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Tumor Cell Image Segmentation Algorithm

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Abstract—**Image segmentation, as a key task in computer vision and image processing, involves the problem of segmenting an image into different regions or objects. Tumor cell image segmentation is an important task in medical image processing, playing a crucial role in disease diagnosis, treatment planning and research. Six algorithms were used for image segmentation of tumor cells and human osteosarcoma cell images, including image segmentation algorithm based on PCNN and NSGA-II, artificial bee colony algorithm, particle swarm optimization algorithm, image segmentation algorithm based on allostatic optimization and gaussians function, image segmentation algorithm based on differential evolution and gaussian function, adaptive thresholding segmentation based on maximizing inter-class variance. Objective quantitative evaluation of image segmentation algorithm results is conducted by using Accuracy, Sensitivity, Fmeasure, Precision, Matthews Correlation Coefficient, Dice Coefficient, Jaccard Index and Specificity as evaluation indicators, and the segmentation image results and performance indicators are analyzed.**

Index Terms—**Tumor cell image; Image segmentation; Performance comparison; Optimization**

I. INTRODUCTION

Cancer is one of the leading causes of death worldwide and poses a significant challenge to public health systems. As an important basis for early diagnosis of cancer, accurate segmentation of tumors is particularly important. Tumors have different characteristics, types, and treatment methods [1], and early detection and diagnosis of cancer are crucial for improving treatment effectiveness and patient survival rates. With the development of imaging technologies such as CT, MRI, PET, etc., doctors can obtain higher resolution and clearer tumor images, which provides a better foundation for tumor cell segmentation. Traditional cell segmentation methods consist of three steps: cell segmentation, feature extraction or selection, and cell classification. Due to the complexity of these methods, they often find it difficult to be effective in practical applications [2]. In order to reduce the workload of doctors and improve the consistency and accuracy of diagnosis, the demand for computer-aided diagnostic systems is increasing, and tumor cell segmentation is a core component of these systems. Tumor cell segmentation technology can help doctors determine the surgical scope, radiation dose distribution, and evaluate treatment efficacy. With the help of medical image segmentation technology, doctors can quickly and accurately analyze medical images and provide accurate diagnosis and treatment results, saving time and reducing misdiagnosis rates. Therefore, the research on medical image segmentation technology plays an important role in the application of the medical field and has great application value and significance [3].

Image segmentation is one of the most popular research fields in computer vision, serving as the foundation for pattern recognition and image understanding [4]. The purpose of image segmentation is to divide an image into regions with isomorphic properties corresponding to objects or object parts [5]. Image segmentation plays a crucial role in image understanding, feature extraction, analysis, and interpretation. It has a wide range of applications in medical science, such as tissue classification, tumor localization, tumor volume estimation, blood cell delineation, surgical planning, atlas matching, and image registration [6]. The so-called image segmentation refers to dividing an image into several non intersecting regions based on features such as grayscale, color, spatial texture, geometric shape, etc [7]. Traditional image segmentation algorithms mainly include threshold based segmentation methods, edge based segmentation methods, and region based segmentation methods [8]. Image segmentation is divided into semantic segmentation, instance segmentation, and panoramic segmentation based on the granularity of segmentation. Medical image segmentation is considered a semantic segmentation task [7]. In the field of medicine, by classifying and summarizing existing medical image segmentation methods, medical image segmentation can be divided into two categories: deep learning based segmentation methods and traditional segmentation methods. Traditional segmentation methods include threshold segmentation, region based segmentation, clustering segmentation, edge detection based segmentation, and model-based segmentation. The segmentation methods based on deep learning include supervised learning, weakly supervised learning, and other methods.

Medical image segmentation is a key step in the field of medical image analysis [9]. In the field of medical image segmentation, researchers use deep learning techniques for tasks such as tumor segmentation [10], cell segmentation [11], and organ segmentation [12]. Automatic tumor segmentation plays an important role in radiotherapy and clinical practice, and is the foundation for implementing subsequent treatment plans. The purpose of tumor cell segmentation is to distinguish tumor cells from surrounding

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normal tissues for further analysis and research. Due to the potential similarity in morphology and staining characteristics between tumor cells and normal cells, tumor cell segmentation becomes a challenging task. Accurate tumor cell segmentation is of great significance for improving the success rate of cancer treatment and the survival rate of patients, helping to determine the treatment area and dose distribution, as well as the precise location of surgery. Tumor cell image segmentation helps analyze the morphological features, growth patterns, and invasiveness of tumors, providing support for the biological understanding of cancer. The challenges of segmentation involve cell adhesion, cell deformation, unclear cell contours, low contrast cell protrusion structures, and background impurities [11]. Although the segmentation methods for different tumor cells vary, the sole purpose of tumor cell image segmentation is to achieve accuracy. Tumor cells typically have different morphologies, with benign tumors typically having smooth, circular, and elliptical boundaries, while most malignant tumors have irregular and needle like shapes [13]. In pathological research, analyzing images of tumor cells, studying the morphological characteristics, grading, and types of tumors, and providing real-time image information during surgical procedures to assist doctors in precise operations.

This article studies the segmentation of tumor cell images, selecting two types of cells: tumor cells and human osteosarcoma cells. Six different segmentation methods are used to segment the images of the two different types of tumor cells. And analyze the segmented image results and performance indicators. The structure of the paper is arranged as follows. The second section introduces six algorithms: image segmentation algorithm based on PCNN and NSGA -II, Artificial Bee Colony algorithms, Particle Swarm Optimization algorithms, image segmentation algorithm based on Allostatic Optimization and Gaussians Functions, image segmentation algorithm based on Differential Evolution and Gaussian function, Adaptive Thresholding Segmentation Based on Maximizing Inter-class Variance; The third section is experimental simulation and result analysis; Finally, there is the conclusion of the paper.

II. IMAGE SEGMENTATION ALGORITHM

A. Image Segmentation Algorithm Based on PCNN and NSGA -II

Pulse Coupled Neural Networks (PCNN) is an image segmentation method used in image theory. The inspiration for Pulse Coupled Neural Networks comes from the neural cortex of animals [14], which is composed of a combination of neural models, each of which is a single-layer neural network. The capture characteristics and features of PCNN models enable them to process images in different ways, and PCNN models are divided into coupled links and uncoupled links. Coupled PCNN models also have many parameters that are not conducive to analyzing network characteristics, while uncoupled PCNN models remove coupled link subsystems while retaining the core subsystems of PCNN models. Therefore, the analysis of uncoupled PCNN models has become an important support for research. In this neural network, a PCNN model consists of a coupled connection subsystem, a feed input subsystem, a modulation subsystem, a dynamic threshold subsystem, and a trigger subsystem. It can be summarized into three parts: signal receiving part, connection module, and pulse output part. The PCNN model is a single-layer feedback network consisting of several interconnected neurons and two-dimensional local connections primarily based on iterative operations.It has significant differences compared to other artificial neural networks. PCNN is a self supervised and self-learning network that does not require prior training and belongs to the third-generation neural network model. It has excellent self-learning image segmentation and self-learning image feature extraction.

