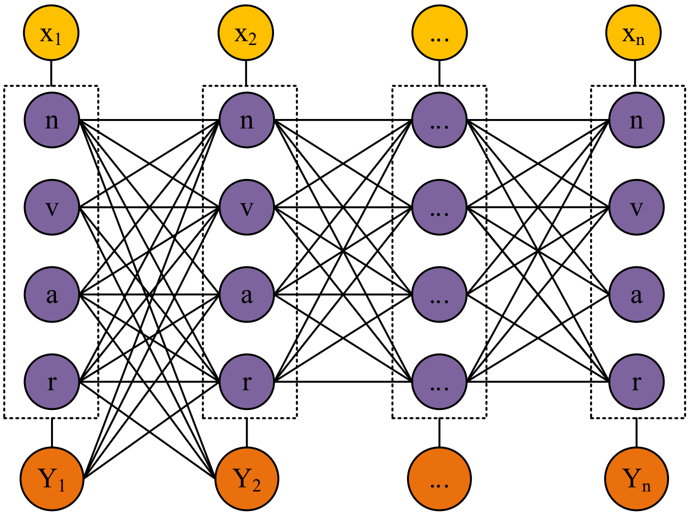
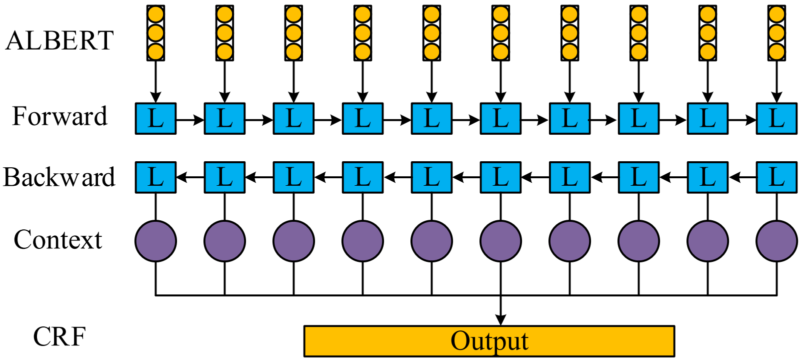


Figure 6 - ALBERT-IBiLSTM model technology roadmap



$$P\left(Y_i \middle| X, Y_1, Y, \ldots, Y_{i-1}, Y_{i+1}, \ldots, Y_n\right) = P\left(Y_i \middle| X, Y_{i-1}, Y_{i+1}\right) \tag{6}$$

In equation (6), X and Y represent random variables, P represents conditional probability, and n represents sequence length. By using conditional probability as the weight of the decoder output, the evaluation score can be calculated using the method shown in equation (7).

$$S(x, y) = \sum_{i=0}^{n} A_{y_i, y_{y+1}} + \sum_{i=1}^{n} P_{i, y_i} \tag{7}$$

In equation (7), S represents the evaluation score, and A represents the transition matrix. By evaluating the score, the maximum probability of sequence labels can be calculated. The study uses a normalization index for calculation, as indicated in equation (8).

$$P(y|x) = \frac{e^{S(x,y)}}{\sum_{i=0}^{n} e^{S(x,y_i)}} \tag{8}$$

In equation (8), $P(y|x)$ means the maximum probability of sequence labels, and e means the natural constant. Combining the ALBERT model with the improved BiLSTM to form a new model Fusion of ALBERT and Improved BiLSTM Model (ALBERT-IBiLSTM). The technical roadmap implementation of this model is shown in Figure 6.

In Figure 6, the ALBERT model is first used for feature extraction to obtain the contextual representation of rice DP data text. Then, BiLSTM is utilized to model the context of pest and disease data text to capture information in the sequence. Finally, the labels in the sequence are calculated using the CRF algorithm, and the obtained label sequence is output.

