MRI Fuzzy Segmentation of Brain Tissue Using IFCM Algorithm with Genetic Algorithm Optimization

Youness Aliyari Ghassabeh, Nosratallah Forghani, Mohamad Forouzanfar, Mohammad Teshnehlab
Electrical engineering department, K. N. Toosi University of Technology
y_aliyari@sina.kntu.ac.ir , n_forghani@ee.kntu.ac.ir, mohamad398@ee.kntu.ac.ir
teshnehlab@eetd.kntu.ac.ir

Abstract

Fuzzy c-mean (FCM) is a common clustering algorithm which is used for segmentation of magnetic resonance (MR) images. However in the case of noisy MR images, efficiency of this algorithm considerably reduces. Recently, researchers have been introduced two new parameters in order to improve performance of traditional FCM in the case of noisy images. New parameters are computed using artificial neural networks and through an optimization problem, where need complex and time consuming computations. In this paper, we present a new method for efficient computation of these two parameters. We used genetic algorithm (GA) optimization method and showed capability of GA for finding optimal values of these parameters. Simplification of computation is advantage of new proposed method. Simulation results using noisy MR images, demonstrated effectiveness of proposed optimization method for noisy MR image segmentation.

1. Introduction

Magnetic resonance imaging (MRI) is an important diagnostic imaging technique used for early detection of abnormal changes in tissues and organ [1]. Segmentation of MR images for computer-aided diagnosis is often required as a preliminary stage. Detection of internal structure in brain MRI is widely used to diagnose several brain diseases such as epilepsy, multiple sclerosis, schizophrenia and alcoholism. Traditionally, segmentation of MR images is performed manually by trained radiologists. However, manual segmentation of these kinds of images is a time consuming job and human mistakes are inevitable. To solve these drawbacks, many computer based segmentation algorithms have been proposed in order to classify MRI regions [2-6]. Some notable algorithms include thresholding, region growing and clustering. Thresholding methods are generally restrictive and have to be combined with other methods [3]. Getting an accurate segmentation using region growing methods require precise anatomical information to locate single or multiple seed pixels for each region [5]. Fuzzy clustering can be considered the most important unsupervised learning algorithm and fuzzy c-mean (FCM) is the most popular fuzzy clustering method among different fuzzy clustering algorithms [7, 8].

Experiments demonstrate that FCM algorithm has an excellent performance on normal brains; however accuracy of this algorithm on abnormal brains with edema, tumor, etc is not efficient [9]. FCM algorithm only takes care to pixels intensity and does not consider their location or neighborhood properties. As a result, noisy images influence effectiveness of this algorithm. Unfortunately, MR images always contain a significant amount of noise caused by operator performance, equipment, and the environment, which can lead to serious inaccuracies with segmentation. Recently, Shen *et al.* [10] introduced new extension of FCM. They introduced two influential factors in segmentation where address issues of neighborhood attraction. First factor is the feature difference between neighboring pixels in the image and the second one is the relative location of the neighboring pixels. Therefore, segmentation is decided not only by the pixel's intensity and considers neighboring pixel's intensities and the locations. Authors in [10] computed these two parameters using an artificial neural network (ANN) and through an optimization problem. In this paper, a new computational method based on genetic algorithms (Gas) introduced in order to compute optimum values of these two parameters. Simulation results using noisy MR images, demonstrated the effectiveness of proposed method in efficient computation of unknown parameters and robustness toward the noise.

2. Improved FCM clustering algorithm

Generally, it is assumed that number of clusters is known in advance. For MR images number of clusters is equal to four cluster, they are: background, gray matter, white matter, cerebrospinal fluid (CSF) [11]. Intensity of background and CSF are nearly same, therefore CSF and background belong to same class and as a result, number of classes reduces to three classes. Most of the well-known fuzzy clustering algorithms are those derived by minimizing a cost function of the form:

$$J_q = \sum_{i=1}^{n} \sum_{j=1}^{m} u_{ij}^q d(x_i, \theta_j) \qquad (1)$$

In (1), θ_j represent the *j-th* cluster, m is number of clusters, n is number of unknown vectors and u_{ij} is membership function of vector x_i to *j-th* cluster that satisfies following conditions [7]:

$$u_{ij} \in [0,1] \text{ , } \sum_{j=1}^{m} u_{ij} = 1 \text{ \& } 0 < \sum_{i=1}^{n} u_{ij} < n \qquad (2)$$