Fig. 1 shows the PCNN neuron model. As shown in Fig. 1, the neuron model of the Pulse Coupled Neural Network mainly consists of three key components: nonlinear connection modulation link, dendritic region and pulse firing mechanism. The receiving area of this model can integrate input signals from the external environment as well as signals from other neurons in the network. This structural design enables PCNN to effectively simulate the information processing process in the biological nervous system.The modulation part is usually obtained by multiplying the L-channel signal L_j with a positive offset and the F-channel signal F_j for modulation. The offset in the model is normalized to 1, and β_j is the connection strength. The corresponding mathematical equation is:

$$F_{ij}[n] = e^{\alpha F\delta n} L_{ij}[n-1] + S_{ij} + V_F \sum M_{ijkl} Y_{kl}[n-1] \quad (1)$$

$$L_{ij}[n] = e^{\alpha L\delta n} L_{ij}[n-1] + S_{ij} + V_L \sum W_{ijkl} Y_{kl}[n-1] \quad (2)$$

$$U_{ij}[n] = F_{ij}[n]\{1 + \beta L_{ij}[n]\} \quad (3)$$

$$Y_{ij}(n) = f(x) = \begin{cases} 1, U_{ij}(n) > \theta_{ij}(n) \\ 0, U_{ij}(n) \le \theta_{ij}(n) \end{cases} \quad (4)$$

$$\theta_{ij}[n] = e^{\alpha\theta\delta n} \theta_{ij}[n-1] + V_\theta Y_{ij} \quad (5)$$

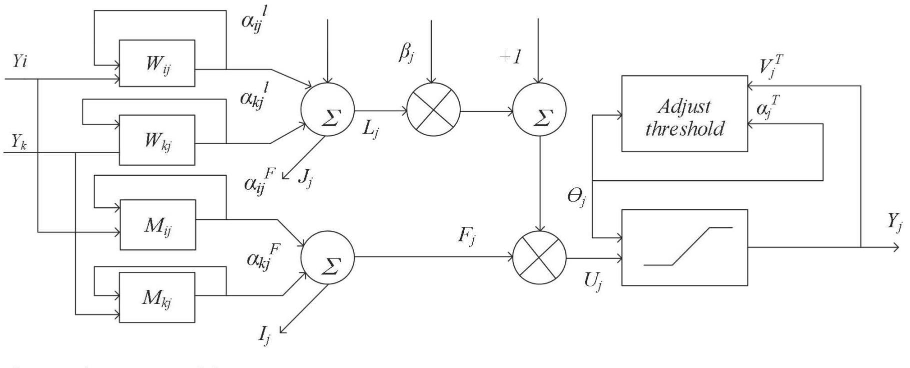


Fig. 1 Pulse coupled neural network neuron model.

where, S is the excitation, F is the feedback, L is the connection, U is the internal motion feature, Y is the pulse output, θ is the dynamic threshold, and the local connection M and W usually follow a Gaussian distribution with constant values. However, due to difficulties such as the difficulty in determining network parameters, a simplified model of neurons has emerged, as shown in Fig. 2. The corresponding mathematical equations are:

$$F_{ij}(n) = S_{ij} \tag{6}$$

$$L_{ij}(n) = \sum_{kl} W_{ijkl} Y_{kl}(n-1) \tag{7}$$

$$U_{ij}(n) = F_{ij}(n)\left(1 + \beta L_{ij}(n)\right) \tag{8}$$

$$\theta_{ij}(n) = e^{-\alpha_\theta} \theta_{ij}(n-1) + V_\theta Y_{ij}(n-1) \tag{9}$$

$$Y_{ij}(n) = f(x) = \begin{cases} 1, U_{ij}(n) > \theta_{ij}(n) \\ 0, U_{ij} \le \theta_{ij}(n) \end{cases} \tag{10}$$

Non-dominated Sorting Genetic Algorithm II (NSGA-II) [15] is an improved version of the Non-dominated Sorting Genetic Algorithm (NSGA) [16]. Fig. 3 shows the algorithm flowchart of NSGA-II, which consists of two key components: first, a fast non dominated sorting mechanism, and second, a crowding comparison operator. On top of the standard genetic algorithm, NSGA-II has made innovative improvements, particularly in optimizing the selection and reproduction mechanisms. This algorithm stratifies the population by evaluating the dominant and non dominant relationships between individuals, thereby distinguishing the strengths and weaknesses of individuals. And based on this, perform the selection operation. This improvement ensures that the algorithm achieves significant and satisfactory results in multi-objective optimization tasks.

The proposal of NSGA-II is aimed at overcoming the limitations of the NSGA algorithm. NSGA-II introduces an elite strategy, which improves the robustness of the algorithm and the accuracy of optimization results. The initial step of the NSGA-II algorithm involves non dominated sorting of individuals in the population. During this process, each individual will receive a rank value that reflects how many other individuals are ranked above them in the ranking. This sorting mechanism is crucial for evaluating the relative performance of individuals in multi-objective optimization problems. To ensure the diversity and good distribution of the population during the evolution process, the NSGA-II algorithm first calculates the aggregation degree of each individual. Individuals are included in a partially ordered set based on their level and clustering. When building a new generation population, the algorithm selects individuals in sequence based on the order of the partially ordered set. During the selection process, priority should be given to individuals with excellent performance and low clustering to ensure that they can enter the next generation's evolutionary cycle. It is worth noting that individuals with lower aggregation actually have larger aggregation distances, which are calculated based on the sum of the distance differences between the individual and neighboring individuals on each sub target. Specifically, by accumulating the distance difference between an individual and neighboring individuals on each sub target, the aggregation distance of the individual can be obtained. This method helps identify and preserve individuals with sparse distributions in the solution space, thereby promoting population diversity. NSGA-II also forms new populations through standard genetic algorithm operations. Merge the parent and child populations, select individuals based on non dominated sorting and crowding degree to form a new parent population. When a certain number of iterations or other termination conditions are reached, the algorithm stops and outputs the optimal solution set in non dominated sorting.

Image segmentation algorithm based on PCNN and NSGA -II. Combining the algorithms of both has improved the accuracy of image segmentation. In image segmentation algorithms, PCNN is generally used for preliminary image segmentation, while NSGA-II is used to further optimize segmentation results.

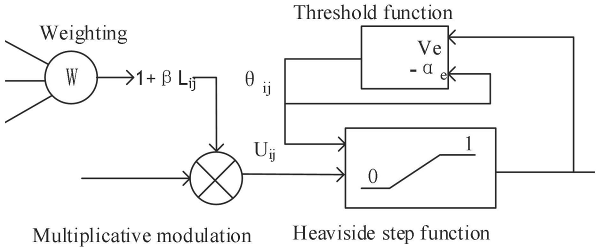


Fig. 2 Simplified model of neurons.

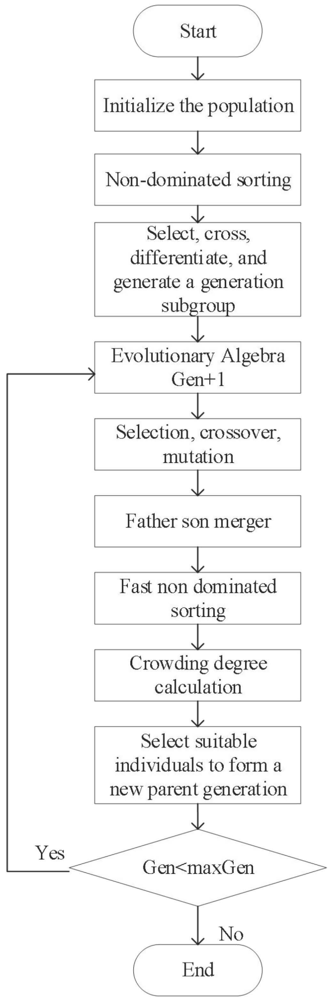


Fig. 3 Algorithm flowchart of NSGA-II.

