# RESEARCH



# A cell P system with membrane division and dissolution rules for soybean leaf disease recognition

Hongping Song<sup>1\*</sup>, Yourui Huang<sup>1,2\*</sup>, Tao Han<sup>1</sup>, Shanyong Xu<sup>1</sup> and Quanzeng Liu<sup>1</sup>

# Abstract

Rapid and accurate identification of soybean leaf diseases is crucial for optimizing crop health and yield. We propose a cell P system with membrane division and dissolution rules (DDC-P system) for soybean leaf disease identification. Among them, the designed Efficient feature attention (EFA) and the lightweight sandglass structure and efficient feature attention (SGEFA) can focus on disease-specific information while reducing environmental interference. A fuzzy controller was developed to manage the division and dissolution of SGEFA membranes, allowing for adaptive adjustments to the model structure and avoiding redundancy. Experimental results on the homemade soybean disease dataset show that the DDC-P system achieves a recognition rate of 98.43% with an F1 score of 0.9874, while the model size is only 1.41 MB. On the public dataset, the DDC-P system achieves an accuracy of 94.40% with an F1 score of 0.9425. The average recognition time on the edge device is 0.042857 s, with an FPS of 23.3. These outstanding results demonstrate that the DDC-P system not only excels in recognition and generalization but is also ideally suited for deployment on edge devices, revolutionizing the approach to soybean leaf disease management.

# Introduction

Soybean is an important global food and oilseed crop, but its growth is often affected by a variety of diseases, resulting in reduced yield and quality [1]. Three categories of pathogens cause leaf diseases in soybeans: fungal, bacterial, and viral [2], which are usually spread by wind, rain, insects, or agricultural practices, resulting in frequent disease occurrences [3], limiting the quality and yield of soybeans and causing significant losses. In China, soybean yields are reduced by approximately 10% per year

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due to diseases and up to 30% in severe cases; therefore, it is important to realize accurate and rapid identification of soybean leaf diseases.

Traditional soybean disease identification methods rely mainly on manual experience and simple image processing techniques, which are not only time-consuming and labor-intensive but also have low accuracy [4]. In recent years, with the development of image processing and artificial intelligence, machine and deep learning have received extensive attention in agriculture, including disease recognition [5], weed detection [6], quality grading [7], and growth monitoring [8]. For disease recognition, Zeng et al. proposed the LDSNet model for maize leaf disease recognition [9] and designed the IDDC module, the feature fusion module CASF, and the ASCE loss function, which resulted in a recognition accuracy of 95.4%. Fu et al. proposed a lightweight CNN model



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# A cell P system with membrane division and dissolution rules for soybean leaf disease recognition (DDC-P system)



# Highlights

- We propose a cell P system with membrane division and dissolution rules for rapid identification of soybean leaf diseases that improves model real-time performance by reducing the amount of computation.
- The EFA and SGEFA membranes were designed to reduce background interference and focus on disease information.
- Fuzzy controllers were designed to control the triggering of membrane division and membrane dissolution rules, thus controlling the number of SGEFA membranes in parallel and dynamically adjusting the model structure to avoid redundancy.
- A self-developed soybean disease dataset containing 8883 images was obtained.
- The method proposed in this study was successfully deployed on edge devices and could provide a new basis for soybean disease diagnosis.

**Keywords** Soybean leaf disease, Cell P system, Efficient feature attention, Fuzzy control, Convolutional neural network, Disease classification

for recognizing pepper leaf disease [10]. The proposed CNN model uses the GGM-VGG16 architecture, which incorporates the Ghost module, global mean pooling, and multi-scale convolution, and achieves 100% recognition accuracy for pepper leaf disease in human palm background images. Yang et al. proposed the LSGNet model to achieve fast identification of tomato diseases [11]. The LSGNet backbone consisted of SGECA and ParcSG modules. The former suppresses the interference of complex environments and focuses on extracting useful feature information. The latter has a global sensing field and provides more detailed feature information for disease identification, and LSGNet achieved an accuracy of 95.54% in recognizing tomato diseases. Lin et al.