$d(x_i, \theta_j)$ is the dissimilarity between x_i and θ_j and $q \in [1, \infty]$ is a parameter called fuzzifier. The common choice for $d(x_i, \theta_j)$ is [7]:

$$d(x_i, \theta_j) = (x_i - \theta_j)^t A(x_i - \theta_j) \qquad (3)$$

Where A is a symmetric positive definite matrix. Partial derivation of J with respect to u_{rs} and θ_j and using gradient descent optimization method [12] (in order to fined optimum values of $u_{ij} \, and \, \theta$) will result:

$$U_{ij} = 1 \Big/ \sum_{k=1}^{m} (d(x_i, \theta_j) / d(x_i, \theta_k))^{(2/q-1)} \qquad (4)$$

$$\theta_j = \sum_{i=1}^{N} u_{ij}^q x_i \Big/ \sum_{i=1}^{N} u_{ij}^q \qquad (5)$$

The feature vectors in MR images represent the pixel's intensity; hence their dimension is equal to one. The FCM algorithm iteratively optimizes cost function using (4), (5). Iterations continue until a termination criterion is met, i.e.: $\theta(t)-\theta(t-1) < \varepsilon$. From (3), it is obvious that FCM algorithm does not consider location or neighborhoods of pixels and only pay attention to pixel's intensity. Therefore, higher membership function depends on similarity between the pixel's intensity and the cluster center. Dependence on intensity increase sensitivity of algorithm to noise. Normally MR images corrupted by noise, therefore pixel's intensity will changed and it will cause generating incorrect membership functions and as a result, inaccurate segmentation. There are some ways to reduce sensitivity of FCM algorithm to noise. For example using low pass filters in order to smooth the image and then applying the FCM algorithm [13]. However low pass filtering, may lead to loose some important details. Different extensions of FCM algorithm were proposed by researchers in order to solve sensitivity to noise. Pham modified objective function and called it robust fuzzy c-mean (RFCM) [14], Krishnapuram and Keller interpreted clustering as a Possiblistic partition and called their new approach Possibilistic c-means (PCM) [15], Shen *et al* presented two influential factors where address issues of neighborhood attraction and called their new approach improver fuzzy c-mean (IFCM) [10]. Considering neighborhood attraction, Shen *et al* define dissimilarity function as below:

$$d(x_i, \theta_j) = |x_i - \theta_j|^2 (1 - \lambda H_{ij} - \xi F_{ij}) \qquad (6)$$

where H_{ij} represents the feature attraction and F_{ij} represents the distance attraction. Magnitudes of two parameters λ and ζ are between 0 and 1; adjust the degree of the two neighborhood attractions. H_{ij} and F_{ij} computed as follow:

$$H_{ij} = \sum_{k=1}^{s} U_{ki} \, g_{jk} \Big/ \sum_{k=1}^{s} g_{jk} \qquad (7)$$

$$F_{ij} = \sum_{k=1}^{s} U_{ik}^2 \, q_{jk}^2 \Big/ \sum_{k=1}^{s} q_{jk}^2 \qquad (8)$$

where g_{jk} and q_{jk} are defined by:

$$g_{jk} = |x_j - x_k| \text{ , } q_{jk} = (a_j - a_k)^2 + (b_j - b_k)^2 \qquad (9)$$

where (a_j, b_j) denote the *j-th* pixel's location. For any input image, defining an objective function and using an ANN, constant parameters λ and ξ are computable.

3. Structure of genetic algorithms

GAs are stochastic search techniques based on mechanism of natural selection and natural genetics. GAs, differing from conventional search techniques, start with an initial set of random solutions called population. Each individual on the population is called a chromosome, representing a solution to the problem at hand. A chromosome is a string of symbols. These symbols are called genes. The chromosomes evolve through successive iterations, called generations. During each generation the chromosomes are evaluated using some measure of fitness function (a function that demonstrates how each solution /chromosome is accurate). To create the next generation, new chromosomes, called offspring, are formed by either merging two chromosomes from current generation using a crossover operator or by modifying genes of a chromosome using a mutation operator. According to fitness function some of parents and offspring are chosen and others will reject in order to keep population size constant. Fitter chromosomes have higher probabilities of being selected. After several generations the algorithms converge to the best chromosome, which hopefully represent the optimum solution to the problem [16]. Initial population is usually considered to be random. The genetic operations mimic the process of heredity of genes to create new offspring at each generation. The evolutionary operation, mimic the process of Darwinian evolution to create populations from generation to generation [17].

