# Research on Brain Image Segmentation Based on FCM Algorithm Optimization

Xinlei Chen(✉), Dongming Zhao, Wei Zhong, and Jiufeng Ye

Suzhou Guangji Hospital, Suzhou 215000, Jiangsu, China

**Abstract.** Brain disease is becoming a threat to human health. Many countries begin to pay attention to the research of brain science. If brain diseases are predicted in advance, diagnosed accurately and treated with comprehensive intervention, the life expectancy of patients will be greatly improved. There are many explorations and applications in the field of computer-aided disease diagnosis, which can significantly improve the efficiency of disease diagnosis. Medical image processing is one of the medical imaging technology. It can help doctors improve the diagnosis quality by processing and analyzing the medical image data by computer. An improved FCM clustering method Sagakfcm algorithm is proposed for brain tissue segmentation in MRI images. Sagakfcm model fully combines the advantages of simulated annealing algorithm and genetic algorithm, so as to obtain the best initial clustering center, reduce the iteration times of fuzzy c-means algorithm, avoid the initial clustering falling into local optimum, and accelerate the operation speed. The algorithm combines Gaussian kernel function to improve the robustness of FCM algorithm.

**Keywords:** Brain disease · Image segmentation · Image processing

## 1 Introduction

As the pace of social life has increased significantly, the pressure on all aspects has increased sharply, and the eutrophication of people's diet has also brought a great burden to the body. The subsequent brain diseases often cause disability and death. With an increasing trend every year, brain diseases have increasingly become a threat to human health, and many countries have begun to pay attention to brain science research. According to incomplete statistics, about 20% of the world's total population is suffering from chronic mental illness. Some common brain diseases in our lives, such as Alzheimer disease (AD) and Parkinson's Diseases, autism, depression, etc. belong to this category of diseases. Brain diseases are more threatening to people's lives than other diseases [1]. According to a research report from a foreign disease prevention and control center, if people's brain diseases are predicted in advance, early and accurate diagnosis, and comprehensive intervention and treatment, then the life expectancy of the patient will be greatly improved. With the development of medical imaging technology in recent years, with the help of accurate deep analysis and induction of brain tissue images, results with


W. Fu et al. (Eds.): ICMTEL 2021, LNICST 388, pp. 278–289, 2021.
https://doi.org/10.1007/978-3-030-82565-2_23

imaging characteristics that are closely related to brain diseases can be found, which is of great significance for the prevention and treatment of brain diseases [2, 3].

Due to the unique and complex brain of human beings, human beings have become the spirit of all things. The human brain has evolved and developed about 5 million years ago, and the maturity of the human brain has gone through millions of years. The brain is connected by tens of billions of neurons, and there are about trillions of synaptic connections between neurons, forming a complex information processing network system. Each neuron contains millions of proteins that perform different functions, so that the brain provides the most important advanced brain functions for humans. With the advancement and development of science and technology, people are gradually aware of the role of the brain, and more and more attention has been paid to human exploration of the mystery of the brain [4]. The study of the brain has become the most esoteric subject in science and the most difficult scientific fortress to overcome. One of the ultimate goals of the research of the Brain Project is to predict brain diseases in advance, which is a major challenge in the health field facing all mankind. The latest statistics show that there are nearly one billion patients with brain diseases in the world, and the annual economic burden caused by this item is about one trillion US dollars. In my country, due to the continuous deterioration of the environment, the aging of the population, the increasingly accelerated social rhythm and the intensified social competition, brain developmental health, mental illness, and neurodegenerative diseases affect the health of people of all ages in our country.

Computer-aided Diagnosis (CAD) is a product of the combination of medical diagnosis and artificial intelligence (AI). There are many explorations and applications in the field of computer-aided disease diagnosis, which can significantly improve the diagnosis of diseases [5]. effectiveness. With the development of modern medicine, a large number of different types of information are often generated during patient visits, including symptoms, signs, laboratory examination results, physical diagnosis results, etc. How to accurately and fully utilize this information has become a problem that must be addressed in clinical work. The computer-aided diagnosis system has opened up an effective way to make full use of various clinical information related to diagnosis [6].