RESULTS AND DISCUSSION

This chapter mainly illustrates on the experiment findings of the rice DP identification algorithm that integrates ALBERT and improved IBiLSTM. The first section is the performance test results of ALBERT-IBiLSTM, and the second section is the real utilization effect of the ALBERT-IBiLSTM model in DP identification.

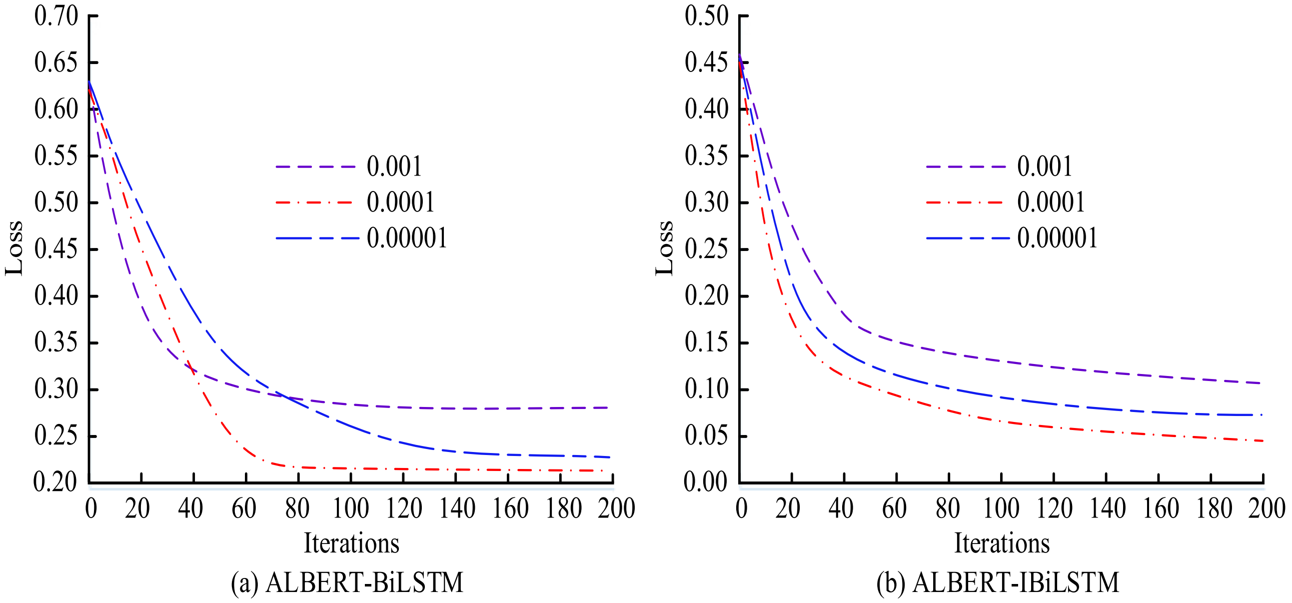
Performance analysis of ALBERT-IBiLSTM model

To identify the effectiveness of the design method, experiments were completed using Python 3.7 on an operation system equipped with an Intel (R) Xeon (R) Gold 6140 @ 2.30GHz central processing unit, RTX 3080Ti graphics card, 32GB of RAM, 1TB hard drive, CUDNN 8.3 DL library, and CUDN10.2 computing platform. The maximum input length of Transformer was set to 64, batch size to 32, initial learning rate (LR) to 0.001, and maximum iteration count to 200. Firstly, the LR of the model was adjusted using the Adam algorithm, and the loss function was used to calculate the loss at different LRs. The results were compared with the ALBERT-BiLSTM model, as shown in Figure 7.