Firstly, PCNN preprocesses and segments the image, and simulates the behavior of neurons in the biological visual system through feature extraction. Afterwards, utilizing the global coupling characteristics of PCNN, the image is preliminarily segmented by grouping pixels based on their similarity. Based on the segmentation results of PCNN algorithm, initialize the population of NSGA-II. Each member of the population represents a possible segmentation outcome. Subsequently, based on NSGA-II, the optimization process is carried out by first selecting individuals, and then selecting individuals with good performance for crossover and mutation operations through fitness evaluation. Crossover is an attempt to combine segmentation parameters of different individuals by generating new ones to produce better segmentation results. Mutation introduces randomness by making small perturbations to individual segmentation parameters to explore other possibilities and regions in the solution space. Non dominated sorting stratification divides individuals in a population based on non dominated relationships, prioritizing the selection of non dominated individuals who perform the best in the population. Calculate the crowding degree between individuals at the same level, and prioritize selecting individuals with higher crowding degrees to maintain population diversity. Generate a new generation of population through mutation, selection, and crossover, and replace a portion of the old population with it.

Finally, when it reaches the preset number of iterations or its fitness does not significantly improve, stop iterating. Select one or more solutions from the final non dominated sorting front as the final segmentation result. The algorithm results provided by PCNN through these operations serve as the starting point for the optimization algorithm of NSGA-II. By utilizing genetic algorithms to optimize segmentation parameters and ultimately improve the quality of segmentation results, the local learning ability of PCNN is combined with the global NSGA-II function to optimize individual algorithm processes and enhance the performance of segmentation algorithms.

B. Artificial Bee Colony Algorithm

Artificial Bee Colony (ABC) is a new population-based metaheuristic method inspired by the foraging behavior of bees [17-18]. Compared to other algorithms, the ABC algorithm significantly enhances its global search capability and demonstrates its unique advantages through its unique collaboration mechanism and division of labor strategy. At the beginning of the algorithm, a certain number of "bees" are randomly initialized, and these bees will randomly search for the optimal solution in the search space of the problem. Hiring bees to search in localized domains in an attempt to improve the current solution. When exploring new solutions, they not only rely on the information in the current strategy, but also adopt specific methods to create new possibilities based on these. At the same time, these exploration processes are similar to the behavior of bees, which selectively search for more optimized solutions by observing specific solutions discovered by hired bees. If the new solution is superior to the current solution, the observation bee will adopt it and continue to search further from it. When the solution cannot be improved for a long period of time, the relevant bees will transform into scout bees, leave the current search area, and randomly explore new solutions in the search space. During the iteration process, if a better solution is discovered, the algorithm will be updated to the optimal solution. If the quality of the solution does not significantly improve or reaches the set number of iterations, the algorithm will terminate. Fig. 4 is a flowchart of the ABC algorithm. At the beginning of the algorithm, the bee colony is initialized using Eq. (11).

$$\mathrm{x}_{id} = L_d + \mathrm{rand}(0,1)(U_d - L_d) \tag{11}$$

where, X_{id} represents the *d*-th dimensional position of honey source i; U_d and L_d are the upper and lower limits of the search space. These bees will randomly search for the optimal solution in the search space of the problem. Hiring bees to search in localized domains, attempting to improve the current solution, and updating according to Eq. (12).

$$\mathrm{v}_{\mathrm{id}} = \mathrm{x}_{\mathrm{id}} + \varphi(\mathrm{x}_{\mathrm{id}} - \mathrm{x}_{\mathrm{jd}}) \tag{12}$$

where, v_{id} is a new honey source generated by hiring bees to search near honey source i, and φ is a random number between $[1,-1]$, which determines the disturbance amplitude. The greedy strategy is used to choose whether to update x_i. After the update, the hired bees flew back to share the information of the honey source. Based on the honey source information shared by the hired bees, the following bees follow the probability according to Eq. (13).

$$p_i = \frac{fit_i}{\sum_{i=1}^{NP} fit_i} \tag{13}$$

The follower bee usually chooses to hire bees according to the roulette wheel method, that is, generates a random number r between $[0,1]$. If $p_i > r$, the follower bee generates a new honey source around the honey source i in the same way as the hired bee, and uses a greedy strategy to choose whether to keep the original honey source. If the honey source x_i still does not update to a better quality honey source after reaching the threshold of iterations, the honey source x_i will be abandoned, and the corresponding hired bees will transform into reconnaissance bees. The reconnaissance bees will randomly generate a new honey source in the search space to replace x_i.

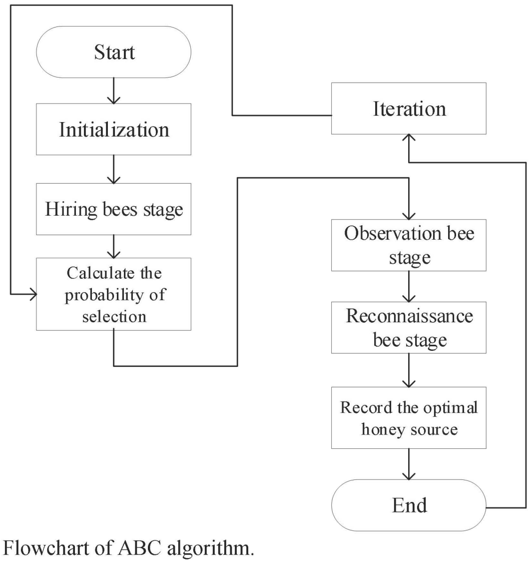


Fig. 4 Flowchart of ABC algorithm.

C. Particle Swarm Optimization Algorithm

Particle Swarm Optimization (PSO) is an optimization algorithm based on swarm intelligence proposed by Eberhart and Kennedy in 1995 [19]. PSO is a population-based stochastic optimization algorithm that is motivated by the intelligent collective behavior of some animals, such as bird flocks or fish schools [20]. Fig. 5 is a flowchart of the PSO algorithm.

The starting point of PSO algorithm is to randomly generate a group of particles in the solution space, where each particle represents an excellent candidate solution for a possible optimization problem. These particles collaborate to explore the solution space during the search process, in order to find the optimal or approximate optimal solution. The characteristics of each particle are characterized by three indicators: its position, velocity, and fitness value. In the iterative process, the fitness function value is first calculated for each particle to quantitatively evaluate the effectiveness of its corresponding image segmentation. Subsequently, based on these fitness values, particles track Gbest (population extremum) and Pbest (individual extremum) in spatial motion to update their position. When updating the position, the particles calculate the fitness value again, compare it with the fitness values of Pbest and Gbest, and then update their position information. This process will continue until the initial set conditions are met and it ends. Particles update their position and velocity through Pbest and Gbest using Eq. (14) and Eq. (15).

$$v_{id}^{k+1} = \omega v_{id}^{k} + c_1 r_1 \left(P_{id}^{k} - X_{id}^{k}\right) + c_2 r_2 \left(P_{gd}^{k} - X_{id}^{k}\right) \tag{14}$$

$$X_{id}^{k+1} = X_{id}^{k} + V_{id}^{k+1} \tag{15}$$

where, V is the velocity, and the current velocity is added to the correction term. c_1 and c_2 are coefficients, and r_1 and r_2 are random numbers. X is the position, and the current position is summed with the velocity.

D. Image Segmentation Algorithm Based on Allostatic Optimization and Gaussians Function

The image segmentation algorithm that combines Allostatic Optimization and Gaussian Functions combines two different algorithms to improve the accuracy and efficiency of segmentation. Allostatic Optimization is a global optimization strategy aimed at finding the optimal solution, while Gaussian Function mixture is commonly used to represent the statistical properties of different regions in an image. The probability density function formula for Gaussian distribution is shown in Eq. (16).

$$f\left(x \mid \mu,\ \sigma^2\right) = \frac{1}{\sqrt{2\sigma^2\pi}} e^{-\frac{(x-\mu)^2}{2\sigma^2}} \tag{16}$$

where, μ represents the mean and σ represents the standard deviation. The mean corresponds to the middle position of the normal distribution.

