MR Brain Image Segmentation Using Clustering Technique

Ock-Kyung Yoon*, Dong-Whee Kim**, Hyun-Soon Kim*, Kil-Houm Park*
*School of Electronic Engineering, Kyungpook national University,
1370 San-Kyuk Dong, Puk-Gu, Taegu, KOREA 702-701
Tel: +82 – 53 – 940 - 8849, Fax: +82 – 53 – 950 – 5505, E-mail: yoon@palgong.knu.ac.kr
**School of Comp. & Inform. Engineering, Taegu University,
5 Naeri JinRyang KyungSan Kyungpook, KOREA 712-714

Abstract: In this paper, an automated segmentation algorithm is proposed for MR brain images using T1-weighted, T2-weighted, and PD images complementarily. The proposed segmentation algorithm is composed of 3 steps. In the first step, cerebrum images are extracted by putting a cerebrum mask upon the three input images. In the second step, outstanding clusters that represent inner tissues of the cerebrum are chosen among 3-dimensional (3D) clusters. 3D clusters are determined by intersecting densely distributed parts of 2D histogram in the 3D space formed with three optimal scale images. Optimal scale image best describes the shape of densely distributed parts of pixels in 2D histogram. In the final step, cerebrum images are segmented using FCM algorithm with it's initial centroid value as the outstanding cluster's centroid value. The proposed segmentation algorithm complements the defect of FCM algorithm, being influenced upon initial centroid, by calculating cluster's centroid accurately. And also can get better segmentation results from the proposed segmentation algorithm with multi spectral analysis than the results of single spectral analysis.

1. Introduction

Magnetic resonance images offer anatomical information for medical examination more accurately than other medical images such as X ray, ultrasonic, and CT images. So MR images are widely used not only for diagnosing brain tumor, heart disease, disk disease, and so on which are difficult to detect by using other images but also for examining anatomical state of tissues. A typical MR analysis of a patient involves multi-modal information in three cross section by itself contains 10-30 2D slices, and generally each slice has three different types of image (T_1-weighted, T_2-weighted, proton density(PD) image) which have different contrast affected by selection of pulse sequence and weighting signal. Thus, even for a single study, there are one hundred or more images to be acquired and analyzed. This naturally burdens the computational requirements for computation time and data analysis. For this reason, an automated algorithm for segmentation and recognition is inevitably required.

Most early reports of MR brain image segmentation are not used the characteristics of each spectral image complementarily but used only the characteristics of each spectral image itself.

C. Tsai et al.[1] used only the characteristics of each spectral image for segmenting MR brain image. Cerebrum region is extracted from PD image and CSF is extracted from T2-weighted image. CSF is appeared as a single mode and located upper part(bright intensities) of the histogram of T2-weighted image. They extracted CSF by thresholding at top 10% of the histogram. The histogram of brain regions(excluding ventricles) for PD images has two distinguishable peak corresponding to white matter and gray matter. White and gray matter are separated by computing thresholds of this mode.

M. C. Clark et al.[2] used knowledge and fuzzy clustering techniques. They oversegment T2-weighted brain image as 10 classes using fuzzy clustering. They determine lower 3 classes as background and upper 7 classes as cerebrum region. CSF and white matter and gray matter are separated from this 7 classes using knowledge.

M. C. Clark et al.[3] segments glioblastoma-multiforme tumor from abnormal slices which is determined by passing through their previous work[2]. Intracranial region of abnormal slice is extracted using quadrangle mask. They made two tumor images which are roughly separated from each T1-weighted image and PD image. And finally they refine tumors using density screening from 2D histogram of PDT1. They used histogram characteristics of T1-weighted image and PD image complementarily to segment brain tumors.