Figures 7 (a) and (b) show the loss curves of the ALBERT-BiLSTM and ALBERT-IBiLSTM models at different LRs, respectively. From Figure 7 (a), at different LRs, the loss of the ALBERT-BiLSTM model gradually decreased and reached stability. When the LR was 0.001, the loss curve of the ALBERT-BiLSTM model reached stability with a loss value of 0.28. When the LR was 0.0001, the loss curve reached stability with a loss value of 0.21. When the LR was 0.00001, that of the ALBERT-BiLSTM model reached a flat state with a loss value of 0.23. From Figure 7 (b), the loss of the ALBERT-IBiLSTM model decreased with increasing iteration times at three different LRs. When the LRs were 0.001, 0.0001, and 0.00001, the loss curves of the model reached a stable state with losses of 0.11, 0.04, and 0.08, respectively. As the LR increased, the loss of both models first decreased and then increased, indicating that an appropriate LR should be selected during model training. Meanwhile, at different LRs, the loss of the ALBERT-IBiLSTM model was smaller than that of the ALBERT-BiLSTM model, demonstrating the high prediction accuracy of the ALBERT-IBiLSTM model. To test the running efficiency of the ALBERT-IBiLSTM model, three indicators including average training time, CPU usage, and memory utilization were calculated and compared with the ALBERT-BiLSTM model and the methods in references (Khan et al., 2023; Puta et al., 2023; Sourav and Wang, 2023). The outcomes are indicated in Table 1.

From Table 1, the average training time of ALBERT-BiLSTM was 81.6 seconds, with a CPU usage rate of 94.3% and a memory usage rate of 66.4%. The average training time, CPU usage, and memory utilization of the method in reference (Khan *et al*., 2023) were 67.9 seconds, 90.6%, and 53.2%, respectively. The three indicator values of the method in reference (Puta *et al*., 2023) were 63.3s, 83.7%, and 51.2%, respectively. The three indicator values of the method in reference (Sourav and Wang, 2023) were 52.5s, 76.2%, and 45.4%, respectively. The three indicators of ALBERT-IBiLSTM were 31.4s, 53.8%, and 36.6%, respectively. Analysis shows that the three indicators

Figure 7 - Loss curves of two models at different learning rates



(a) ALBERT-BiLSTM

(b) ALBERT-IBiLSTM

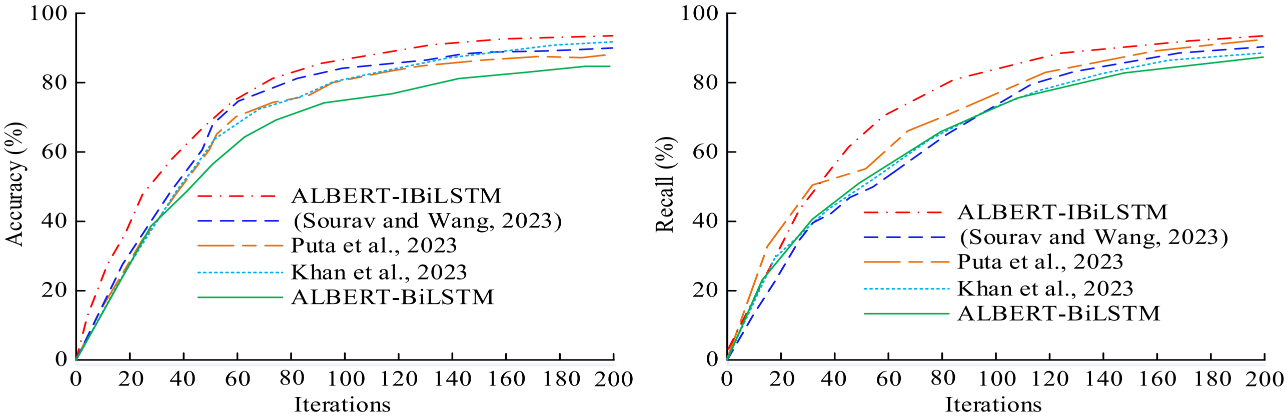
of the ALBERT-IBiLSTM model are greatly lower than those of the other four models, indicating its high operational efficiency. To assess the comprehensive effectiveness of the ALBERT-IBiLSTM model, the accuracy, recall, and F1 score of ALBERT-IBiLSTM, reference (Sourav and Wang, 2023), reference (Putra, Salfiati & Wirman, 2023), reference (Khan *et al*., 2023), and ALBERT-BiLSTM were calculated separately. The results are shown in Figure 8.