In image segmentation, Gaussian mixture is commonly used to simulate the grayscale distribution of regions in the image, while Allostatic Optimization algorithm is used to find the optimal solution and parameters in these mixed simulations to achieve more accurate segmentation. These two methods are suitable for processing images with foreground distribution and complex backgrounds. In image segmentation, Gaussian Function mixture models can be used to describe the grayscale distribution of each region in the image. It is a soft clustering method that allows points in an image to belong to multiple clusters, each defined by a Gaussian Function. This method can handle blurry boundaries and overlapping areas in images. The Allostatic Optimization algorithm refers to a global optimization technique applied in the process of image segmentation, which can be used to optimize the parameters of Gaussian Functions or to select the best features and model structures to improve segmentation accuracy. This algorithm first uses Gaussian Function mixture to initialize image segmentation, and then iteratively improves the segmentation results through Allostatic Optimization until a global optimal solution is found or a certain termination condition is reached. This image segmentation algorithm that combines Allostatic Optimization and Gaussian Function mixture may be suitable for medical image analysis, satellite image processing, and other fields that require precise segmentation. Allostatic Optimization may mean that the algorithm considers the overall information of the image rather than local regions during the segmentation process, which helps capture global context and improve segmentation accuracy. Gaussian mixture can be used to model the pixel distribution of each region in an image, which enables the algorithm to handle regions with complex statistical properties. At the same time, it provides a soft segmentation method that allows pixels to belong to multiple categories, which helps to handle fuzzy boundaries and overlapping areas. The algorithm may use iterative methods to continuously optimize parameters to improve segmentation results until convergence. Combining multi-scale analysis to capture features at different resolutions and enhance the algorithm's segmentation ability for objects of different sizes.

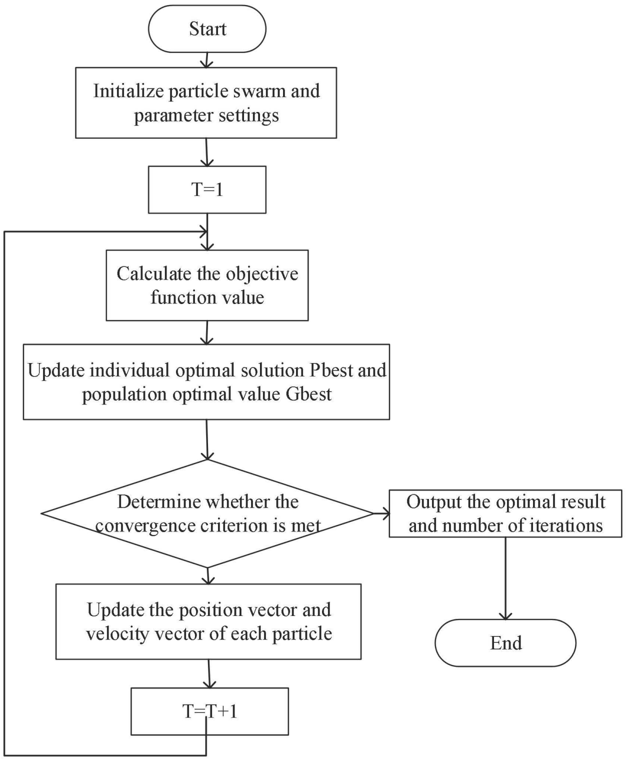


Fig. 5 PSO algorithm flowchart.

The specific steps of the algorithm include initialization, selecting the initial Gaussian component and corresponding parameters. Performing probability calculations may involve reclassification of pixels or merging of regions. The Allostatic Optimization strategy is used to optimize the parameters of the Gaussian Function, which may include updating the mean, variance, and weights. Repeat the iterative process until the final termination condition is met.

E. Image Segmentation Algorithm Based on Differential Evolution and Gaussian Function

The hybrid image segmentation algorithm of Differential Evolution and Gaussian Function combines two different algorithms to improve the accuracy and efficiency of segmentation. Combining Differential Evolution and Gaussian Functions for image segmentation can create a powerful optimization framework, whose basic steps may include first initializing the population, using Differential Evolution algorithm to initialize a population, where each individual represents a potential image segmentation solution. Afterwards, Gaussian blur is applied to the original image, which helps smooth the image, reduce noise, and preserve important structural features. Define a fitness function to evaluate the quality of each individual by designing a fitness function. This function can be based on the accuracy, consistency, or other relevant criteria of image segmentation. Iteratively update the population through the mutation, crossover, and selection steps of Differential Evolution algorithm. The mutation step generates new candidate solutions by randomly selecting individuals from the population and performing linear combinations; The crossover step is used to combine the mutated solution with the current solution to generate new offspring; The selection process is based on the fitness function to select individuals for the next generation. Differential Evolution algorithm is a population-based heuristic optimization algorithm.

The reason why the Differential Evolution algorithm has been widely adopted in optimization problems in engineering and scientific fields is due to its simplicity, efficiency, and ease of implementation. The core mechanism of this algorithm imitates the laws of evolution in nature, covering three basic steps: mutation, crossover, and selection. In the mutation process, the algorithm randomly selects three independent individuals within the population, calculates their differences, and adds them to the fourth individual to create a mutation vector. This process promotes the evolution of the population towards a better solution by simulating the phenomenon of variation in biological evolution. This is a crucial step for algorithms to explore new solution spaces. Combining these two algorithms can create a powerful optimization framework for better application in image segmentation. Differential Evolution process is shown in Fig. 6.

F. Adaptive Thresholding Segmentation Based on Maximizing Inter-class Variance

The adaptive threshold segmentation algorithm based on maximizing inter class variance is one of the image segmentation techniques. Its segmentation principle is based on the assumption that the grayscale range of the threshold t is 0, 1, $\cdots$, $L-1$, and the probability of pixels with grayscale level i appearing is given by Eq. (17).

$$p_i = \frac{n_i}{N}, \sum_{i=1}^{L-1} p_i = 1 \tag{17}$$

Divide the image into two parts: background and foreground, with the following formula.

Partial probability of foreground:

$$w_0(t) = \sum_{t=0}^{t} p_i \tag{18}$$

Average of the prospect section:

$$\mu_0(t) = \sum_{i=0}^{i} \frac{i_{pi}}{w_0} \tag{19}$$

Background probability:

$$w_1(t) = \sum_{i=t+1}^{L-1} p_i \tag{20}$$

Mean value of background section:

$$\mu_1(t) = \sum_{i=t+1}^{L-1} \frac{ip_i}{w_1} \tag{21}$$

Variance between two groups:

$$\mathrm{f}(\mathrm{t}) = \mathrm{w}_0(\mathrm{t})\mathrm{w}_1(\mathrm{t})(\mu_0(\mathrm{t}) - \mu_1(\mathrm{t}))^2 \tag{22}$$

The core idea of this method is to maximize the variance between the foreground and background classes after segmentation, thereby achieving more accurate segmentation. The steps of this algorithm include image preprocessing, typically including grayscale, denoising, and other steps to simplify the problem and improve segmentation quality. Perform histogram analysis and calculate the grayscale histogram of the image. Maximizing inter class variance is to find a suitable threshold that maximizes the variance between the foreground and background classes after segmentation. This usually involves calculating the cumulative distribution function of the histogram and finding the local maximum of the cumulative distribution function.