designed a peanut leaf disease monitoring system based on a lightweight deep learning model [12], which facilitates disease detection, improves monitoring efficiency, and reduces labor costs. Meanwhile, a large number of researchers have utilized deep learning to recognize soybean leaf diseases, advancing research on soybean diseases [13]. Pan et al. proposed the TFANet model to achieve the recognition of multi-categories of soybean leaf diseases [14]. The main component is the TFA module, which achieves powerful feature extraction capability by two-stage aggregation of feature information from different convolutional layers to achieve powerful feature extraction capability. TFANet has only 1.18 MB of parameters, and the accuracycan reach 98.18%. Yu et al. addressed the problems of high complexity, high computational volume, and difficulty in applying current deep learning-based disease diagnosis models to commonly used portable mobile terminals, etc., and proposed a light-weight soybean disease diagnosis model based on the attention mechanism and residual neural network, named RANet18 [15], with a model size of only 40.64 MB and an accuracy of 96.5%. Karlekar et al. proposed a soybean leaf disease classifier called SoyNet [16]. The SoyNet consists of two modules. The first module segmented the background. The second module was used to recognize the segmented leaf image with an accuracy of 98.14%. Zhang et al. designed a multi-feature fusion Faster R-CNN model for the accurate detection of soybean leaf diseases in complex scenes with an accuracy of 83.34% [17]. Wang et al. proposed a convolutional neural network-based image recognition model for different disease stages of soybean leaves [18] to address the problem of insufficient data to realize the recognition of soybean bacterial spot disease with an accuracy of 99.64%. Bevers et al. produced a soybean leaf disease dataset with eight categories and used transfer learning to achieve 96.8% accuracy in recognizing the original field soybean disease images [19]. Santana et al. collected hyperspectral images of soybean rust and used machine learning to classify them. Experimental results showed that the SVM algorithm achieved an accuracy of more than 90% [20]. Stone et al. analyzed the associations of soybean dwarf virus isolates with soybean aphid vectors and severe diseases, and constructed a soybean dwarf virus isolate global phylogenetic research system [21]. Zhu et al. proposed an improved YOLO model [22]; that can detect soybean pests with complex backgrounds, and the detection mAP of common soybean pests reached 86.9%. Tetila et al. used the YOLOv3 model to realize the real-time detection of soybean pests [23].

From the above studies, it can be seen that to achieve fast and accurate identification of diseases on soybean leaves, related studies have mainly focused on lightweight [24], and the soybean disease identification models with the smaller models mentioned above were mainly realized by constructing small model architectures using depth-separable convolutions. However, there are other methods to make the model lightweight, such as model pruning [25], knowledge distillation [26], and model compression [27]. Although these methods have made significant progress in speeding up models and reducing their complexity, they are more applicable to large models and less effective on small model architectures with fewer channels and fewer layers [28]. The model selection layer pruning method for small model architectures is an effective approach [29, 30], where the efficiency can be improved by removing all layers from the network while maintaining the network performance. However, the method of culling or merging layers, while reducing the network depth to reduce latency, also introduces a serious problem: the kernel size increases. In this case, although the depth is reduced, the computational effort of a single convolutional operation increases significantly owing to the increase in the kernel size, resulting in the delay reduction effect being canceled out.

To this end, we propose a cell P system with membrane division and dissolution rules to achieve the rapid identification of soybean diseases. The model can dynamically adjust the model architecture without increasing the kernel size, thus realizing the fast identification of soybean diseases. The main contributions of this study are as follows:

(1) A cell P system with membrane division and dissolution rules (DDC-P system) was proposed. The DDC-P system can dynamically adjust the model structure, avoid model redundancy, and achieve the rapid and accurate identification of soybean diseases.

(2) To efficiently extract soybean leaf features and reduce the number of model parameters, we designed a membrane with a lightweight sandglass structure and efficient feature attention (SGEFA).

(3) A fuzzy controller was designed to realize the control of membrane division and membrane dissolution rule triggering using a fuzzy controller, which can dynamically adjust the number of SGEFA in parallel in the DDC-P system more effectively.

(4) In addition, we designed efficient feature attention (EFA) to reduce the interference of complex environments on the model performance and focus on extracting key disease feature information.

### **Materials and methods**

### Soybean disease dataset

The dataset used for the experiment was a soybean disease dataset collected from 2023 to 2024 in Huainan City (32.6264° N, 116.9969° E), Anhui Province, China. Soybean leaf images were captured using a Fuji digital camera and the rear camera of a Honor cellphone. The soybean disease dataset contained 8883 images with real field and pure white backgrounds, which were classified into three main categories: healthy, insect pests, and disease. The images are uniformly resized to  $256 \times 256$  pixels and randomly divided into train, test, and validation sets in the ratio of 8:1:1. Figure 1 shows example images for each category. Table 1 presents the specific division results for the soybean disease dataset.

# DDC-P system

The p system is a computational model inspired by the structure of biological cell membranes [31]. The p system enables parallel computation by simulating biochemical reactions and information transfer processes in the cells.



(a)Diseases

Fig. 1 Example images of the soybean disease dataset

Table 1	Division	of sov	/bean	disease	dataset
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Classes	Train set	Validation set	Test set	Total
Diseases (0)	3747	468	469	4684
Healthy (1)	931	117	116	1164
Insect pests (2)	2428	303	304	3035
Total	7106	888	889	8883

The p system can be of three types: cell, tissue, and neural p systems. Cell P systems are widely used in various fields [32, 33]. To accurately and quickly recognize soybean diseases, we combined the p system and convolutional neural network to propose a new hypergraph cell P system model called the DDC-P system. The overall architecture of the DDC-P system is shown in Fig. 2. The