4. New optimization approach based on GA

As mentioned in the previous section, domain of variables λ and ξ is [0, 1]. We considered required precision is four places after the decimal point (precision is variable and it can be assigned a big number, but here four place after decimal point is enough). The required bits for each variable, is calculated as follows:

$$2^{m_i - 1} < 10^4 < 2^{m_i} - 1 \text{ , } (i=1, 2) \qquad (10)$$

Conversion from binary format to decimal is simply computed by:

X_j=decimal (binary string) / (2^m-1)

Total bits required for simultaneous computation of λ and ξ is m = m_1 + m_2. If precision is set to four places after decimal point, total number of 28 bits are required (m_1 =m_2=14), the first 14 bits represent the λ and next 14 bits represent the ξ. We considered population size equal to 20 and then generated a random initial population. Cost function J_q in (1) is defined as fitness function and used for evaluation of initial chromosomes. In this stage some chromosomes are strong and others are weak (some of them produce lower value for fitness function and vice versa). For selection stage a roulette wheel approach is adopted. Construction of roulette wheel is as follows [17]:
Procedure: Roulette wheel

Step 1.Calculate the fitness value for each chromosome.
Step 2 .Compute summations of all fitness values and calculate the total fitness.
Step3. Divide each fitness value to total fitness and get the selection probability for each chromosome (noted by p_k).
Step4. Calculate cumulative probability q_k for each chromosome $q_k = \sum p_j$.

In selection process, roulette wheel spin 20 (population size) time. Each time a single chromosome is selected for a new population in the following manner [18]:

Procedure: selection

Step1. Generate a random number r from the rang [0, 1]
Step2. If $r<=q_1$, then select the first chromosome, otherwise select the k-th chromosome such that $q_{k-1}< r < q_k$.

After selection part, a new population will produce that chromosomes with higher selection probability will remain and others will clear. Now, crossover and mutation operators produce new chromosomes. Consider probability of crossover is set to 0.2 and probability of mutation is set to 0.01(it means that 4 chromosomes from total population of 20 will change using crossover operator and 6 genes from 560 (28×20) genes will converted using mutation operator). Crossover procedure can describe as follows [17]:

Procedure: cross over
Begin
$0 \rightarrow k$;
While (k<= population size) do
Random number from [0, 1] $\rightarrow r_k$
If ($r_k<0.2$) then select k-th chromosome as one parent for crossover.
end
$k\rightarrow k+1$;

end
end

Mutation procedure is done as follows:

Step1.choose 6 genes from total 560 genes (we considered mutation rate is equal to 0.01).
Step2. Change current value of selected genes (if they are one, alter them to zero and vice versa).

After completion of above processes, a new population is produced and the current iteration is completed. We iterated the above procedures until a certain criterion is met. At this point, the most fitted chromosome represented the optimum values of λ and ξ.

5. Simulation results

Simulations are done on one sample T1 weighted MR image. In first experiment, noise is absent and in second and third experiments noise is present and effect of noise increases. In each experiment, parameters λ and ζ are computed using proposed optimization method based on genetic algorithm. Then we used IFCM clustering algorithm in order to segment MR images. Figure 1 shows a noiseless MR image and segmented images, form left to right they are, original image, white matter, gray matter and CSF.
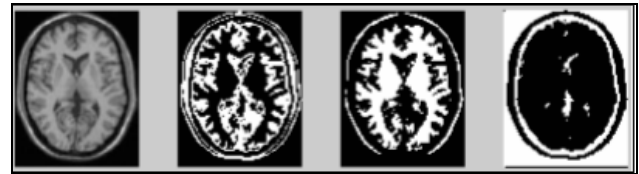

Figure 1. From left to right: original noiseless image: white matter, gray matter, CSF.

In the second experiment, T1 weighted MR image destroyed with Gaussian noise. Figure 2 demonstrates the results of segmentation. In third experiment, we increased amount of Gaussian noise and corrupted the original image. Figure 3 shows results of segmentation in this case. Table 1 shows values of λ and ζ for each experiment. It is clear that for every new input image values of λ and ζ will change.
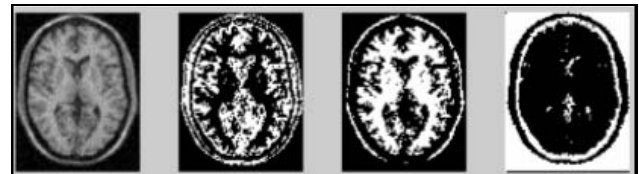

Figure 2. From left to right: corrupted MR image, white matter, gray matter and CSF.

New proposed algorithm based on GA makes it available to compute λ and ζ without using ANN.