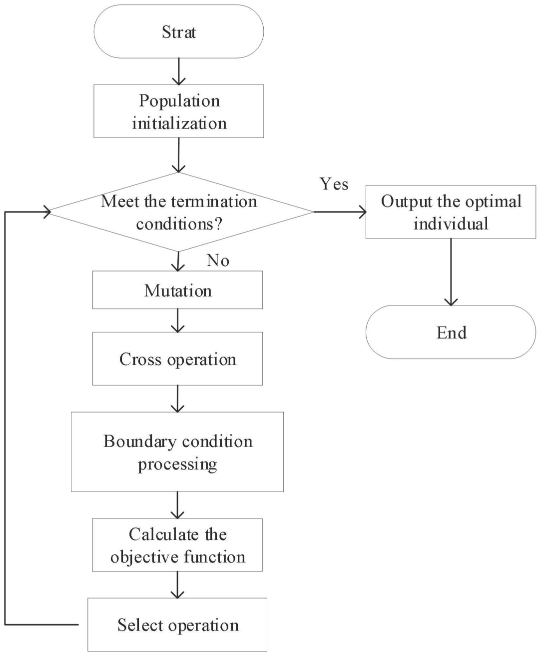


Fig. 6 Flowchart of differential evolution algorithm.

Subsequently, the threshold is determined based on the principle of maximizing inter class variance to determine the segmentation threshold, and finally image segmentation is performed. This algorithm has adaptability, robustness, and is simple and efficient. The algorithm can automatically determine the optimal threshold based on the pixel intensity distribution of the image, and is suitable for different images and scenes. The implementation of adaptive threshold segmentation algorithm based on maximizing inter class variance is relatively simple, with small computational complexity, and suitable for real-time or resource limited application scenarios. And by maximizing the inter class variance, the algorithm can effectively handle noise and lighting changes in the image.

III. SIMULATION EXPERIMENT AND RESULT ANALYSIS

A. Image Segmentation Performance Indicators

In order to provide an objective quantitative evaluation of tumor cell image segmentation algorithms, Accuracy, Sensitivity or Fmeasure, Precision, MCC (Matthews Correlation Coefficient), Dice Coefficient, Jaccard Index and Specificity were introduced as evaluation indicators to assess the segmentation results.

(1) Accuracy. It is a commonly used metric to evaluate the performance of segmentation algorithms, which measures the proportion of correctly predicted samples by the model to the total number of samples. In multiclass and binary classification problems, accuracy is often used to provide an overall perspective to observe the predictive ability of the model. The formula for calculating accuracy is:

$$Accuracy=\frac{TP+TN}{TP+TN+FP+FN} \tag{23}$$

where, TP (True Positive) is the true number of instances, which refers to the number of samples that can be predicted as positive categories in the model. TN (True Negatives) is the number of true negative cases, which refers to the number of samples that can be predicted as negative categories in the model. FP (False Positive) is the number of false positives, which refers to the number of samples in the model that are incorrectly predicted as positive categories. FN (False negatives) refers to the number of false negatives, which is the number of samples in the model that were incorrectly predicted as negative categories.

(2) Sensitivity. It is an important indicator used to evaluate the performance of classification models, especially in binary classification problems. Its formula is:

$$Sensitivity=\frac{TP}{TP+FN} \tag{24}$$

(3) Fmeasure. It is an indicator used to evaluate the performance of binary classification problem models, especially when precision and recall are equally important. Fmeasure is the harmonic mean of precision and recall, which strikes a balance between the two. Its formula is:

$$F_1=2\times\frac{Precision\times Recall}{Precision+Recall} \tag{25}$$

(4) Precision. also known as the correct prediction value, it is a key indicator used to evaluate the performance of classification models. Especially for handling binary classification problems. The measurement of accuracy is the proportion of positive categories that are actually positive categories in the model prediction. Its formula is as follows:

$$Precision=\frac{TP}{TP+FP} \tag{26}$$

(5) MCC (Matthews Correlation Coefficient). It is an indicator used to evaluate the performance of classification models in binary classification problems. Its formula is as follows:

$$MCC=\frac{TP\times TN-FP\times FN}{\sqrt{(TP+FP)\times(TP+FN)\times(TN+FP)\times(TN+FN)}} \tag{27}$$

(6) Dice Coefficient. It is a measure used to evaluate the quality of cell segmentation, especially in medical image processing. It is based on the set theory of samples, considering the true examples and the total number of both to measure the accuracy of segmentation. Its formula is as follows:

$$Dice=\frac{2\times TP}{2\times TP+FP+FN} \tag{28}$$

(7) Jaccard Index. In image segmentation, it is used to measure the similarity between real markers and segmentation results.

(8) Specificity. It is an important indicator used to evaluate the performance of classification models, especially in binary classification problems. Specificity measures the proportion of samples correctly predicted as negative categories by the model to all actual negative category samples. Its formula is as follows:

$$Specificity=\frac{TN}{TN+FP} \tag{29}$$

B. Image Segmentation and Objective Evaluation

Test 1: For the segmentation effect of tumor cell images

Select cell images stored in. tif file format with a size of for testing and research. The specific images are shown in Fig. 7, and three cell images (a), (b) and (c) are selected. Six image segmentation algorithms were used to compare the segmentation of cell (a) in Fig. 7, and the results are shown in Fig. 8. Table I analyzes the evaluation indicators of the segmented image and the real image. Similarly, six image segmentation algorithms were used to compare the segmentation of cell (b) in Fig. 7. The results are shown in Fig. 9, and Table II analyzes the evaluation indicators between the segmented images and the real image. Six image segmentation algorithms were used to compare the segmentation of cell (c) in Fig. 7. The results are shown in Fig. 10, and Table III analyzes the evaluation indicators of the segmented image and the real image.

Test 2: Segmentation effect on human osteosarcoma cell images

Select cell images stored in. jpg file format with a size of 696×520 for testing and research. The specific images are shown in Fig. 11, and three cell images (a), (b) and (c) are selected. Six image segmentation algorithms were used to compare the segmentation of cell (a) in Fig. 11, and the results are shown in Fig. 12. Table IV analyzes the evaluation indicators of the segmented image and the real image. Six image segmentation algorithms were used to compare the segmentation of cell (b) in Fig. 11. The results are shown in Fig. 13, and Table V analyzes the evaluation indicators between the segmented images and the real image. Six image segmentation algorithms were used to compare the segmentation of cell (c) in Fig. 11. The results are shown in Fig. 14, and Table VI analyzes the evaluation indicators between the segmented images and the real image.

For the analysis of image segmentation performance indicators, Particle Swarm Optimization algorithms have a high classification accuracy in the accuracy evaluation indicators, and most of them are correctly classified. The adaptive threshold segmentation algorithm based on maximizing inter class variation can effectively identify the majority of correct results in sensitivity or true positive rate performance indicators. Fmeasure is the harmonic mean of accuracy and recall, used to evaluate the performance of binary classification models. In the analysis of this performance indicator, Particle Swarm Optimization algorithms have relatively accurate results. Similarly, Particle Swarm Optimization algorithms has achieved high segmentation accuracy in MCC, Dice Coefficient, and Jaccard Index. In the analysis of Accuracy, Image Segmentation Algorithm Based on Differential Evolution and Gaussian Function has the highest accuracy.Overall, when selecting algorithms for medical tumor cell segmentation, the performance of the algorithm should be balanced according to the needs of the actual application scenario for specific applications.