Fig. 2 Membrane structure of the DDC-P system

DDC-P system consists mainly of an input membrane, n SGEFA membranes, an EFA membrane, and an output membrane. A membrane can be contained by more than one membrane at the same time in the hypergraph cell P system, in which the input membrane type is contained by n SGEFA membranes simultaneously, and the input membranes are indicated by dashed lines in Fig. 2. When the soybean disease image enters the DDC-P system, the shallow features of the image are first extracted by two  $3 \times 3$  convolutions in the input membrane, and then the feature maps are passed into n parallel SGEFA membranes after reducing the number of parameters of the model by using  $3 \times 3$  maximum pooling. In the SGEFA membrane, feature information is efficiently extracted, and then the feature maps are transferred text  $Imput, SGEFA_1, SGEFA_2, \dots, SGEFA_n, EFA, Output$ the EFA membrane, which first splices the n feature maps according to the channel direction and further fuses the feature information through a 3×3 convolution. Then, the EFA module is connected to the module to highlight the key information and suppress the interference of the background information, and then transfers the feature maps to the output membrane. In the output membrane, a  $1 \times 1$  convolutional layer was used to integrate the feature maps, and global average pooling was used to fuse the feature information. Finally, the softmax function was used to classify soybean leaf disease. The detailed

Table 2	Detailed	configuration	of DDC-P	system
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Membrane labelling	Configuration	Input shape	Output shape
Input	Conv (k=3, s=2), BN, ReLU	256×256×3	63×63×64
	Conv (k=3, s=1), BN, ReLU		
	Maxpool ( $k=3, s=2$ )		
SGEFA <sub>1</sub>	Conv (k = 1, s = 1), BN, ReLU	63×63×64	63×63×64
	PWConv ( $k = 1, s = 1$ )	63×63×64	63×63×32
	EFA	63×63×32	63×63×32
	PWConv ( $k = 1, s = 1$ )	63×63×32	63×63×48
	DWConv ( $k=3, s=2$ )	63×63×48	63×63×48
•••			
SGEFA <sub>n</sub>	Conv (k=3, s=2), BN, ReLU	63×63×64	63×63×64
	PWConv ( $k = 1, s = 1$ )	63×63×64	63×63×32
	EFA	63×63×32	63×63×32
	PWConv ( $k = 1, s = 1$ )	63×63×32	63×63×48
	DWConv ( $k=3, s=2$ )	63×63×48	63×63×48
EFA	Conv (k=3, s=1), BN, ReLU	63×63×[48×n]	63×63×128
	EFA	63×63×128	63×63×128
Output	Conv (k = 1, s = 1), BN, ReLU	63×63×128	1×1×3
	FC		

configuration information of the model is presented in Table 2.

### **Evolution rules**

DDC-P system is formally defined as:

$$\Pi = (V, O, H, \mu, \omega_1, \cdots, \omega_{n+3}, R_1, \cdots, R_{n+3}, i_0)$$
(1)

Where:

(1) V is a not empty finite alphabet whose object is the feature of the image;

(2)  $O \subseteq V$  is the output alphabet and the output algorithm results;

(3)  $H = \{Input, SGEFA1, SGEFA2 \dots, SGEFA_n, EFA, Out-$ , *H* is a set of membrane labels;

(4)  $\mu$  is a membrane structure, as shown in Fig. 2;

(5)  $\omega_i (1 \leq i \leq n+3)$  represents the multiset of objects in a region *i*, corresponding to the feature map composed of features in each membrane;

(6)  $R_i (1 \le i \le n+3)$  is a set of evolution rules in each region of membrane structure;

(7)  $i_0$  is the label of the output membrane from the membrane systems,  $i_0 = \text{Output}$ .

The evolution rules in the DDC-P system include communication rules, membrane division rules, and membrane dissolution rules. It is worth noting that membrane division rules and membrane dissolution rules cannot be used simultaneously in the same membrane.

Communication rules:

$$r: u \to v$$
 (2)

Where: u, v are the multiple sets of objects in each membrane, that is the image feature map, indicates that the feature map within the membrane changes from u to v after executing the rules, which include convolution operations, pooling operations, etc.;  $v \in \{v_{here}, v_{in}, v_{out}\}$ , Where  $v_{here}$  is to indicate that the feature map  $\nu$  stays in the current membrane after the rule is executed,  $v_{in}$ is to indicate that the feature map v leaves the current membrane after the rule is executed and enters the child membrane contained by the current membrane, and  $v_{out}$ is to indicate that the feature map v leaves the current membrane after the rule is executed and enters the parent membrane containing the current membrane.

Membrane division rules:

$$[E]_i \to []_j[]_k \tag{3}$$

Where: E is the condition that needs to be satisfied to execute the membrane division rules, i, j, and k are the membrane labels. After executing the membrane division rule, the current membrane splits into two membranes, 
 Table 3
 Fuzzy control tables for inputs and outputs

Val_acc	D				
	Р	Z	N		
Н	E	0	F		
Μ	E	0	0		
L	E	E	E		

and both membranes have the same substances and rules as before

Membrane dissolution rules:

$$[F]_i \to \delta \tag{4}$$

Where: F is the condition that needs to be satisfied to execute the membrane splitting rules, *i* represents the membrane label. The membrane was dissolved after executing the membrane dissolution rules.