In this paper, we propose 3 step automated segmentation algorithm which uses T1-weighted, T2-weighted, and PD images complementarily. In the first step of segmentation, cerebrum regions are extracted by putting the cerebrum mask on the three input images. Cerebrum mask is made from PD image by using histogram thresholding, morphological operation, and labeling algorithm. In the second step, outstanding clusters that represent inner tissues of the cerebrum are chosen among 3D clusters. 3D clusters, have similar t1, t2, and pd values, are shown in the 3D spaces composed of t1, t2, and pd axes. 2D histogram serves information for the distribution of 3D clusters. Therefore we can analogize the shape of 3D clusters by intersecting densely distributed parts of pixels, peaks, of three 2D histograms (t1t2, t2pd and pdt1). Peaks are found by scale space filtering and it's second derivative. There are many peak extracted images for a 2D histogram cause scale parameter of scale space filtering is varied. Optimal scale image, best describes 2D histogram, is selected among these peak extracted images using graph structure. We make 3D space using optimal scale image and find 3D clusters by intersecting each peaks in the space and select outstanding clusters. FCM algorithm is widely used in image processing, because it has robust characteristics for ambiguity and noise-contained image. But it may consume high amount of CPU time and memory for large data sets and influenced on the initial centroid value. In the final step, cerebrum images are segmented using FCM algorithm with it's *initial* centroid value as the outstanding cluster's centroid value

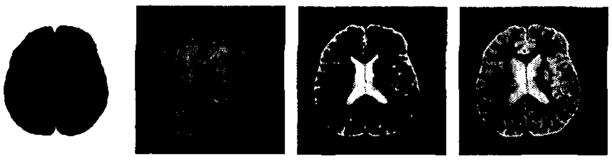
The remainder of the paper is divided into three sections. Section 2 describes the proposed MR brain image segmentation algorithm. Section 3 presents the experimental results and compare with the results of single spectral analysis. The last section conclude with the future directions.

2. Segmentation

2.1 Extraction of the cerebrum region

Histogram of PD image is formed with background mode and CSF, white, and gray matter mode. Bimodal characteristics of PD image make easy for elimination of background and extraction of the cerebrum region.

The first step in the segmentation process is to isolate the cerebrum region from the bone, muscle, and fat tissues. Cerebrum images of the same shape are obtained by putting the cerebrum mask on the three input images. Cerebrum mask is made by elimination of the background noise and removing uninterested region outside the cerebrum such as bone, muscle, and fat. A single threshold from iterative thresholding is applied to the PD image to eliminate the background. Bone and soft tissues are eliminated by using morphological erosion operation. A morphological erosion operation with a NxN rectangular shaped structural element is applied to the thresholded image. After erosion, labeling algorithm is applied to the eroded image and find the biggest region. The biggest region may have a hole due to thresholding. After dilation and filling the biggest region, we can get the cerebrum mask image like Fig. 1(a). This mask is used to extract the cerebrum image from the input images as shown in Fig. 1(b), (c), and (d).



(a) (b) (c) (d)

Fig. 1. Cerebrum mask image and cerebrum images (a) cerebrum mask image from PD image, (b) cerebrum image from T1-weighted image, (c) cerebrum image from T2-weighted image, and (d) cerebrum image from PD image.

2.2 Segmentation of the cerebrum region

Pixels in T1-weighted, T2-weighted, and PD images have gray level values between 0 to 255 and are corresponded to a single point of 3D space composed of T1 and T2, PD axes. Cerebrum tissues to segment can be regarded as a set of pixels, which have similar t1 and t2, pd values. They made clusters crowded adjacent area in the 3D space. So, we can segment cerebrum region by separating these clusters. When pixels, distributed in the 3D space, are projected to the three planes of the space, 2D histogram is made by accumulated pixel numbers at each point of the plane.

2.2 Scale space filtering

Scale space filtering is a qualitative signal description method that deals gracefully with the problem of scale by treating the size of the smoothing filter as a continuous parameter. As the scale parameter is varied, scale space filtered image is varied.