Figures 8 (a), (b), and (c) show the accuracy, recall, and F1 score of 5 models, respectively. From Figure 8 (a), the accuracy of different models increased with the amount of iterations. When the amount of iterations arrived 200, the accuracy of ALBERT-IBiLSTM, the method in reference (Sourav and Wang, 2023), the method in reference (Puta *et al*., 2023), the method in reference (Khan *et al*., 2023), and ALBERT-BiLSTM was 95.49%, 92.71%, 93.73%, 90.16%, and 87.32%,

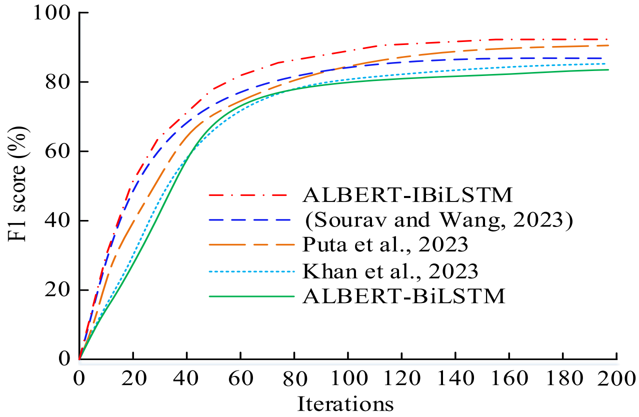
Table 1 - Average training time, CPU usage, and memory utilization of different models

Model	Average training time (s)	CPU usage rate (%)	Memory utilization (%)
ALBERT-BiLSTM	81.6	94.3	66.4
Khan *et al*., 2023	67.9	90.6	53.2
Puta *et al*., 2023	63.3	83.7	51.2
Sourav and Wang, 2023	52.5	76.2	45.4
ALBERT-IBiLSTM	31.4	53.8	36.6

Figure 8 - Accuracy, recall, and F1 score of different models



(a) Accuracy of different models (b) Recall rates of different models



(c) F1 values for different models

respectively. From Figure 8 (b), the recall rates of the five models were 95.03%, 91.55%, 93.81%, 89.82%, and 86.59%, respectively. From Figure 8 (c), the F1 scores of the five methods were 94.76%, 90.03%, 93.77%, 90.38%, and 86.81%, respectively. It can be observed that the three indicators of the ALBERT-IBiLSTM model are higher than the other four models, indicating that its comprehensive performance is good.