At present, the auxiliary diagnosis of brain diseases is mainly performed by clinicians by observing brain images to perform feature extraction and judgment based on experience. Doctors need to view a large number of pictures for analysis. This not only greatly increases the workload of clinicians, but also because of doctors' experience and technical level. Different, it is easy to cause missed diagnosis or misdiagnosis. With the aid of modern medical imaging technology for auxiliary diagnosis, it has a positive effect on the prevention and treatment of brain diseases.

In order to better recognize images of patients with brain diseases, first use segmentation algorithms on brain tissue images to segment the parts that need to be observed, and then extract appropriate features for areas with research needs and lesion features, and finally extract the features Information induction and identification. Accurate segmentation, proper selection of features and classifiers can improve recognition accuracy, which is of great significance to patients and doctors.

## 2 Research Status

Since the brain science plan was put forward in the 1990s, with the advancement of diagnostic technology and molecular biology technology, mankind has had a breakthrough understanding of this complex and mysterious organ of the brain. At present, many research units at home and abroad focus on intelligent diagnosis of brain imaging. For example, overseas Harvard Medical School, Stanford University, University of Washington, Northwestern University Molecular Imaging Center, Duke University, Massachusetts General Hospital, etc., as well as medical imaging of Chinese Academy of Sciences, Tsinghua University, Huazhong University of Science and Technology, Nanjing University, Southeast University and other units in China The laboratories have achieved certain results [7, 8].

Xiong Zhiqi, a brain scientist at the Chinese Academy of Sciences, proposed that early diagnosis and early intervention of brain diseases are the key means to treat brain diseases. He Yongqi thought about multi-modal neuroimaging technology and brain connectionomics methods to explore the altered patterns of brain structure and functional connection in the dementia stage and dementia stage of Alzheimer's disease. Li Haijiao and others use multi-modal magnetic resonance imaging for joint exercises to provide information on brain tissue anatomy, function, and metabolism [9].

Based on the clinical data of 128 patients with cerebral infarction admitted from March 2009 to February 2011, Huang Yuanbing screened and classified OCSP based on their clinical signs and main symptoms. Zhang Daoqiang and others proposed to use a multi-modal correlation vector regression machine to predict the value of clinical variables through the learning of multi-modal features [10]. Fei et al. adopted a brain-connected network classification method based on discriminative subgraph mining. Ke Shanhong and others applied FCM (Fuzzy means clustering) algorithm and its kernel method version KFCM (Kernel-basedFCM) to segmentation of MR images [11–15]. Maitra et al. used the improved orthogonal wavelet transform Slantlet transform and proposed a new image feature extraction algorithm based on the wavelet transform. E1-Dahshan et al. adopted a three-step joint algorithm and introduced an artificial neural network (Artificial-Neural Network, ANN). Chaplot et al. used the Daubechies-4 wavelet transform to extract the approximate coefficients and detail coefficients of the image, and input the features obtained from the wavelet transform into the Self-Organizing Map (SOM) [16, 17]. The experimental data showed that the result of the SOM clusterer could reach 94%. However, the disadvantage is that after image feature extraction, there is a lack of information screening, which leads to a feature dimension of 4761, a sharp increase in calculation load, and a reduction in calculation performance. For MRI images, Wu proposed to use a forward neural network as a classifier [18–20].

## 3 Introduction to the Image Processing Process

Medical image processing is one of the medical imaging technologies. It uses computers to process and analyze medical image data to help doctors improve the quality of diagnosis.

For medical imaging of the brain, only from the superficial perspective, only the external planar imaging of the brain tissue can be seen. The detailed information inside the tissue is difficult to find through direct observation with the naked eye. At this time, it is necessary to perform brain imaging. The series of processing and analysis, and the general steps related to it are as follows see Fig. 1.

