Cerebrospinal Fluid Image Segmentation using Spatial Fuzzy Clustering Method with Improved Evolutionary Expectation Maximization

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Abstract-Visualization of cerebrospinal fluid (CSF), that flow in the brain and spinal cord, plays an important role to detect neurodegenerative diseases such as Alzheimer's disease. This is performed by measuring the substantial changes in the CSF flow dynamics, volume and/or pressure gradient. Magnetic resonance imaging (MRI) technique has become a prominent tool to quantitatively measure these changes and image segmentation method has been widely used to distinguish the CSF flows from the brain tissues. However, this is often hampered by the presence of partial volume effect in the images. In this paper, a new hybrid evolutionary spatial fuzzy clustering method is introduced to overcome the partial volume effect in the MRI images. The proposed method incorporates Expectation Maximization (EM) method, which is improved by the evolutionary operations of the Genetic Algorithm (GA) to differentiate the CSF from the brain tissues. The proposed improvement is incorporated into a spatial-based fuzzy clustering (SFCM) method to improve segmentation of the boundary curve of the CSF and the brain tissues. The proposed method was validated using MRI images of Alzheimer's disease patient. The results presented that the proposed method is capable to filter the CSF regions from the brain tissues more effectively compared to the standard EM, FCM, and SFCM methods.

I. INTRODUCTION

The cerebrospinal fluid (CSF) flow plays an important role in detecting neurological diseases; one of them is Alzheimer's disease [1-3]. Often, these diseases are detected by analysing the substantial changes in the normal CSF volume and pressure. The fluid is produced in the choroid plexus, in which the flow is streamed from the lateral ventricles to the foramen of Monroe and other parts of the brain, including third ventricle, forth ventricle, aqueduct of Sylvius, median, and the foramen of Magendie and Luschka. The CSF eventually fills up the subarachnoid space around the brain, which channels the fluid in the spinal cord. The CSF flow dynamic commonly moves in the form of pulsatile motion that is controlled during respiration. To elucidate this

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S.Y. and K.K. are with Department of Human and Information Sciences, School of Information Science and Technology, Tokai University, Hiratsuka, Japan (e-mail: 8adi2203@gmail.com; kagayaki@keyaki.cc.utokai.ac.jp). complex behaviour, the analysis of the CSF flow dynamics is assisted by the use of magnetic resonance imaging (MRI) technique. This is due to the fact that this biomedical imaging technique allows the measurement of CSF volumetric over a specific range of time, mostly quantified by the cardiac cycles [4-6]. In the past few years, there are a number of studies that have focused on analysing the pulsatile motion of the CSF flow based on the MRI images [7-10]. However, due to the inhomogeneous of the pulsatile motion during the cardiac cycles as well as the varieties of symptoms of the diseases, the analysis of the CSF pulsatile motion has become a prominent and challenging study [7].

Among the existing image segmentation methods [11-14], the fuzzy clustering methods have been widely implemented for the image segmentation problem. The methods employ fuzzy-based classification to group the pixels based on the membership values that formulate according to the intensity values. Compared to the other clustering methods, the fuzzy clustering methods allow the pixels to be classified into more than one group, which useful to handle the measurement noise. Despite of this advantage, these methods show a lack of capability in handling the partial volume effect [11]. Furthermore, the methods also present an extensive use of computational time compared to the other conventional methods [15-17]. To address these limitations, novel researches have improved the fuzzy clustering methods by incorporating the spatial information gathered from the neighbouring pixels [12, 18]. In these methods, the membership values of the neighbouring pixels are included in the membership value of the current pixel. Therefore, this allows the methods to avoid the partial volume effect in the images during the segmentation. Alternatively, the deformable models, which are mostly utilized by active contour approaches to solve level set formulations, are also applied to find the surface evolution of certain regions in the images. In recent years, Li et al. [12] had integrated this model to improve the spatial fuzzy clustering (SFCM) methods. The proposed method shows that the deformable model is effective in differentiating the boundary wall in the brain MRI images [19-21]. Due to the optimization problem applied in the previous researches, it is suggested that the use of evolutionary computation (EC) such as Genetic Algorithm (GA) [32] methods may provide prospective improvements for better segmentation accuracy [16, 22].