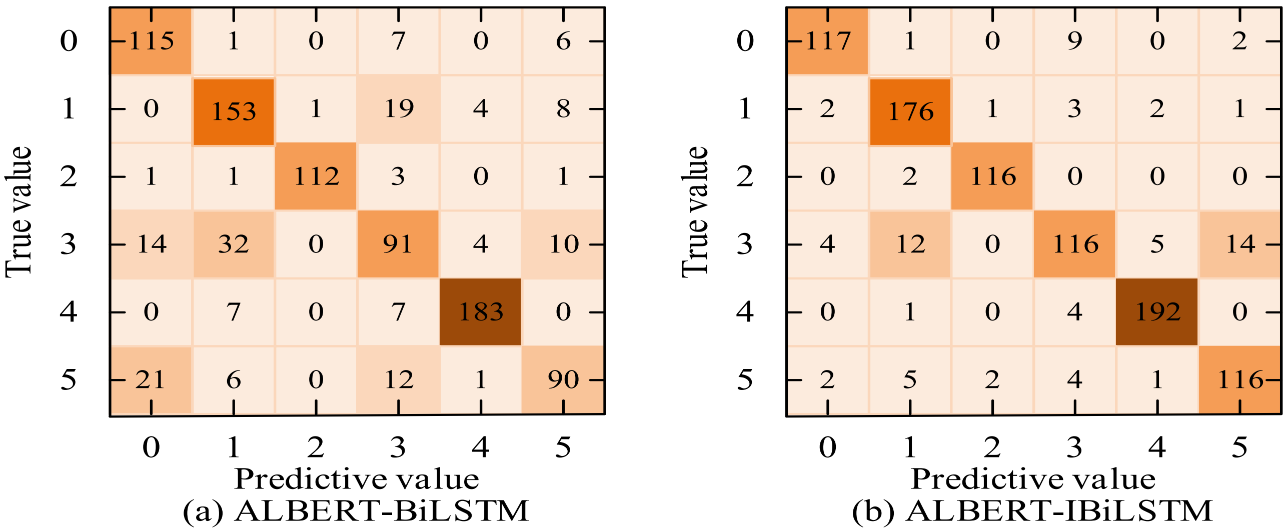
Application analysis of ALBERT-IBiLSTM in rice disease and pest identification

To verify the actual effectiveness of ALBERT-IBiLSTM in identifying rice DPs, the PlantVillage dataset was introduced. 1000 rice DP data were selected and broken into a test set and a training set in a 6:4 ratio. The selected data includes 5 types of rice pests and diseases, specifically rice blast disease, rice planthopper, rice bacterial stripe disease, rice blast disease, and rice bacterial leaf blight, represented by 0, 1, 2, 3, 4, and 5, respectively. Firstly, the recognition performance of ALBERT-IBiLSTM on the test set was verified and compared with the results of ALBERT-BiLSTM. The confusion matrices of the two models are denoted in Figure 9.

Figures 9 (a) and (b) show the confusion matrix of the ALBERT-BiLSTM and ALBERT-IBiLSTM models, respectively. From Figure 9(a), the ALBERT-BiLSTM model had recognition rates of 89.1%, 82.7%, 94.9%, 60.3%, 92.9%, and 69.2% for six types of rice pests and diseases, respectively. From Figure 9(b), the ALBERT-IBiLSTM model had recognition rates of 90.7%, 95.1%, 98.3%, 76.8%, 97.5%, and 89.2% for six types of rice pests and diseases, respectively. Outcomes illustrates that the ALBERT-IBiLSTM model has a significantly higher recognition rate for various pests and diseases than other models, indicating its good performance. To prove the effectiveness of various modules of the ALBERT-IBiLSTM model, ablation experiments were organized on the PlantVillage dataset, and the outcomes are indicated in Table 2.

From Table 2, in the ablation experiment, the accuracy of ALBERT-IBiLSTM was 0.893, an improvement of 20.5% compared to ALBERT, 14.2% compared to ALBERT-LSTM, 6.9% compared to ALBERT-BiLSTM, and 5.8% compared to BiLSTM-CRF. The macro average precision of ALBERT-IBiLSTM was 0.726, and the macro average recall and F1 score

Figure 9 - Confusion Matrix between ALBERT BiLSTM Model and ALBERT IBiLSTM



	0	1	2	3	4	5
0	115	1	0	7	0	6
1	0	153	1	19	4	8
2	1	1	112	3	0	1
3	14	32	0	91	4	10
4	0	7	0	7	183	0
5	21	6	0	12	1	90