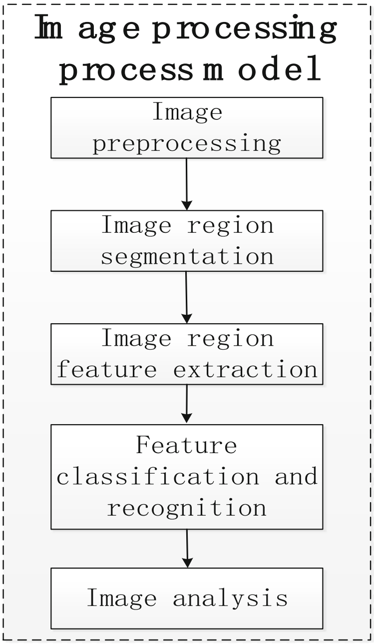


**Fig. 1.** Image processing flowchart

(1) Image preprocessing;
(2) Segmentation of the region of interest in the image;
(3) Perform feature extraction on the acquired region;
(4) Input the features into the relevant classifier to complete the classification and recognition of the target area;
(5) Analyze the image according to the results; in the brain image analysis process, the image is preprocessed to reduce the interference of the offset field on the segmentation. In the process of medical image processing, segmentation is a step that cannot be ignored. It is the premise of other image processing. Segmentation is actually to separate the target area in the image from the background area according to the needs of the user. The feature extraction process is the process of extracting information from other features such as color feature, shape feature or texture of the segmented region of interest. The process of image recognition is to take the extracted data information as input, and then divide the data with the same characteristics into the same category, so as to achieve the purpose of image recognition.

# 4 Key Technologies for Segmentation

## 4.1 Principle of FCM Algorithm

The FCM algorithm is obtained by Bezdek improving the Hard C-Means (HCM) clustering method proposed by Dunn in 1973. The FCM clustering algorithm divides the feature points in the feature space $X = \{x_1, x_2, \ldots, x_n\}$ into c categories ($2 \leq c \leq n$), the cluster center of each category is $\mathbf{v}_i \in R$, and the cluster center matrix is $V = \{v_1, v_2, \ldots, x_c\}$, the membership of the i-th category of any feature point $c_i \in R$ is $V = \{v_1, v_2, \ldots, x_c\}$, $U$ is its fuzzy membership matrix. After normalizing it, the sum of the membership degrees of the data set is equal to 1, $u_{ij}$ introduces Between [0,1], that is, $u_{ij}$ satisfies the following conditions:

$$\sum_{i=1}^{c} u_{ij} = 1, \ \forall j = 1, \ldots, n \tag{4-1}$$

The generalized form of the objective function of FCM:

$$J_{FCM} = \sum_{i=1}^{c} \sum_{j=1}^{n} u_{ij}^{m} d_{ij}^{2} \tag{4-2}$$

In formula (4-2), $d_{ij} = \left\| x_j - v_i \right\|$ is the distance between the $i$ cluster center and the $j$ th data point For the Euclidean distance, $m$ is the fuzzy index. When $m \in [1, \infty)$, $m = 1$, it means hard C-means clustering. With the increase of $m$, the result is more fuzzy, Usually $m = 2$ is used in the experiment. The objective function can be expressed as the sum of the squares of the weighted distances from all sample points in the data set to each cluster center. The best classification result is that the sample points are divided into the class with the smallest difference from it, so the clustering goal of the FCM algorithm is to find the minimum value of the cost function $J_{FCM}$. That is to find the optimal clustering center and the optimal membership matrix to minimize the cost function $J_{FCM}$. Under the constraints of Eq. (4-1), the minimum value of Eq. (4-2) is solved and solved by Lagrange multiplier method. Construct a new objective function:

$$\overline{J}_{FCM} = J_{FCM} + \lambda\left(1 - \sum_{j=1}^{c} u_{ij}\right) = \sum_{i=1}^{c} \sum_{j=1}^{n} u_{ij}^{m} d_{ij}^{2} + \lambda 1 - \left(\sum_{j=1}^{c} u_{ij}\right) \tag{4-3}$$