### Design of fuzzy controller

To realize the dynamic adjustment of the number of SGEFA membranes in parallel in the DDC-P system, we designed a fuzzy controller that calculates the validation set accuracy (Val\_Acc) and the rate of change of the validation set accuracy (D) every 20 epochs and takes Val\_Acc and D as the inputs to the fuzzy controller, and the outputs are the execution or not of the membrane division and dissolution rules.

Use the fuzzy mathematics library in Python to define the fuzzy sets of inputs and outputs, where the Val\_acc is in the interval [0, 1], and its fuzzy subset is set to  $\{H, M, L\}$ , where H is a high accuracy, ranging from 0.9 to 1. M is of medium accuracy, ranging from 0.6 to 0.9. L is low accuracy, with a range from 0 to 0.6. The D is in the interval [-1, 1], and its fuzzy subset is set to  $\{P, Z, N\}$ , which is P positive change, ranging from 0.15 to 1. Z is no change, ranging from – 0.15 to 0.15. N denotes negative change, ranging from – 1 to -0.15. The output set is  $\{E, F, O\}$ , where E denotes the condition required to satisfy the membrane division rule to execute the membrane division rule, F denotes the condition required to satisfy the membrane dissolution rule to execute the membrane dissolution rule, and O means that the condi-

tions needed for neither the membrane division rules nor the membrane dissolution rules are satisfied and the current membrane structure does not change. Table 3 lists the designed fuzzy control tables.

### EFA membrane

To highlight the key feature information and suppress the interference of background information and noise on the model performance, we design an EFA membrane in the DDC-P system, whose main module is the EFA module. Different from channel attention and spatial attention, we weight each feature to highlight important features. Figure 3 shows the designed EFA module.

As shown in Fig. 3, the EFA module encodes the feature map using both Global average pooling (GAP), Pooling along the horizontal coordinate direction (XAP), and Pooling along the vertical coordinate direction (YAP). Thus, GAP is represented by Eq. (5), XAP by Eq. (6), and YAP by Eq. (7).

$$z_{c} = \frac{1}{H \times W} \sum_{0 \leqslant i < H, 0 \leqslant j < W} u_{c}\left(i, j\right)$$
(5)



$$z_{c}\left(h\right) = \frac{1}{W} \sum_{0 \leq i < H} u_{c}\left(h, i\right)$$
(6)

$$z_{c}(w) = \frac{1}{H} \sum_{0 \leq i < W} u_{c}(i, w)$$
(7)

Where:  $z_c$  is the feature map on the c-th channel, H and W denote the height and width of the input feature map, respectively,  $u_c$  is the feature map on the c-th channel,  $z_c(h)$  is the output along the x-direction on the c-th channel, and  $z_c(w)$  is the output along the y-direction on the c-th channel.

Next, feature maps  $z_C(H)$  and  $z_C(W)$  are cascaded and fed into a  $1 \times 1$  convolution with shared weights, which is more conducive to accurately locating the position of key features, to obtain a new feature map  $z_C(W + H)$ , and  $z_C(W + H)$  obtained from Eq. (8).

$$z_C \left( W + H \right) = Conv \left( \left[ z_C \left( H \right), z_C \left( W \right)^{-1} \right] \right)$$
 (8)

Where:  $Conv(\cdot)$  denotes the 1×1 convolution of the BN layer for ReLU using the activation function first, [a, b] denotes the cascading of the feature maps a and b in the direction of the channel, and  $z_C(W)^{-1}$  denotes the feature map after converting the size of  $z_C(W)$  from  $C \times 1 \times W$  to  $C \times W \times 1$ .

Subsequently, feature map  $z_C(W + H)$  is split into two feature maps  $z_C(H')$  and  $z_C(W')$  along the channel direction, and the size of  $z_C(W')$  is converted from  $C \times W \times 1$  to  $C \times 1 \times W$ . The resulting feature maps  $z_C$ ,  $z_C(H')$ , and  $z_C(W')$  are activated using a sigmoid function to obtain the attention weights  $g^C$ ,  $g^H$ , and  $g^W$ denoted by Eq. (9).

$$\begin{cases} g^{C} = \sigma \left( z_{C} \right) \\ g^{H} = \sigma \left( z_{C} \left( H' \right) \right) \\ g^{W} = \sigma \left( z_{C} \left( W' \right) \right) \end{cases}$$
(9)

Finally, the input *Z* is multiplied sequentially with  $g^C$ ,  $g^H$ , and  $g^W$  to obtain the final output *Z'*, represented by Eq. (10).

$$Z' = g^C \times \left( g^W \times \left( g^H \times Z \right) \right) \tag{10}$$

Thus, we can see that the EFA module not only locates key disease information more accurately but also reduces the impact of background information and other information on model performance.