For a continuous 2D signal $f(x, y)$, its scale space filtering is defined as follows[4].

$$F(x,y,\tau) = f(x,y) * g(x,y,\tau)$$
$$= \int\int_{-\infty}^{\infty} f(u,v)\frac{1}{2\pi\tau^2}\exp\left[-\frac{(x-u)^2+(y-v)^2}{2\tau^2}\right]dudv$$

Where, "*" denotes 2D convolution and $g(x, y, \tau)$ is 2D scale space filter. Scale space filtering smoothed wide area of 2D input image as scale constant τ increased. We call $F(x, y, \tau)$ as "scale space image". Zero-crossings in the first derivative of scale space image correspond to the peaks and valleys. In the second derivative, peaks have negative values and valleys have positive values at each zero-crossing. Second derivative of $F(x, y, \tau)$ can be got convolving $f(x, y)$ and $\nabla^2 g(x, y, \tau)$[4].

$$\nabla^2 F(x,y,\tau) = \nabla^2\{f(x,y) * g(x,y,\tau)\}$$
$$= f(x,y) * \nabla^2 g(x,y,\tau)$$

$$\nabla^2 g(x,y,\tau) = \frac{\partial^2 g(x,y,\tau)}{\partial^2 x^2} + \frac{\partial^2 g(x,y,\tau)}{\partial^2 y^2}$$
$$= -\frac{1}{\pi\tau^4}\left[1-\frac{x^2+y^2}{2\tau^2}\right]\exp\left[-\frac{x^2+y^2}{2\tau^2}\right]$$

Peaks are extracted where $\nabla^2 F(x, y, \tau)$ has negative values,. We call this peak extracted image as "*peak image*". Scale space filtering takes long time as the scale constant increased, scale space filter $g(x, y, \tau)$ also grow larger. We can improve this problem using two 1D filter h_1 and h_2.

$$\nabla^2 g(x,y,\tau) = h_1(x)h_2(y) + h_2(x)h_1(y)$$
$$h_1(\xi) = \frac{1}{(2\pi)^{1/2}\tau^2}(1-\frac{\xi^2}{\tau^2})\exp\left[-\frac{\xi^2}{2\tau^2}\right]$$
$$h_2(\xi) = \frac{1}{(2\pi)^{1/2}\tau^2}\exp\left[-\frac{\xi^2}{2\tau^2}\right]$$

A computational point of view, the total number of operations reduced at each pixel from m^2 to m, where the size of the filter is m x m pixels.

Scale space filtering for 2D histogram generates more meaningless peaks as scale constant becomes smaller, on the other hand it doesn't show prominent ones as τ becomes larger. Once scale constant is about 40, the filter includes most 2D histogram and peaks in the peak images have the merged shape of several prominent ones.

So peak images of which scale constant is more than 40 don't affect to find prominent peaks. Therefore we let the maximum scale constant as 40 and make peak image until it becomes 11. Second derivatives of scale space filter have meaningless small value, where the value of x and y is more than $|3\tau|$. So, we made a 2D window between -3τ and 3τ for second derivatives of scale space filter.

2.2.2 Automatic selection of optimal scale

"*Optimal scale image*" is peak image which best describes the shape of 2D histogram and its scale constant is "*optimal scale*". Optimal scale is found by examining the variation of the peaks in peak image. The variation of the peaks can be described one of four cases as follows.

① the case that new peaks are generated.
② the case that one peak is divided into more than two peaks.
③ the case that more than two peaks are merged into one peak.
④ the case that the shape only of the peak is changed.

The variation of peaks are represented by using graph structure and optimal scale is selected by searching this structure. Information of peaks is represented as nodes and the peak relationship between two adjacent peak images are represented by using directional edges. In the node structure, we put the value of start scale constant which a peak starts, and a counter, next node pointer, previous node pointer. A counter counts the number of scale constant, which the peak is continuously existent in the scale range, starting from start scale constant.