(1) The degree of membership is solved. According to formula (4-3), the objective function $\overline{J}_{FCM}$ is derived from the degree of membership $u_{ij}$ to obtain 0:

$$\frac{\partial \overline{J}}{\partial u_{ki}} = \sum_{i=1}^{c} \sum_{j=1}^{n} m u_{ij}^{m-1} d_{ij}^{2} - \lambda = 0 \tag{4-4}$$

From the above formula:

$$\mathbf{u}_{ij} = \left(\frac{\lambda}{m d_{ij}^{2}}\right)^{\frac{1}{m-1}} \tag{4-5}$$

Because of $\sum_{k=1}^{c} u_{kj} = 1,\ \forall j = 1, \ldots, n$, there is

$$\sum_{k=1}^{c} \left( \frac{\lambda}{md_{ij}^2} \right)^{\frac{1}{m-1}} = 1 \tag{4-6}$$

From the above formula:

$$\lambda^{\frac{1}{m-1}} = \frac{1}{\sum_{i=1}^{c} \left( \frac{1}{md_{kg}^2} \right)^{\left(\frac{1}{m-1}\right)}} \tag{4-7}$$

Incorporate formula (4-7) into formula (4-5) to obtain the degree of membership:

$$u_{ij} = \frac{\frac{1}{\sum_{k=1}^{c} \left( \frac{1}{md_{kj}^2} \right)^{\left(\frac{1}{m-1}\right)}}}{(md_{ij}^2)^{\frac{1}{m-1}}} = \left[ \sum_{k=1}^{c} \left( \frac{d_{ij}^2}{d_{kj}^2} \right)^{\frac{1}{m-1}} \right]^{-1} \tag{4-8}$$

(2) Find the clustering center $v_i$, according to formula (4-3), the objective function $\overline{J}_{FCM}$ to the clustering center $v_i$, find the partial derivative 0:

$$v_i = \frac{\sum_{j=1}^{n} u_{ij}^m x_j}{\sum_{j=1}^{n} u_{ij}^m} \tag{4-9}$$

Although the traditional FCM algorithm has good stability, the segmentation effect is poor. The algorithm in this paper has obvious advantages in both stability and segmentation effect, which is about 0.02 higher than other algorithms, which can affect the subsequent recognition effect.

## 4.2 Based on KFCM Simulated Annealing Genetic Algorithm

The traditional FCM algorithm ignores the spatial information of neighboring pixels when segmenting an image, and is susceptible to noise interference during segmentation, making the segmentation result unsatisfactory. WU and Yang proposed an improved FCM algorithm, in which the kernel function is used for distance measurement for the first time. Compared with the traditional Euclidean measure, the robustness of the algorithm is enhanced.

Simulated Annealing Genetic Algorithm: Based on the simulation statistics of the annealing process of high-temperature objects in physics, the Simulated Annealing Algorithm (SA) is finally derived. Because this algorithm is very similar to the process of solving random problems, it is widely used Solve the global optimal solution and achieved good results. In addition to accepting the global optimal solution, the simulated annealing algorithm (SA) uses the Metropolis criterion to accept the non-local optimal solution to a limited extent, and repeats the Metropolis process, so that the probability of acceptance is gradually oriented to 0, so as to ensure that it will not fall into the local optimal solution. The algorithm finally converges to all the optimal solutions with probability 1, but because the search process of the algorithm is random, sometimes the algorithm cannot search the whole world, and it may also jump out of the optimal solution. Genetic algorithm is easy to fall into the problem of local optimization when searching for local optimization, but its ability to search for the whole world is relatively strong. If the two algorithms are combined to complement each other, the algorithm can be more effective and converge to the global optimal solution. Genetic simulated annealing algorithm is an improved algorithm that combines the advantages of traditional genetic algorithm (GA) and simulated annealing algorithm. In principle, this algorithm has many similarities with traditional genetic algorithm. Like the traditional genetic algorithm, the implementation process of the simulated annealing genetic algorithm is to first initialize the population and individuals, calculate the fitness value of the individual according to the fitness function, and then perform operations such as selection, crossover, and mutation to generate new individuals, and then be independent Perform the operation of the simulated annealing algorithm on a single individual among them, and then evaluate the fitness of the simulated annealing to generate new individuals, and iterate this process repeatedly until the end conditions are met, and the output is confirmed as the current optimal individual. Simulated annealing genetic algorithm has the advantages of genetic algorithm and simulated annealing algorithm, so the algorithm model effectively avoids the premature problem of traditional genetic algorithm in the optimization process. In this paper, the simulated annealing genetic algorithm is used for cluster analysis, and the initial clustering center is optimized by the simulated annealing genetic algorithm. According to different situations, the coding method and fitness function suitable for the situation are designed and used to solve the corresponding fitness. Value, so that the global optimal solution can be solved efficiently and quickly.