# SGEFA membrane

Sandler et al. proposed a lightweight model called MobileNetV2 [34], which is characterized by its efficient

efficient feature attention (SGEFA), and the specific

structure of the three is shown in Fig. 4. In Fig. 4, we see that the SGEFA module has a similar structure to the original hourglass block, but there are also differences. First, the SGEFA module does not use residual connections. The main reason is that dynamically adjusting the number of SGEFA membrane parallels will only change the width of the model and will not change the depth of the model. The problem of gradient vanishing is not serious, so the residual connections are of limited usefulness but instead add unnecessary computational overhead. Therefore, we remove the residual connections and the first depth-separable convolution. Second, to efficiently extract feature information, we add the EFA module between the two pointwise convolutions to improve the feature extraction capability without significantly increasing the number of parameters of the model. Finally, we only use the ReLU6 function as the activation function in the first pointwise convolution, which has the advantage of retaining more feature information. The ReLU function and ReLU6 function are shown in Eqs. (11) and (12).

$$ReLU6(x) = max(6, max(0, x))$$
 (11)

$$ReLU(x) = max(0, x) \tag{12}$$

Therefore, assume that the input of the SGEFA module is Z and its output is:

$$Z' = DWConv\left(PWConv2\left(EFA\left(PWConv1(Z)\right)\right)\right) (13)$$

Where DWConv is deep convolution, PWConv1 and PWConv2 are pointwise convolution, and EFA is the EFA module.

### Performance evaluation metrics

We choose accuracy, precision, recall, F1 score, ROC curve, and PR curve as the performance evaluation metrics of the model. The formulas for accuracy, precision, recall, and F1 score are as follows:

$$Accuracy = \frac{TP + TN}{TP + FN + FP + TN} \times 100\%$$
(14)

$$Precision = \frac{TP}{TP + FP} \tag{15}$$



Fig. 4 Specific structure of the three modules. (a) Inverted residual block in MobileNetV2, (b) Raw hourglass block, (c) SGEFA module

$$Recall = \frac{TP}{TP + FN} \tag{16}$$

$$F1 = \frac{2 \times Precision \times Recall}{Precision + Recall}$$
(17)

Where: TP denotes the number of true positive results, FP denotes the number of false positive results, FN denotes the number of false negative results, and TN denotes the number of true negative results.

The receiver operating characteristic (ROC) curve demonstrates the overall performance of the model by plotting the relationship between the model's true positive rate (TPR) and false positive rate (FPR), while the area under the ROC curve (AUC) is closer to 1, which indicates model performance.

$$TPR = \frac{TP}{TP + FN} \tag{18}$$

$$FPR = \frac{FP}{FP + TN} \tag{19}$$

The PR curve shows the relationship between precision and recall at different thresholds. AP (average precision) represents the average precision at different recall rates. Usually, the closer the AP is to 1, the better the model performance is. Meanwhile, the number of parameters and frames per second (FPS) are chosen to evaluate the performance of the model in real applications. The number of parameters is an important indicator of inference speed and model size. FPS represents the number of images predicted by the model per second for speed evaluation.

$$FPS = \frac{Total \ of \ images}{Time} \tag{20}$$

## **Experiments and results**

This study uses Python and TensorFlow deep learning frameworks for experiments. All experiments were performed on Windows 10, using an Intel (R) Core (TM) i7-9700 K CPU and an NVIDIA RTX2070 GPU. Our hyperparameters are set as follows: the loss function is a cross-entropy loss function, and we use the Adam optimizer with the batch size set to 32.

# Determination of the parallel number(n) of SGEFA membrane

The n is set to avoid model redundancy and better adapt to the input data. Therefore, we set the epoch to 300, the maximum number of times the membrane division rule can be used to 10, and the maximum number of times the membrane dissolution rule can be used to 5. The initial number of parallel SGEFA membranes is set to 1; the number of n is added to 1 after each execution

**Table 4** The course of Val\_acc and N in the experiment

Iteration Val_acc (%)		n
0	0	1
1	76.01%	2
2	88.29%	3
3	96.06%	4
4	97.41%	4
5	95.50%	3
6	97.07%	4
7	98.20%	4
8	98.09%	4
9	97.97%	4
10	97.41%	4
11	97.86%	4
12	97.64%	4
13	97.86%	4
14	97.64%	4
15	98.31%	4

 Table 5
 Experimental results of the DDC-P system with different

n	Val_loss	Val_acc (%)	Test_loss	Test_acc (%)
1	0.2320	91.10%	0.2121	92.35%
2	0.1297	96.28%	0.1493	94.71%
3	0.0786	97.52%	0.0817	96.85%
4	0.0341	98.76%	0.0476	98.43%

of the membrane division rule, and the number of n is subtracted from 1 after each execution of the membrane dissolution rule. 20 epochs are taken as a round, and the Val\_acc is printed once in each round. The rate of change of the validation set accuracy is calculated as D, denoted by Eq. (21). Val\_acc and D are used as inputs to the fuzzy controller to regulate the application of membrane division and dissolution rule, while also updating the frequency of their usage. The model stops running when it reaches the maximum epoch, the maximum number of uses of the membrane division rules, or the maximum number of uses of the membrane dissolution rules.

$$D_i = Val\_acc_i - Val\_acc_{i-1}$$
(21)



Fig. 5 Confusion matrix of the DDC-P system with different n

Where:  $Val\_acc_i$  is the current validation set accuracy,  $Val\_acc_{i-1}$  is the last validation set accuracy, and *i* is the number of rounds.