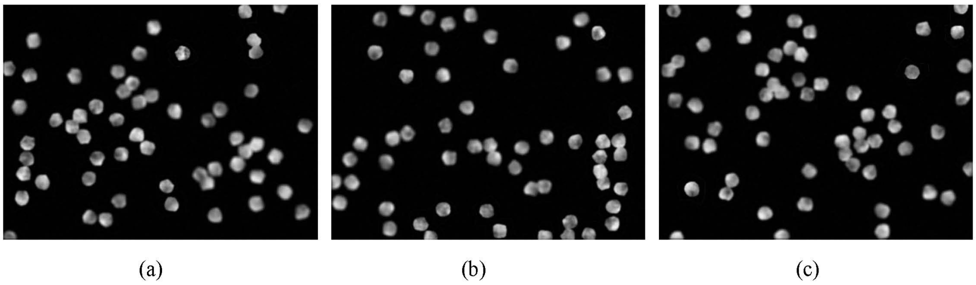
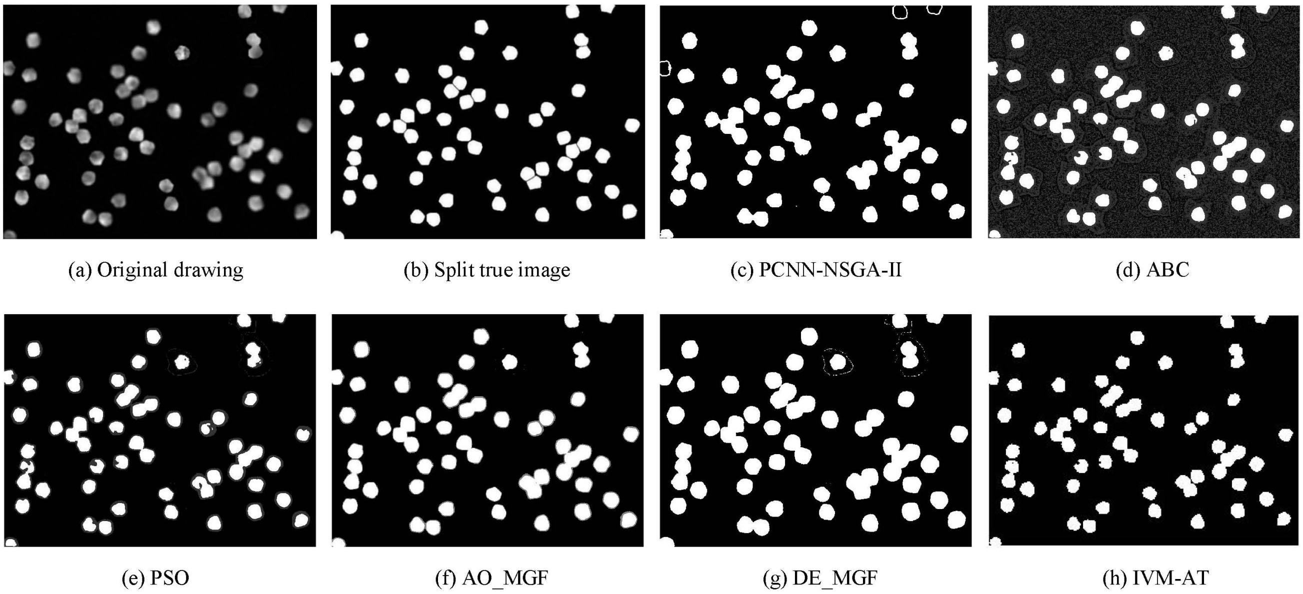

(a) (b) (c)

Fig. 7 Tumor cell image.

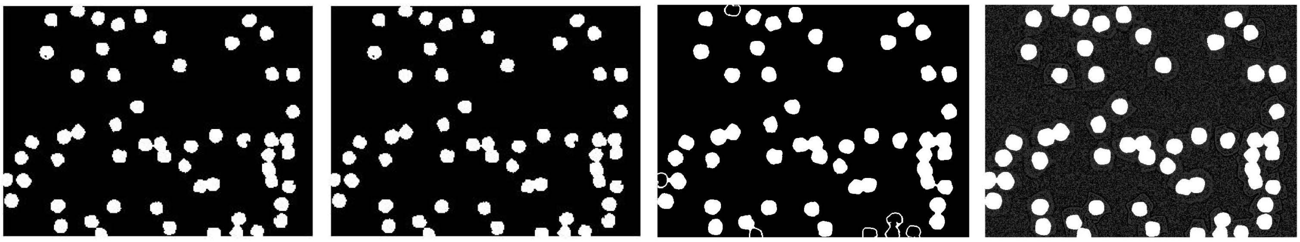

(a) Original drawing (b) Split true image (c) PCNN-NSGA-II (d) ABC

(e) PSO (f) AO_MGF (g) DE_MGF (h) IVM-AT

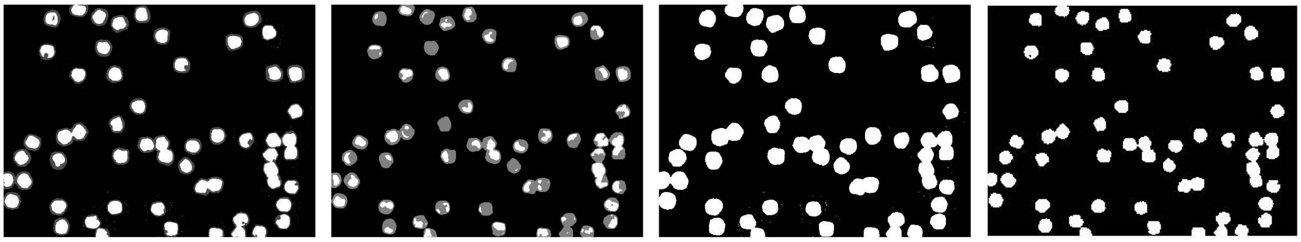
Fig. 8 Different algorithms for cell segmentation.

TABLE I. PERFORMANCE INDICATORS OF DIFFERENT ALGORITHMS

	ACC	SEN	F1	PREC	MCC	DICE	JI	SPEC
PCNN-NSGA-II	0.9451	0.9107	0.8279	0.7589	0.8003	0.8279	0.7064	0.9510
ABC	0.5284	0.9689	0.4167	0.2654	0.3184	0.4167	0.2632	0.4356
PSO	0.9476	0.8424	0.8509	0.8596	0.8192	0.8509	0.7405	0.9703
AO_MGF	0.9247	0.7259	0.8080	0.9108	0.7694	0.8080	0.6778	0.9801
DE_MGF	0.9247	0.7259	0.8080	0.9109	0.7695	0.8080	0.6778	0.9802
IVM-AT	0.9417	0.9839	0.8011	0.6756	0.7869	0.8011	0.6682	0.9359