## 4.3 KFCM Segmentation Based on Simulated Annealing Genetic Algorithm

### 4.3.1 Chromosome Coding and Population Initialization

Due to the uncertainty of the initial cluster centers in the clustering process, the simulated annealing genetic algorithm used in this paper is required to initialize the initial cluster centers. There are many ways to encode chromosomes in genetic algorithms. Choosing an appropriate encoding method will affect the subsequent calculation methods of genetic operators such as crossover, mutation, and fitness, and ultimately affect the evolution speed and results of the entire genetic operator, so choose the appropriate one. Genetic operators are very important. Commonly used genetic operators include binary encoding methods, symbol encoding, real number encoding, etc. Binary encoding is simple to operate, but has poor local search capabilities, it is difficult to achieve the optimal goal, and it takes a long time; symbol encoding is different from general Using numbers for encoding, using letters instead of numbers for chromosome encoding, requires higher design requirements for subsequent operators; real number encoding is encoding in the form of real number solution space, and there is no limit to the length range of chromosomes, and each gene corresponds to A number, the advantage is that the search space is large, it is easy to search for the optimal solution, and it does not need to be decoded frequently. This article will choose the real number encoding method for encoding. For $n$ data samples, the dimension is $d$, and each chromosome $V_i = \{v_1, v_2, \ldots, v_c\}$, If there are c cluster centers, it can be expressed as the length $l = c \times d$. A chromosome can look like this:

$$V_i = \left\{ \underbrace{a_{11}a_{12}\ldots a_{1d}}_{v_1} \underbrace{a_{31}a_{22}\ldots a_{2d}}_{v_2} \cdots \underbrace{a_{c1}a_{c2}\ldots a_{cd}}_{c_c} \right\} \tag{4-10}$$

For the gene values of all individuals in the initial population, in actual operation, they are represented by randomly generated numbers, and these numbers are required to conform to a uniform distribution.

### 4.3.2 Calculation of Fitness

The performance of genetic algorithm depends on the selection of fitness function to a certain extent. According to the fitness value determined by the fitness function, it will directly affect the adaptability of the population to the environment. It is precisely because of it that the survival of the fittest of the population will occur. Therefore, the choice of fitness function is very important. Usually in practical applications we will Objective function to calculate fitness function. Suppose the objective function is $J_{KFCM} = f(x)$, and generally speaking, the minimum value of the objective function is the optimal solution of the problem, and to calculate the maximum fitness value of the population, we need According to the following fitness function $Fit(f(x)) = 1/(1+f(x))$ In addition, the selection of fitness function should try to avoid the phenomenon of premature in the early stage of algorithm iteration. The purpose of this is to ensure the diversity and diversity of individual populations. The formula of the fitness function used in this article is:

$$Fit(f(x)) = \frac{1}{1 + \sum_{i=1}^{c} \sum_{k=1}^{n} u_{ik}^{m} \|\Phi(x_k) - \Phi(v_i)\|^2} \tag{4-11}$$