Graph structure, first, generates starting(root) node and nodes of peaks existing in the peak image for scale constant of 40 and then examine the variation of the peak by decreasing the scale constant. For the cases of ①, ②, and ③, new nodes are generated and their starting scales are stored and their counters are initialized as 1. For the case of ④, only the counter is increased. Once the graph structure is completed, we find the scale range that its corresponding peak exists for the longest time on each path by searching all paths from starting node to terminal nodes. For the case that new peak is generated, it is the case that valleys at the previous step become peaks by scale variation. If the scale range of the valley is longer than that of peak, the peak can not be regarded as a prominent one. In this case, we do not find the longest scale range of peak existence. After finding the longest scale range at each path, we determine the range which scale range of each path is superimposed as "*variable range*". Peak image according to variable range includes all the prominent peaks of 2D histogram. Optimal scale is the smallest value of the variable range cause peak image of small scale constant describes 2D histogram better than bigger one.

2.2.3 3-dimensional clustering

The 3 dimensional clustering is composed of 3D cluster finding process and cerebrum image segmenting process using FCM algorithm with 3D cluster's centroid as it's centroid. The 3D cluster finding process selects outstanding clusters among 3D clusters by intersecting peaks of optimal scale image in the space. The methods are first, assigning different label to each peaks in optimal scale image and get three label pair (L_t1, L_t2, L_pd) by projecting cerebrum pixel's t1 and t2, pd value to the each plane of the space. We regard this label pair as 3D cluster. And calculate total pixel number belong to each 3D cluster and center value of that. After this process, all 3D clusters information in the cerebrum image is found. Outstanding clusters are determined comparing 3D cluster's total pixel number and save their information such as label pair, pixel number, and center value. Outstanding clusters are corresponded to cerebrum tissues, which we are going to segment.

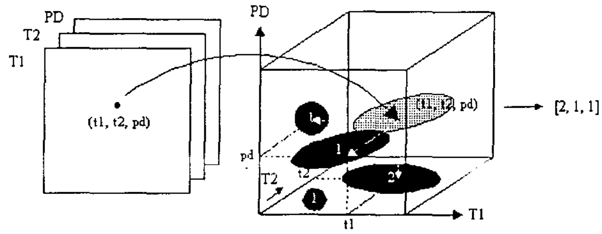
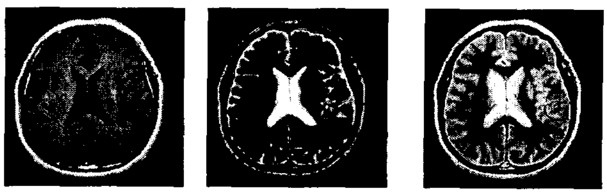


Fig. 3. Acquiring process of 3D cluster's label pair at each cerebrum pixels.

Fig. 3 Shows acquiring process of cluster's label pair at each pixel in cerebrum image. Segmenting process of cerebrum image is used FCM algorithm with 3D cluster's centroid as it's centroid.

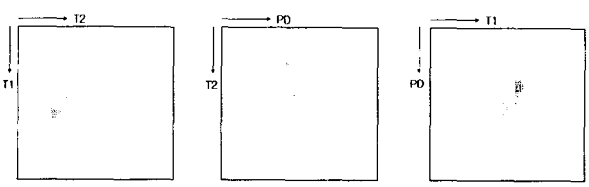
3. Experimental results and discussions

MR brain data used in this research is 256 x 256 8bits/pixel images, which acquired 256 x 256 16 bits/pixel Dicom 3.0 format from Siemens 1.5 Tesla Magnetom. We do this work at Pentium pro 200 MHz using Visual C++ 5.0. Fig. 4 shows the example of input image which used in this research. 2D histogram from T1-weighted image and T2-weighted image, PD image is shown in Fig. 5. Dark region represents densely distributed region of pixels.



(a) (b) (c)

Fig. 4. Input images (a) T1-weighted image, (b) T2-weighted image, and (c) PD image.



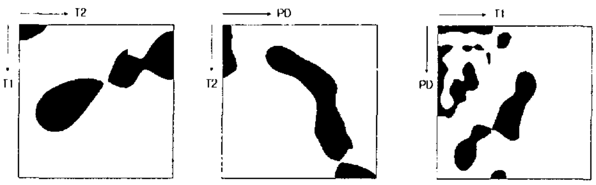
(a) (b) (c)

Fig. 5. 2 dimensional histogram (a) T1T2 histogram, (b) T2PD histogram, and (c) PDT1 histogram.