(a) Original drawing (b) Split true image (c) PCNN-NSGA-II (d) ABC

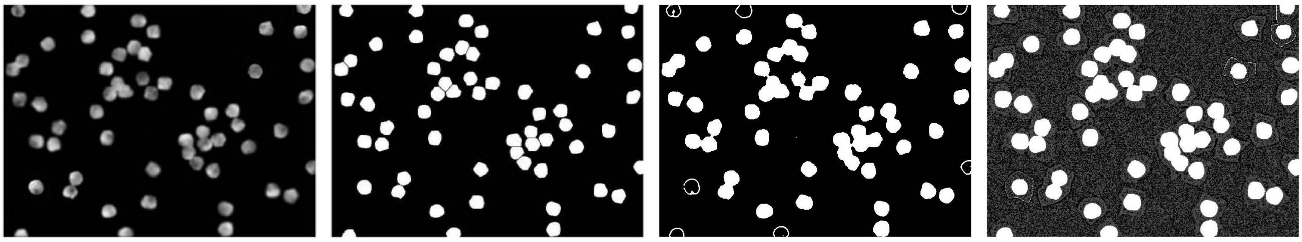


(e) PSO (f) AO_MGF (g) DE_MGF (h) IVM-AT

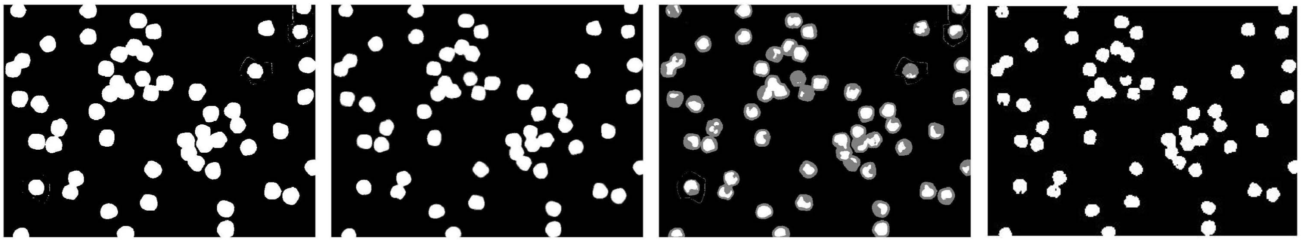
Fig. 9 Different algorithms for cell segmentation.

TABLE II. PERFORMANCE INDICATORS OF DIFFERENT ALGORITHMS

	ACC	SEN	F1	PREC	MCC	DICE	JI	SPEC
PCNN-NSGA-II	0.9404	0.9109	0.8073	0.7249	0.7797	0.8073	0.6769	0.9451
ABC	0.5300	0.9668	0.4146	0.2639	0.3175	0.4146	0.2615	0.4392
PSO	0.9490	0.8481	0.8525	0.8569	0.8216	0.8525	0.7429	0.9702
AO_MGF	0.7018	0.2110	0.2358	0.2674	0.0543	0.2358	0.1337	0.8387
DE_MGF	0.9280	0.7345	0.8136	0.9117	0.7766	0.8136	0.6858	0.9807
IVM-AT	0.9427	0.9852	0.8029	0.6775	0.7892	0.8029	0.6707	0.9370



(a) Original drawing (b) Split true image (c) PCNN-NSGA-II (d) ABC

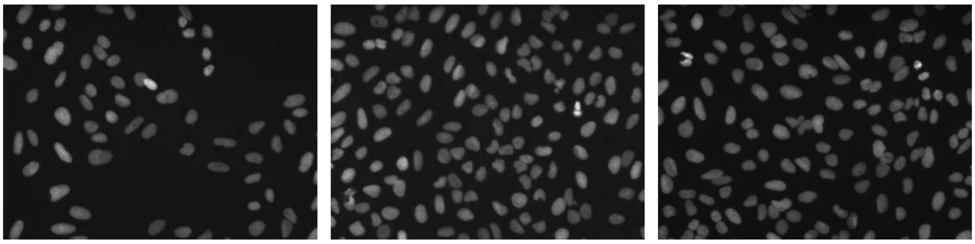


(e) PSO (f) AO_MGF (g) DE_MGF (h) IVM-AT

Fig. 10 Different algorithms for cell segmentation.

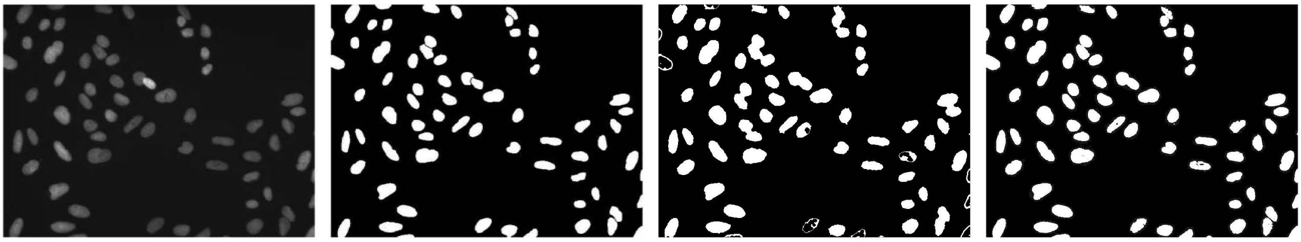
TABLE III. PERFORMANCE INDICATORS OF DIFFERENT ALGORITHMS

	ACC	SEN	F1	PREC	MCC	DICE	JI	SPEC
PCNN-NSGA-II	0.9411	0.9079	0.8078	0.7276	0.7801	0.8078	0.6776	0.9463
ABC	0.5292	0.9683	0.4118	0.2615	0.3172	0.4118	0.2593	0.4391
PSO	0.9509	0.8676	0.8534	0.8396	0.8240	0.8534	0.7442	0.9673
AO_MGF	0.7057	0.2156	0.2423	0.2764	0.0639	0.2423	0.1378	0.8425
DE_MGF	0.9256	0.7220	0.8071	0.9151	0.7700	0.8071	0.6766	0.9816
IVM-AT	0.9437	0.9857	0.8042	0.6791	0.7909	0.8042	0.6725	0.9381

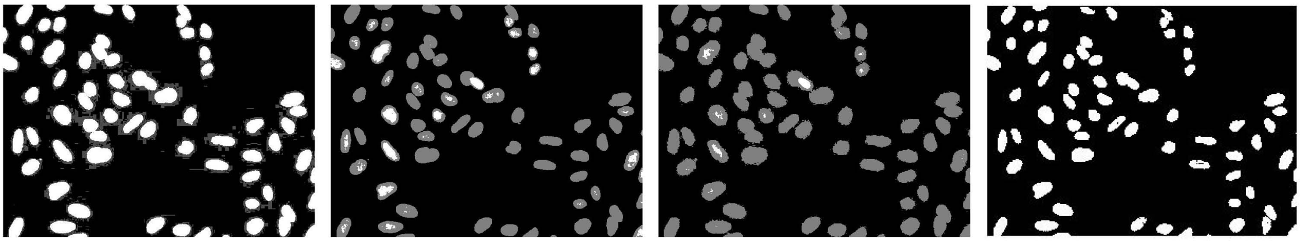


(a) (b) (c)

Fig. 11 Image of human osteosarcoma cells.