### 4.3.3 Simulated Annealing Genetic KFCM Algorithm Flow

In order to avoid repetition, the implementation of the following algorithm is based on the above chromosome coding, initial population and fitness. The algorithm flow chart is shown in Fig. 2:

(1) Initialize various control parameters: population number *Gsize*, evolutionary algebra *Gmax*, crossover probability *Pc*, mutation probability *Pm*, annealing initial temperature, temperature cooling coefficient $K$, termination temperature *Ta*;

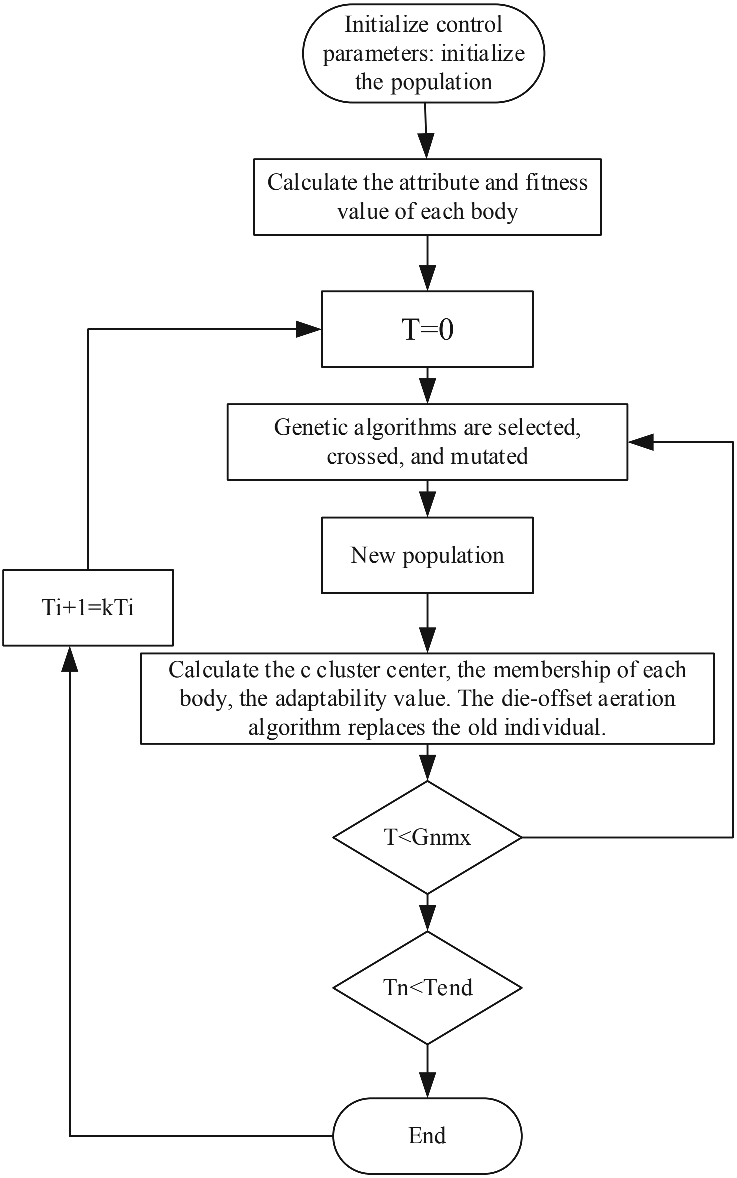


**Fig. 2.** Algorithm flow chart

(2) Initialize the genetic algebra $t = 0$, the fuzzy coefficient $m = 0$, and set their initial values to 0, randomly generate c cluster center matrices and use these cluster center matrices to form an initial population representation for $V_i = \{v_1, v_2, \ldots, v_c\}$;