In this paper, the current research on developing an effective segmentation method based on spatial fuzzy clustering method is extended by incorporating an improved Expected Maximization (EM) method using evolutionary operations of the GA method. The aim of this contribution is

to overcome the partial volume effect of the MRI images that may reduce the accuracy of image segmentation. The proposed method is developed based on two main stages: genetic EM filtering, and spatial fuzzy clustering stages. In the genetic EM filtering stage, the improved evolutionary EM method was used to filter the original MRI image. In the spatial fuzzy clustering stage, the filtered image produced by the previous stage was used to determine the initial centroids for the clustering process. After the segmentation was performed, the geometric-based level set model was applied in the post-processing stage to identify the curve of the specific regions for segmenting the CSF from the brain tissues. The effectiveness of the proposed algorithm was evaluated using real MRI image dataset gathered from Alzheimer's Disease Neuroimaging Initiative (ADNI) [29]. The results showed that the segmentation accuracy of the proposed method had outperformed those of the existing EM, FCM, and SFCM methods.

II. PROPOSED METHOD

A. Genetic Expectation Maximization Filtering

The EM method is often used to estimate the parameters in the mixture modeling approach. The method is generally developed based on the iterative technique, which aims to optimize the likelihood function when information is insufficient. In the context of image segmentation, this missing information is usually formulated as the class membership of the intensity values in the images. Accordingly, let x_i be the intensity value of the *i*th pixel in the image *I*. In general, given *C* number of classes, the intensity value x_i may belong to one of the classes with different probabilities, $f(x_i)$. Thus, the probability of the intensity value x_i may belong the class as given as the following equation:

$$f(x_i) = \sum_{j=1}^C w_j f_j(x_i|p_j) \tag{1}$$

where w_j is the weighting coefficient of the *j*th cluster and p_j is a parameter set containing two vectors; mean, μ_j , and covariance matrix, $\dot{\Sigma}_j$. In most cases, the distributions of the probabilities for intensity values are illustrated using histogram, in which the modes may represent the classes or clusters of the images. Based on this equation, the parameter set is commonly unknown and often estimated using the iterative optimization method, namely EM method. However, this usually required an extensive amount of computational time.

Recent researches showed that this limitation is overcome by incorporating metaheuristics methods such as the GA method [25]. In general, the GA method is a metaheuristics optimization method that utilizes stochastic searching strategy based on the enhancement of fitness function. In this paper, the fitness function of the searching strategy is modified, in which is aimed to find the plausible parameter sets, p_j , that may minimize the errors of the likelihood function in the EM method. Firstly, a population of *NP* solutions, *S*; which is formed by a randomly selected parameter set, is initiated as follows

$$S_{(t)} = \{s_{1(t)}, s_{2(t)}, s_{3(t)}, \dots, s_{NP(t)}\}$$
(2)

where for *l*th solution, in which $l = \{1,2,3,...,NP\}$, the solution is formed as follows

$$s_{l(t)} = \{a_{l(t)}, b_{l(t)}\}$$
 (3)

The vectors of the solution, $a_{l(t)}$ and $b_{l(t)}$, represent the vectors of the parameter set in the model, μ_j and $\dot{\Sigma}_j$, respectively. These vectors are initiated randomly within a specific range of values. Then, the fitness value of each *l*th solution is computed according to the following equation:

$$f(s_{l(t)}) = \sum_{j=1}^{C} w_j f_j(x_i | s_{l(t)})$$
(4)

After that, the selection operation is performed to randomly select a number of solutions that produced plausible fitness values. These solutions are used for crossover operation, in which one of the vectors of the solutions is switched into another solution. Based on a certain threshold, the mutation operation is executed onto a randomly chosen solution. In this operation, one of the vectors is randomly updated. Next, the fitness values of the updated solutions are calculated and the solution that produced plausible fitness value among other solutions in the population is selected as the global best solution. The procedure is repeated until the maximum number of iterations is reached.

After that, the maximization step is performed. In this step, the parameter set, p_j , is updated by maximizing the likelihood function using the determined weighting coefficient found in the previous step. This may involve the update of the parameter vectors μ_j and Σ_j , by calculating the following equations:

$$\mu_{j(t+1)} = \frac{1}{N} \sum_{i=1}^{N} \frac{f(p_j | x_i) x_i}{w_{j(t+1)}}$$
(5)

$$\Sigma_{j(t+1)} = \frac{1}{N} \sum_{i=1}^{N} \frac{f(p_j | x_i) (x_i - \mu_{j(t+1)}) (x_i - \mu_{j(t+1)})^T}{w_{j(t+1)}}$$
(6)

The whole procedure is repeated until the value of the likelihood function converges or the maximum number of iterations is reached.