Table 4 shows the overall change process of Val\_acc and D during the experiment, from which we can see that n has been increasing to 4 and then decreasing to 3, and then increasing to 4 again and then remaining unchanged, which indicates that the number of SGEFA parallels being 4 is the best choice. However, the Val\_acc of the model keeps changing when the value of n is 4. Also, the division of training into rounds of 20 epochs as a round may affect the determination of n. To demonstrate the accuracy of n, we build different DDC-P systems based on different values of n appearing in Table 4, set the epoch to 100, and evaluate the performance of the DDC-P systems at different n.

Table 5 shows the experimental results of the DDC-P system with different n. From Table 5, we can see that the Val\_acc for n of 4 is 98.76% and the test set accuracy (Test\_acc) is 98.43%, which are both the highest among all four models. The validation set loss (Val\_loss) is 0.0341, and the test set loss (Test\_loss) is 0.0476, which are both the lowest among the four models, which can show that an n value of 4 is the best choice. Meanwhile, Fig. 5 shows the confusion matrix of the DDC-P system on the test set for different values of n. The number of correct recognitions of Category 1 by the DDC-P system for n of 4 is second only to that of the DDC-P system for n value of 2. However, the number of correct recognitions for both Category 0 and Category 2 is the highest among all n values. Also, the total number of correct recognitions is the highest of all n values, which also shows that n of 4 is the best choice. Therefore, it is feasible to use a fuzzy controller to control the triggering of membrane division rules and membrane dissolution rules to control the number of SGEFA parallels, and the DDC-P system can dynamically adjust the model structure according to the inputs to avoid model redundancy.



 Table 6
 Experimental results of ablation experiments on the test set



Fig. 6 Results of ablation experiments on three categories

 Table 7
 Performance of the DDC-P system with the comparison models

Model	Accuracy (%)	Precision	Recall	F1	Parame- ter count (MB)
DenseNet121	96.85%	0.9733	0.9766	0.9748	28.87
ResNet101	96.29%	0.9692	0.9715	0.9703	166.77
MobileNetV2	88.75%	0.9353	0.8876	0.8993	11.14
EfficientNetB0	93.14%	0.9114	0.9497	0.9280	17.98
InceptionV3	95.84%	0.9585	0.9714	0.9643	87.21
DDC-P system	98.43%	0.9870	0.9877	0.9874	1.41

### **Rblation experiment**

We designed the attention module EFA in the DDC-P system, and to verify the effect of the EFA module on the model performance, we conducted ablation experiments with an epoch set to 100. Table 6 shows the experimental results of the ablation experiments. It can be seen that the use of the EFA module increases the accuracy by 1.36% and precision, recall, and F1, which indicates that the EFA module can improve the performance of the DDC-P system. Figure 6 shows the specific recognition results for the three categories of soybean leaves on the test set, and the use of the EFA module increases the number of Category 0 and Category 2 recognized correctly. Therefore, using the EFA module can suppress the interference of the background on the model and improve the overall performance of the DDC-P system.

### Comparison with different models

To validate the classification performance of the DDC-P system, we conducted comparison experiments between the DDC-P system and some classical models under the same training conditions, choosing DenseNet121 [36], ResNet101 [37], MobileNetV2. EfficientNetB0 [38], and InceptionV3 [39] models to compare with the overall performance of the DDC-P system with the epoch set to 100. Table 7 shows the overall performance of the DDC-P system with the comparison models on the test set.

Table 7 clearly shows that the accuracy, precision, recall, and F1 of the DDC-P system are 98.43%, 0.9870, 0.9877, and 0.9874, respectively, which are optimal among all the models compared to the classical models mentioned above, suggesting that optimal experimental results are obtained for the DDC-P system. Simultaneously, the DDC-P system is only 1.41 M, possessing the least number of parameters. The results show that the DDC-P system has better performance in soybean leaf disease identification and can accurately identify soybean leaf diseases, while the parameter count of the DDC-P system is significantly lower and easier to implement on edge devices.

Figure 7 shows the confusion matrix between the DDC-P system and the comparison models on the test set. In Category 1, all models except MobileNetV2 achieve 100% recognition. In Category 2, InceptionV3 and the DDC-P system have an equal number of correct recognitions and are the highest among all models. On Category 0, the DDC-P system correctly recognized the highest number of all models. In addition, the DDC-P system had the highest overall number of correct identifications. This indicates that the DDC-P system is optimal for soybean leaf recognition.