(3) Calculate the membership matrix $U$ and fitness $\mathrm{Fit}(f(x))$ of each body in the population $S(t)$ using formula (4-9) in the KFCM algorithm $\overline{f} = \frac{1}{Gsize}\sum_{k=1}^{Gsize} f(k)$, if $\left|\overline{f(t)} - \overline{f(t-1)}\right| < \varepsilon$.
The average fitness value changes very little from the average fitness value before evolution. When $t = G\max$ (that is, the set evolutionary algebra is reached), select the individual with the highest fitness $S$ in the population and turn to (9); Otherwise, go to (4);

(4) Perform a selection operation on the t generation population according to the selection operator, and get $M$ individuals to form a subpopulation $S^{*}(t)$;

(5) Perform crossover operations on the individuals in the subpopulation $S^{*}(t)$ according to the probability of the size of $Pc$ to obtain a new population $S^{**}(t)$;

(6) Perform a mutation operation on individuals of the population $S^{**}(t)$ with the mutation probability $Pm$ according to the mutation operator to obtain the population $S^{***}(t)$:

(7) According to the simulated annealing operator, call the simulated annealing algorithm on the individuals of the population $S^{***}(t)$ to obtain the new population $S^{****}(t)$;

(8) Calculate the fitness of all individuals in $S(t)+S^{***}(t)$, and eliminate M individuals with smaller fitness values to form a new generation of population $S(t+1)$; $t = t + 1$; return (3);

(9) If $T_i < T_{\mathrm{end}}$, calculate the individual $V_i = \{v_1, v_2, \ldots, v_c\}$ chromosome length *len*, determine the initial cluster number as $c = len$;

(10) Call the KFCM algorithm with $c$ and $V_i = \{v_1, v_2, \ldots, v_c\}$ as the initial values, so as to get the final. The clustering center and membership matrix of.

## 5 Summary

This study proposes an improved FCM clustering method—SAGAKFCM algorithm, which is used to segment brain tissue in MRI images. The SAGAKFCM model fully combines the strong local search ability of the simulated annealing algorithm and the global search ability of the genetic algorithm, thereby obtaining the best initial clustering center, reducing the number of iterations of the fuzzy C-means algorithm, and avoiding the initial clustering from falling into the local maximum. Excellent, speed up the calculation speed. The algorithm combines the Gaussian kernel function to improve the robustness of the FCM algorithm. Under the influence of different intensities of noise, the segmentation time of this algorithm is 1–3 times less than the traditional FCM algorithm, ARKFCM algorithm, and FCMLSM algorithm. The segmentation accuracy index SA is about 0.02 larger than that of ARKFCM and FCMLSM. And the algorithm can obviously overcome the influence of noise on the segmentation result. Comparing various algorithms to segment brain white matter and gray matter in clinical brain images can also find the advantages of this algorithm, which provides a very reliable reference basis for segmenting real brain MRI images.

**Funding.** Science and Technology Demonstration Project of Suzhou Science and Technology Bureau, Big Data Analysis Processing and Clinical Application Research of Psychiatry (No. SS201706).

Guiding project of Suzhou Science and Technology Bureau, Research on Auxiliary Recognition of Alzheimer's Disease Based on Gaussian Probability Brain Image Segmentation Model (No.SYSD2019146).