Table 1. Values of ζ and λ in different experiments

	First experiment	Second experiment	Third experiment
λ	0.6523	0.7041	0.7783
ζ	0.4557	0.4987	0.5567

Experimental results demonstrate improved performance of FCM clustering algorithm against noisy MR images. New proposed algorithm based on GA, simplifies computation of λ and ζ without using complicated ANN.
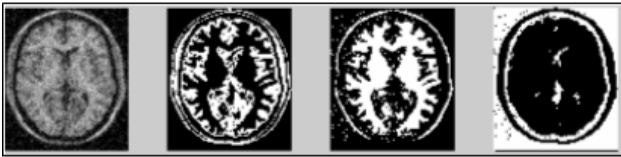

Figure 3. From left to right: corrupted MR image, white matter, gray matter and CSF.

6. Conclusion

There are different source of noise arises from environment, operator and equipments. These sources influence the medical images. As a result, performance of traditional FCM for segmentation of noisy images reduces. IFCM algorithm is proposed to solve sensitivity of FCM algorithm to noise. This version of FCM introduces two new parameters λ and ζ in order to consider pixel's neighborhood and location effect. The new parameters are computed using an ANN through optimization of an objective function. In this paper a new method based on GAs is introduced for computation of the optimal values of these parameters. Simplified computation of λ and ζ is an Advantage of the proposed algorithm compared with ANN optimization technique. Simulation results demonstrated effectiveness of the new proposed method to find optimal values of λ and ζ, that are used for efficient segmentation of noisy MR images.

7. References

[1] A. Huang, R. Abugharbieh, R. Tam and A. Traboulsee, "Automatic MRI Brain Tissue Segmentation using a Hybrid Statistical and Geometric Model ", 3rd IEEE International Symposium on Biomedical Imaging, April 2006.

[2] L. Lemieux, G. Hagemann, K. Krakow, and F. G. Woermann, "Fast, accurate, and reproducible automatic segmentation of the brain in T1-weighted volume MRI data," *Mag. Reson. Med.*, vol. 42, pp. 127-135, 1999.

[3] H.Suzuki and J.Toriwaki, "Automatic Segmentation of Head MR Images by Knowledge Guided Thresholding" Computer Medical Imaging,vol 15, No 4, 1991.

[4] K. V. Leemput, F. Maes, D. Vandermeulen, and P. Suetens, "Automated model-based tissue classification of MR images of the brain," *IEEE Trans. Med. Imag.*, vol. 18, no. 10, pp. 897-908, Oct. 1999.

[5] R.Pohle and L.D. Toennies, "Segmentation of Medical Images using Adaptive Region Growing ", Proc, SPIE, Medical Imaging, vol. 4322, 2001.

[6] S. R. Kannan, "Segmentation of MRI Using New Unsupervised Fuzzy C Mean Algorithm" GVIP (5), No. V2, January 2005.

[7] S. Theodoridis, K. Koutroumbas, *Pattern Recognition,* Academic Press; 2nd edition February 2003.

[8] J. C. Bezek, *Pattern Recognition with Fuzzy Object Function Algorithms* New York: Plenum, 1981

[9] D.L Pham and L.Prince, "Adaptive Fuzzy Segmentation of Magnetic Resonance Images", IEEE trans. On Medical Imaging, vol. 18, September 1999.

[10] S. Shen, W. Sandham, M. Grant and A. Ster, "MRI Fuzzy Segmentation of Brain Tissue Using Neighborhood Attraction with Neural-Network Optimization", IEEE Trans. On Information Technology is Biomedicine, vol 9, No 3, September 2005.

[11] M. C. Clark, L. O. Hall, D. B. Goldgof, "MRI Segmentation using Fuzzy Clustering Technique", IEEE Engineering in Medicine and Biology, vol. 13, no. 5, 1994.

[12] B.Widrow, S. Stearns, *Adaptive Signal Processing*, Prentice-Hall, 1985.

[13] R. C. Gonzales, R. E. Woods, *Digital Image Processing* ,Prentice Hall; 2nd edition ,January 15, 2002.

[14] D.L. Pham, " Spatial Models for Fuzzy Clustering ", Computer Vision Image Understanding, Vol. 84, 2001.

[15] R.R. Krishnapuram and J.M. Keller," A Possibilistic Approach to Clustering" ,IEEE Trans. Fuzzy Systems, Vol 1, No. 2, May 1993.

[16] D. Goldberg, *Genetic Algorithms in Search, Optimization and Machine Learning*, Addison-Wesley ,MA ,1989.

[17] M. Mitchel, *An Introduction to Genetic Algorithms*, MIT Press, Fifth printing, 1999.

[18] M.Gen and R. Cheng, "Genetic Algorithms and Engineer Design ", John Wiley, 1997.