(a) ALBERT-BiLSTM

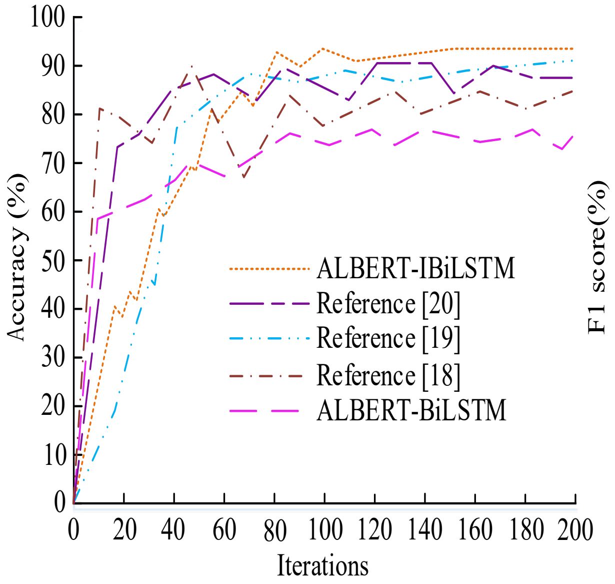
	0	1	2	3	4	5
0	117	1	0	9	0	2
1	2	176	1	3	2	1
2	0	2	116	0	0	0
3	4	12	0	116	5	14
4	0	1	0	4	192	0
5	2	5	2	4	1	116

(b) ALBERT-IBiLSTM

Table 2 - ALBERT-IBiLSTM model ablation experiment results

Model	Accuracy	Precision	Recall rate	F1 score
ALBERT	0.688	0.526	0.806	0.769
ALBERT-LSTM	0.751	0.563	0.861	0.787
ALBERT-BiLSTM	0.824	0.634	0.894	0.829
BiLSTM-CRF	0.835	0.688	0.903	0.836
ALBERT-IBiLSTM	0.893	0.729	0.942	0.885

Figure 10 - The accuracy of different models on the PlantVillage dataset



were 0.942 and 0.885, respectively, which were higher than other modules in the model. This proved the effectiveness of the ALBERT-IBiLSTM model and further verified its high recognition accuracy. Finally, the PlantVillage dataset was applied to train the model, calculate its accuracy, and compare it with other models. The results are shown in Figure 10.

From Figure 10, after training the models using the PlantVillage dataset, as the amount of iterations increased, the accuracy of each model showed an upward trend and gradually stabilized. When the amount of iterations was 200, the accuracy of ALBERT-IBiLSTM, the method in reference (Sourav and Wang, 2023), the method in reference (Puta *et al*., 2023), the method in reference (Khan *et al*., 2023), and ALBERT-BiLSTM was 94.3%, 88.9%, was 90.7%, was 85.1%, and 76.4%, respectively. Compared with other models, the accuracy of ALBERT-IBiLSTM has significantly improved, further proving that this model can effectively detect rice DPs.

CONCLUSIONS

In recent years, there have been frequent occurrences of DPs in the process of rice cultivation. Accurately identifying DPs can help detect their existence as early as possible and take preventive measures to protect the health of rice. The traditional methods for identifying rice DPs are not effective. Therefore, a rice DP identification model based on ALBERT-IBiLSTM was designed by combining the ALBERT model with BiLSTM network and introducing CRF algorithm to optimize BiLSTM. The outcomes denoted that the average training time of the ALBERT-IBiLSTM model was 31.4 seconds, with a CPU usage rate of 53.8% and a memory utilization rate of 36.6%, significantly lower than the three indicators of other models, proving that the ALBERT-IBiLSTM model has high running efficiency. The accuracy, recall, and F1 score of the ALBERT-IBiLSTM model were 95.49%, 95.03%, and 94.76%, respectively, which were significantly higher than other models, proving its good comprehensive performance. The ALBERT-IBiLSTM model could achieve a recognition rate of up to 98.3% for six types of rice DPs, proving its good effectiveness in practical applications of rice DP recognition. Although significant results have been achieved in the research, there are still some shortcomings. Rice may suffer from different DPs at different growth stages, in different regions, and under different climatic conditions. However, the study only analyzed six types of rice DPs. Therefore, future research will introduce more types of DPs to further validate the model, to improve its robustness and practicality.

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