## References

1. Fuchs, A.III. Shape and Size of Neurons. Neurocytology, Springer International Pub-lishing (2015). https://doi.org/10.1007/978-3-319-06856-5
2. Sandeep, C., Patnaik, L.M., Jagannathan, L.M.: Classification of magnetic resonance brain images using wavelets as input to support vector machine and neural network. Biomed. Sig. Process. Control **1**(1), 86–92 (2006). https://doi.org/10.1016/j.bspc.2006.05.002
3. Zhang, Y., Wu, L., Wang, S.: Magnetic resonance brain image classification by an improved artificial bee colony algorithm. Progress Electromagnet. Res. **116**(2011), 65–79 (2011)
4. Jayachandran, A., Dhanasekaran, R.: Brain tumor detection and classification of MR images using texture features and fuzzy SVM classifier. Res. J. Appl. Eng. Technol. **6**(12), 2264–2269 (2013)
5. Sumitra, N., Saxena, R.: Brain tumor classification using back propagation neural network. Int. J. Image, Graph. Sig. Process. **5**(2), 45–50 (2013). https://doi.org/10.5815/ijigsp.2013.02.07
6. Nanthagopal, A.P., Sukanesh, R.: Wavelet statistical texture features-based segmentation and classification of brain computed tomography images. IET Image Proc. **7**(1), 25–32 (2013)
7. Saritha, M., Joseph, K.P., Mathew, A.T.: Classification of MRI brain images using combined wavelet entropy based spider web plots and probabilistic neural network. Pattern Recogn. Lett. **34**(16), 2151–2156 (2013)
8. Sudeb, D., Manish, C., Malay, K.K.: Brain Mr Image Classification Using Multiscale Geometric Analysis of Ripplet. **137**(1), 1–17 (2013)
9. Padma, A., Sukanesh, R.: Segmentation and classification of brain CT images using combined wavelet statistical texture features. Arab. J. Sci. Eng. **39**(2), 767–776 (2013). https://doi.org/10.1007/s13369-013-0649-3
10. Manoochehri, M., Kolahan, F.: Integration of artificial neural network and simulated annealing algorithm to optimize deep drawing process. Int. J. Adv. Manuf. Technol. **73**(1–4), 241–249 (2014). https://doi.org/10.1007/s00170-014-5788-5
11. Rabeh, A.B., Benzarti, F., Amiri, H.: Segmentation of brain MRI using active contour model. Int. J. Imaging Syst. Technol. (2017)
12. Ng, C.R., et al.: Double segmentation method for brain region using FCM and graph cut for CT scan images. In: IEEE International Conference on Signal & Image Processing Applications IEEE (2016)
13. Du, B.J.M.H, Kardan, M., Spann, M.: Texture feature performance for image segmentation. Pattern Recogn. 23(3), 291–309 (1990)
14. Haralick, R.M., Shanmugam, K., Dinstein, I.: textural features for image classification. IEEE Trans. Syst. Man Cybern. **SMC-3**(6), 610–621 (1973). https://doi.org/10.1109/TSMC.1973.4309314
15. Rachmadi, M.F., del Maria, C., Valdés-Hernández, M.L., Agan, F., Di Perri, C., Komura, T.: Segmentation of white matter hyperintensities using convolutional neural networks with global spatial information in routine clinical brain MRI with none or mild vascular pathology. Comput. Med. Imaging Graph. **66**, 28–43 (2018). https://doi.org/10.1016/j.compmedimag.2018.02.002

16. Wells, W.M., Colchester, A., Delp, S. (eds.): MICCAI 1998. LNCS, vol. 1496. Springer, Heidelberg (1998). https://doi.org/10.1007/BFb0056181
17. Aslam, A., Ekram Khan, M.M., Beg, S.: Improved edge detection algorithm for brain tumor segmentation. Procedia Comput. Sci. **58**, 430–437 (2015). https://doi.org/10.1016/j.procs.2015.08.057
18. Upadhyay, A., Kanchan, K., Goyal, P.G., Yerramilli, A., Gorai, A.K.: Development of a fuzzy pattern recognition model for air quality assessment of Howrah City. Aerosol Air Qual. Res. **14**(6), 1639–1652 (2014). https://doi.org/10.4209/aaqr.2013.04.0118
19. Xinlei, C., Ren Xiaogang, W., Yue, Y.J.: Design and realization of a comprehensive management system for severe mental disorders based on FLUX mode. J. Med. Imag. Health Inf. **10**(2), 522–527 (2020). https://doi.org/10.1166/jmihi.2020.2898
20. Gore, J.C.: Principles and practice of functional MRI of the human brain. J. Clin. Invest. **112**(1), 4–9 (2003). https://doi.org/10.1172/JCI200319010