(a) Original drawing (b) Split true image (c) PCNN-NSGA-II (d) ABC

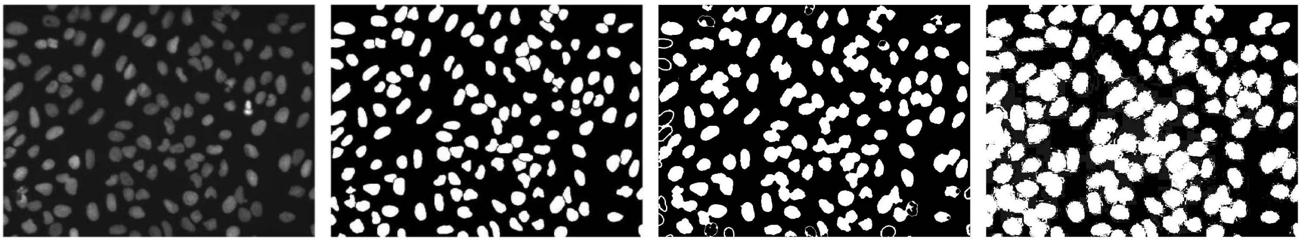


(e) PSO (f) AO_MGF (g) DE_MGF (h) IVM-AT

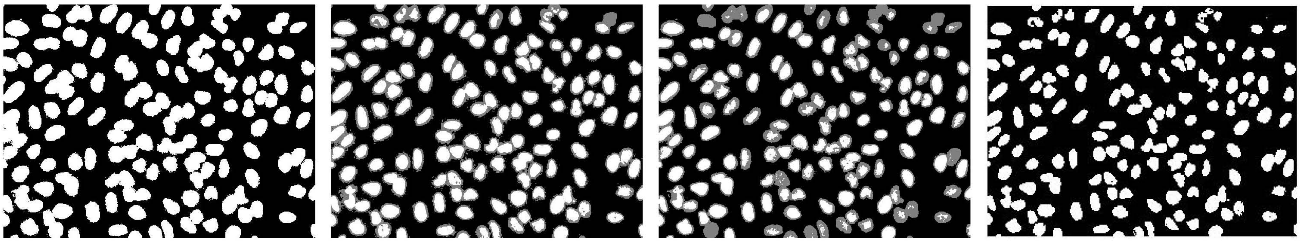
Fig. 12 Different algorithms for cell segmentation.

TABLE IV. PERFORMANCE INDICATORS OF DIFFERENT ALGORITHMS

	ACC	SEN	F1	PREC	MCC	DICE	JI	SPEC
PCNN-NSGA-II	0.9321	0.9171	0.7763	0.6730	0.7496	0.7763	0.6344	0.9343
ABC	0.9319	0.8762	0.8185	0.7679	0.7794	0.8185	0.6928	0.9438
PSO	0.8908	0.6266	0.7494	0.9322	0.7050	0.7494	0.5993	0.9839
AO_MGF	0.6884	0.1874	0.2079	0.2334	0.0170	0.2079	0.1160	0.8282
DE_MGF	0.9162	0.7024	0.7909	0.9049	0.7488	0.7909	0.6541	0.9784
IVM-AT	0.9374	0.9547	0.7908	0.6749	0.7710	0.7908	0.6540	0.9350



(a) Original drawing (b) Split true image (c) PCNN-NSGA-II (d) ABC

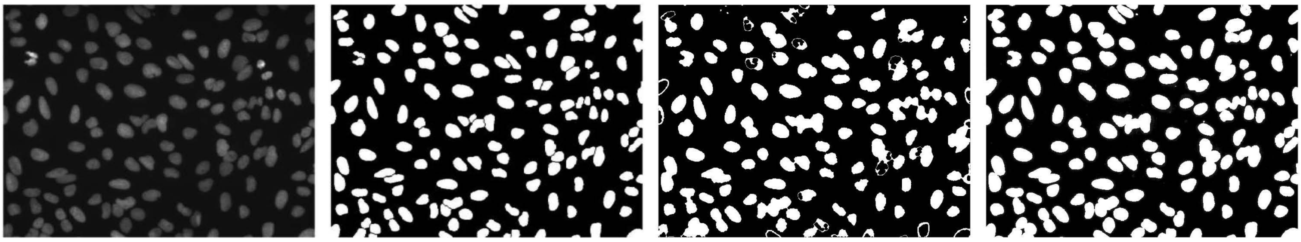


(e) PSO (f) AO_MGF (g) DE_MGF (h) IVM-AT

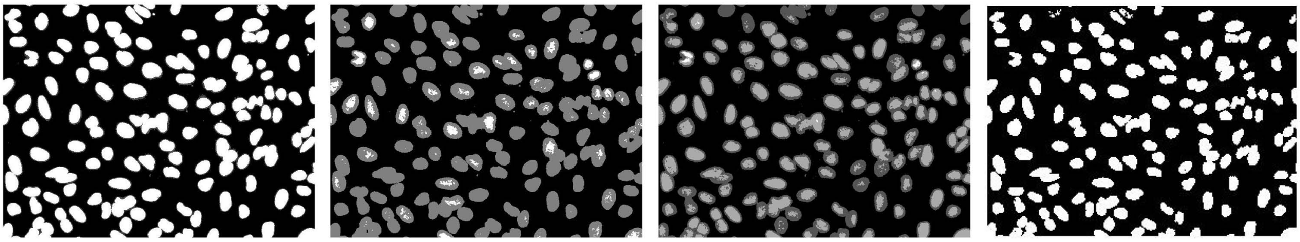
Fig. 13 Different algorithms for cell segmentation.

TABLE V. PERFORMANCE INDICATORS OF DIFFERENT ALGORITHMS

	ACC	SEN	F1	PREC	MCC	DICE	JI	SPEC
PCNN-NSGA-II	0.8363	0.9281	0.7530	0.6334	0.6630	0.7530	0.6038	0.8026
ABC	0.7240	0.9362	0.7276	0.5950	0.5256	0.7276	0.5718	0.5861
PSO	0.8613	0.8543	0.8160	0.7810	0.7069	0.8160	0.6892	0.865
AO_MGF	0.5533	0.3788	0.2701	0.2098	-0.0162	0.2700	0.1561	0.6020
DE_MGF	0.8445	0.7790	0.8107	0.8450	0.6808	0.8107	0.6816	0.8935
IVM-AT	0.8354	0.9743	0.7409	0.5977	0.6706	0.7409	0.5884	0.7911



(a) Original drawing (b) Split true image (c) PCNN-NSGA-II (d) ABC



(e) PSO (f) AO_MGF (g) DE_MGF (h) IVM-AT

Fig. 14 Different algorithms for cell segmentation.

TABLE VI. PERFORMANCE INDICATORS OF DIFFERENT ALGORITHMS

	ACC	SEN	F1	PREC	MCC	DICE	JI	SPEC
PCNN-NSGA-II	0.8942	0.9222	0.7931	0.6957	0.7369	0.7931	0.6572	0.8864
ABC	0.8747	0.9386	0.8136	0.7181	0.7365	0.8136	0.6858	0.8485
PSO	0.8992	0.7838	0.8392	0.9031	0.7705	0.8392	0.7231	0.9575
AO_MGF	0.6032	0.2584	0.2213	0.1935	-0.0383	0.2213	0.1244	0.6994
DE_MGF	0.8466	0.6658	0.7831	0.9506	0.6954	0.7831	0.6435	0.9754
IVM-AT	0.9160	0.9490	0.8392	0.7521	0.7931	0.8392	0.7229	0.9061

IV CONCLUSION

This article uses six image segmentation algorithms to segment two different tumor cells. The segmented image results are observed and performance indicators are compared and analyzed. The six algorithms share common characteristics, such as good segmentation results when processing independent and complete cells, accurate segmentation of individual cell contours, and accurate recognition of complete cells. When processing cells at image boundaries, image segmentation algorithms based on PCNN and NSGA-II can segment the contours of cells, but cannot recognize all cells as a whole. For overlapping cells in an image, the boundary and contour of the cells cannot be accurately segmented at the junction of two cells. Artificial Bee Colony algorithm, Particle Swarm Optimization algorithm, image segmentation algorithm based on Allostatic Optimization and Gaussians Functions, image segmentation algorithm based on Differential Evolution and Gaussian Function, Adaptive Thresholding Segmentation Based on Maximizing Inter-class Variance has the same problem, as it can recognize the overall outline of overlapping and connected cells, but the boundaries of internal connections cannot be accurately identified. The Artificial Bee Colony algorithm and Particle Swarm Optimization algorithm have blurred edge segmentation in some tumor image segmentation.

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