Figure 8 shows the ROC curves of the DDC-P system with the comparison models, where the ROC curves with each of the three categories as positive classes are plotted. The DDC-P system obtains the largest AUC of 0.9990, and EfficientNetB0 obtains the smallest AUC of 0.9808 when Category 0 is used as the positive class. When using Category 1 as the positive class, the AUC of all models except EfficientNetB0 is equal to 1. When Category 2 is used as a positive class, the DDC-P system has an AUC of 0.9989, and EfficientNetB0 has an AUC of 0.9754, with the former being the largest and the latter the smallest of all models. Overall, it can be seen that the ROC curve of the DDC-P system is closer to the vertical axis, and the AUC is optimal among all models, indicating that the DDC-P system can better recognize soybean leaf diseases. Figure 9 shows the PR curves of the DDC-P system with the comparison models, which are also plotted separately for each of the three categories as the positive class. In the figure, the DDC-P system obtains a maximum AP of 0.9991 when Category 0 is used as



Fig. 7 Confusion matrix of the DDC-P system with the comparison models

the positive class. When Category 1 is used as a positive class, only DenseNet121, ResNet101, and the DDC-P system have an AP equal to 1. When using Category 2 as a positive class, the DDC-P system has an AP of 0.9979, the largest of all models. However, EfficientNetB0 obtains the smallest AP for all three PR curves. This indicates that the DDC-P system performs best among all models, and EfficientNetB0 performs worst.

# Experiments on the Auburn soybean disease image dataset

The Auburn soybean disease image dataset [19] is a collection of soybean leaf disease images, consisting of 8 categories and a total of 9,648 images. Table 8 provides the details of the Auburn soybean disease image dataset. The images are uniformly resized to  $256 \times 256$  pixels and randomly divided into training, testing, and validation sets in the ratio of 8:1:1.

Figure 10 shows the variation process of n in the DDC-P system on the dataset. Setting the epoch to 1000

and the rounds to 30 results in an iteration of 34. The membrane division rule can be utilized up to a maximum of 10 times, while the membrane dissolution rule can be applied up to 5 times. It can be seen from the Fig. 10 that an n value of 5 is the optimal choice.

Figure 11 shows the confusion matrix of the DDC-P system compared to other models on the Auburn soybean disease image dataset. It can be seen that the DDC-P system can correctly classify soybean leaf disease categories even on unbalanced samples. Table 9 presents the overall performance of the DDC-P system compared to other models on the Auburn soybean disease image dataset. The performance metrics of the DDC-P system are 94.40% accuracy, 0.94443 precision, 0.9411 recall, and 0.9425 F1 score, which are the highest among all models. The experimental results demonstrate that the DDC-P system maintains excellent recognition ability even on samples with more complex and uneven backgrounds, indicating a stronger generalization capability.



Fig. 8 ROC curves for the DDC-P system and the comparison models



Fig. 9 PR curves of the DDC-P system with comparison models

Classes	Train set	Validation set	Test set	Total
Bacterial Blight (0)	386	49	49	484
Cercospora Leaf Blight (1)	1278	160	160	1598
Downey Mildew (2)	522	65	65	652
Frogeye Leaf Spot (3)	1232	154	154	1540
Healthy (4)	1306	163	163	1632
Potassium Deficiency (5)	826	104	104	1034
Soybean Rust (6)	1303	162	162	1627
Target Spot (7)	865	108	108	1081
Total	7718	965	965	9648

## Deployment on edge devices

Unitree Go1 is a high-mobility quadruped robot. To verify the feasibility of the DDC-P system in real-field operations, we deployed the DDC-P system with the comparison models on a Jetson Xavier NX controller with an internal block of 64G memory. Figure 12 shows a field scene where the DDC-P system was deployed on the Unitree Go1 and tested in a soybean field. Figures 13 and 14 show the running time and FPS of the DDC-P system and the comparison models on Unitree Go1, respectively. The test set contains 889 images of soybean leaves, and the DDC-P system has a running time of 38.1s and an FPS of 23.3, with the former being the shortest among all models and the latter being the largest among all models. Therefore, the DDC-P system has faster real-time recognition speed and better real-time performance.

### Discussions

There are about 120 known soybean diseases in the world, 52 of which are found in China. The annual loss due to diseases is about 10%, and in severe cases, it can

be up to 30%. Therefore, realizing rapid and accurate identification of soybean leaf diseases is of great research significance for both the quality and yield of soybeans. In this paper, a cell P system with membrane division and membrane dissolution rules (DDC-P system) was constructed to recognize soybean leaf diseases. 8883 soybean leaf disease images were collected for experiments. The experimental results show that the DDC-P system is a rapid and accurate soybean leaf disease recognition model that can be easily ported to edge devices. To further evaluate the recognition ability of the DDC-P system on soybean diseases, we compared the DDC-P system with the latest soybean disease recognition models. In Table 10, we list the model name, publication date, dataset, accuracy, and model parameter count. From Table 10, we can see that the accuracy rates of the listed models are more than 95%, which indicates that all of these models have excellent performance. Among them, the accuracy of the DDC-P system is the best among all models, and the model size is only a little bit larger than TFANet, which shows that the DDC-P system has obvious advantages in soybean leaf disease recognition.