Table. 1. Variable range and optimal.

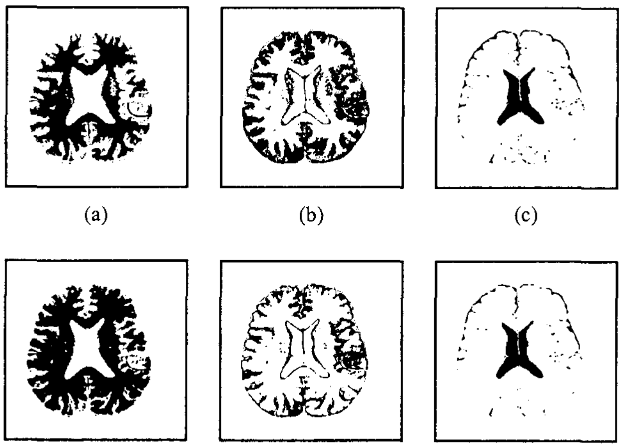
2D histogram of T1T2	Variable range	31 – 25
	Optimal scale	25
2D histogram of T2PD	Variable range	25 – 16
	Optimal scale	16
2D histogram of PDT1	Variable range	24 – 11
	Optimal scale	11

Table 1 shows the process of finding optimal scale of 2D histogram. In the case of input image, ten paths are made at graph structure for the case of 2D histogram of T1T2. Seven paths are ignored for new peak paths and variable range is acquired from the rest three paths as 38 to 14. Optimal scale is determined as 14. By the same methods, variable range and optimal scale for 2D histogram of T2PD and PDT1 was determined as the rest of table 1. Fig. 6 shows the optimal scale image and black region represents peaks.



(a) (b) (c)

Fig. 6. Optimal scale image (a) optimal scale image of T1T2, (b) optimal scale image of T2PD, and (c) optimal scale image of PDT1.



(a) (b) (c)

(d) (e) (f)

Fig. 7. The segmentation results (a)(b)(c) the result of proposed segmentation algorithm, (d)(e)(f) the result of single spectral analysis(T2-weighted image), (a)(d) white matter, (b)(e) gray matter, and (c)(f) CSF.

The result of proposed segmentation algorithm and the result of single spectral analysis[4] are compared in Fig. 7. Fig. 7(a) and (d) are the segmentation result of white matter. Fig. 7(a) is the result of proposed method and (d) is the result of single spectrum image. It is shown that (a) is more accurately segmented than (d). In the case of gray matter and CSF, proposed methods have also good results. White matter is thick in the result of single spectrum image cause gray matter is included at that region. CSF in the result of single spectrum image is thin cause boundary part of CSF is included at the gray matter. But the result of proposed method, white matter and gray matter, CSF are segmented accurately without inclusion of other region.

4. Conclusion

In this paper, we proposed an automated segmentation algorithm for MR brain images using T1-weighted, T2-weighted, and PD image complementarily. The proposed three-step segmentation algorithm was extracted cerebrum images and made 2D histogram from three cerebrum images. Peak images were made using scale space filtering and it's second derivatives. Graph structure was made and searched to determine optimal scale. We found 3D clusters in the 3D space composed of three optimal scale image. Outstanding clusters are determined among 3D clusters comparing the total pixel number and save their centroid values. Finally, cerebrum images are segmented using FCM algorithm with the outstanding cluster's centroid value as FCM algorithm's initial centroid value. The proposed method complements the defect being influenced upon initial centroid of the FCM algorithm with calculating accurate cluster's centroid. And also can get better segmentation results from the proposed segmentation algorithm with it's multi spectral analysis than the method of single spectral analysis.

The segmentation of MR images, which is valuable in analysis of MR data itself, becomes the basis of MR data compression, reconstruction of 3D image, and quantifying a specific tissue for medical examinations. In a future study, we are going to analyze the lesion volume quantitatively and reconstruct the 3D volume of MR data based on segmentation.

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