B. Spatial Fuzzy Clustering for Image Segmentation

The SFCM method has become a prominent clustering method for image segmentation. This method permits the segmentation of different regions of the images by assigning fuzzy-based membership values based on the pixel intensity. The membership values allow the pixels to be grouped in more than one class, in which provides more robust capability for handling the image noise. The segmentation of the image can be represented as an optimization problem, which aims to minimize the following objective function:

$$J = \arg\min\sum_{i=1}^{N} \sum_{j=1}^{C} u_{ij}^{\alpha} \|x_{i} - y_{j}\|^{2}$$
(7)

where *N* is the total number of pixels, and α is the parameter that controls the fuzziness of the segmentation, in which usually $\alpha > 1$. For each iteration, the membership value of each pixel and the corresponding centroid are updated. The

spatial information utilized by the SFCM method is derived by using the following equation:

$$h_{ij} = \sum_{k \in w(x_i)} u_{ik} \tag{8}$$

where $w(y_i)$ is the square window centred on the current pixel x_i [12, 18]. Obviously, the spatial value of a pixel for a cluster is relatively large if the majority of its neighbouring pixels belong to the same cluster. This information is exploited into the following membership function:

$$u_{ij}' = \frac{u_{ij}^{\alpha} h_{ij}^{\beta}}{\sum_{k=1}^{C} u_{ki}^{\alpha} h_{kj}^{\beta}}$$
(9)

where α and β are the predefined control parameters. As a result, spatial information exploited by the SFCM method may useful to handle misclassified pixels due to the noise exhibited within the images more effectively [18]. Figure 1 illustrates the overall procedure for the proposed method.



Figure 1. Flowchart of proposed method

III. RESULTS AND DISCUSSION

The proposed method was evaluated using real Alzheimer's disease patient MRI brain images. The images were collected from ADNI database. A number of 15 images were selected. The images were acquired using 3.0T Philips Medical Systems based on the following setup: flip angle=15.0 degree, slice thickness=10.0mm, TE=4.60ms, TR=11.12ms.

The accuracy of the proposed method was measured using similarity index. The similarity index, *SI*, was calculated as follows:

$$SI = \frac{G \cap S}{G + S} \tag{10}$$

where G and S are the ground truth and segmentation produced by the methods, respectively. Table 1 shows the mean similarity index produced by the proposed method compared to the other methods. The ground truths of these images are generated by the manual segmentation performed by experts. Despite of the presence of partial volume effect, the proposed method has shown potential capability in sustaining the robustness of the segmentation accuracy.

Figure 2 illustrates the example of the CSF segmentation produced by the proposed method compared to those produced by the existing EM, FCM, and SFCM methods. The CSF segmentation is performed using geometric-based level set model in a post-processing stage of each method. Based on this example, the EM method has included some pixels that are suffered by the partial volume effect in the segmented images. Even though the FCM, and SFCM methods have shown the capability to overcome this limitation, the proposed method has presented better segmentation results by including some pixels that are actually present in the ground truth. This suggests the important characteristics of the proposed method in dealing with the partial volume effect in the images.

TABLE I. MEAN SIMILARITY INDEX PRODUCED BY THE METHODS

Region	Mean Similarity Index			
	EM	FCM	SFCM	Proposed
WM	0.66±0.15	0.72±0.09	0.87±0.02	0.93±0.06
GM	0.57±0.12	0.65±0.12	0.81±0.05	0.90±0.07
CSF	0.42±0.10	0.61±0.09	0.75±0.13	0.87±0.06

EM FCM

SFCM

Proposed



Figure 2. CSF segmentation resultd by the methods.

IV. CONCLUSION

In conclusion, the new pre-processing stage of the spatial fuzzy clustering method has shown potential achievements in dealing with the partial volume effect in the real Alzheimer's disease MRI images. This may lead to further investigations of the dynamic changes of the CSF flows that may be caused by such disease.

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