In this study, the DDC-P system was implemented to recognize soybean leaf diseases, and according to the results of the confusion matrix, only healthy leaves were completely and correctly identified, but both diseases and insect pests were misclassified. The reasons for the misclassification of diseased and insect-infested leaves may be twofold; on the one hand, the early diseased and insect-infested leaves are not characterized, thus leading to model misclassification. On the other hand, for soybean leaves, disease and insect pests sometimes occur together, and there are similarities between the characteristics, which can also lead to model misclassification.



Fig. 10 The variation process of the value of n



Fig. 11 Confusion matrix of the DDC-P system

 Table 9
 Performance of the DDC-P system with the comparison models

Model	Accuracy (%)	Precision	Recall	F1
DenseNet121	91.40%	0.9299	0.9014	0.9133
ResNet101	81.87%	0.8599	0.8072	0.8143
MobileNetV2	82.38%	0.8429	0.8399	0.8275
EfficientNetB0	89.53%	0.8940	0.8821	0.8870
InceptionV3	89.84%	0.9292	0.8771	0.8944
DDC-P system	94.40%	0.9443	0.9411	0.9425



Fig. 12 Soybean field trial scene

In this study, the DDC-P system was implemented to recognize soybean leaf diseases, and according to the results of the confusion matrix, only healthy leaves were completely and correctly identified, but both diseases and insect pests were misclassified. The reasons for the misclassification of diseased and insect-infested leaves may be twofold; on the one hand, the early diseased and insect-infested leaves are not characterized, thus leading to model misclassification. On the other hand, for soybean leaves, disease and insect pests sometimes occur together, and there are similarities between the characteristics, which can also lead to model misclassification.

# Conclusion

In this paper, we propose a cell P system with membrane division and membrane dissolution rules (DDC-P system) for rapid, accurate identification of soybean leaf diseases. In the DDC-P system, the SGEFA membrane effectively extracts features and reduces the number of model parameters, and the EFA membrane focuses on key features and suppresses the interference of background on the performance. Meanwhile, a fuzzy controller is designed to control the division and dissolution of the SGEFA membrane to dynamically adjust the DDC-P system and avoid model redundancy. 8883 soybean leaf



Fig. 13 Runtime of the DDC-P system with the comparison models on Unitree Go1



Fig. 14 FPS of the DDC-P system with the comparison model on Unitree Go1

 Table 10
 Comparison of the DDC-P system with recent studies

Models	Publica- tion date	Datasets	Accu- racy (%)	Parame- ter count (MB)
TFANet [14]	2023.09	ASDID	98.18%	1.18
Swin Transformer [18]	2023.09	Private	99.64%	-
TRNet18 [40]	2023.09	Private	99.53%	42.70
RANet18 [15]	2023.06	Private	96.50%	40.64
DenseNet201 [19]	2022.11	ASDID, PDDB	96.75%	-
VirLeafNet-3 [41]	2021.03	Private	97.40%	-
SoyNet [16]	2020.05	PDDB	98.14%	-
DDC-P system (Ours)	2024.08	Private	98.43%	1.41

disease images were collected for experiments, and the test set accuracy of the DDC-P system was 98.43%, F1 was 0.9874, and the model size was 1.41 MB. On public datasets with larger volumes of data, more complex contexts, and imbalanced samples, the DDC-P system achieves an accuracy of 94.40% with an F1 score of 0.9425. The average disease recognition time on the edge device was 0.042857s, and the FPS was 23.3.

The experimental results demonstrate that the DDC-P system exhibits excellent recognition capabilities on datasets with complex backgrounds and diverse disease types. Furthermore, it can achieve efficient real-time inference on edge devices. Additionally, the DDC-P system can dynamically adjust its model structure to accommodate different research tasks, making it highly applicable to other agricultural disease recognition scenarios. However, we also observe that the DDC-P system requires a more refined tuning strategy when applied to larger or more diverse agricultural datasets. Moreover, there is a certain degradation in recognition performance on images with obscure disease features. These aspects will be the focus of our future research efforts.

### Acknowledgements

Not applicable.

#### Author contributions

HPS and YRH analyzed the data and conducted experiments. HPS drafted the manuscript, while YRH and TH reviewed the manuscript. SYX and QZL analyzed soybean leaf disease recognition and created the graphical abstract. All authors read and approved the manuscript.

### Funding

This study was supported by the National Natural Science Foundation of China (61772033), and Collaborative Innovation Project of Colleges and Universities of Anhui Province, China (GXXT-2023-068).

### Data availability

Direct URL to Auburn Soybean Disease Image Dataset: https://doi.org/10.506 1/dryad.41ns1rnj3.

### Declarations

Ethics approval and consent to participate

Not applicable.

### **Consent for publication**

All authors have read and agreed to submit the manuscript.

### **Competing interests**

The authors declare no competing interests.

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### Received: 5 December 2024 / Accepted: 9 March 2025 Published online: 18 March 2025

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