

# Graph Theory Based Algorithm for Magnetic Resonance Brain Images Segmentation

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**Abstract**—Image segmentation is often required as a preliminary and indispensable stage in the computer aided medical image process, particularly during the clinical analysis of magnetic resonance(MR) brain images. The segmentation of magnetic resonance image (MRI) is a challenging problem that has received an enormous amount of attention lately. In this paper, we propose a simple and effective segmentation method combining watershed algorithm and normalized cuts (CWNC) for MR brain images. An initial partitioning of the MRI into primitive regions is set by applying the watershed transform. The latter process uses a region similarity graph representation of the image regions. And then the graph is segmented by normalized cuts algorithm. The efficacy of the proposed algorithm is demonstrated by extensive segmentation experiments using both simulated and real MR images and by comparison with other published algorithms.

## I. INTRODUCTION

Magnetic resonance imaging (MRI) is an advanced medical imaging technique, which is widely used in many medical applications because of its high spatial resolution and soft-tissue contrast [1]. With the increasing size and number of medical images, the use of computers in facilitating their processing and analysis has become necessary. MRI possesses good contrast resolution for different tissues and has advantages over computerized tomography (CT) for brain studies [2]. Because of the advantages of MRI over other diagnostic imaging [3], the majority of researches in image segmentation pertain to its use for MRI images [4] [5].

The task of image segmentation can be stated as the partition of an image into a number of non-overlapping regions, each with distinct properties. In general, the interesting tissues in brain are white matter (WM), gray matter (GM), and cerebral spinal fluid (CSF). Changes in the composition of these tissues in the whole volume or within specific regions can be used to characterize physiological processes and disease entities [6] or to characterize disease severity [7]. Brain image segmentation of MRI means to specify the tissue type for each pixel or voxel in a 2D or 3D data set, respectively, on the basis of information available from

both MRI images and the prior knowledge of brain. It is an important first step in many medical research and clinical applications, such as quantification of tissue volume, visualization and analysis of anatomical structures, multimodality fusion and registration, functional brain mapping, detection of pathology, surgical planning, and surgical navigation. It is also a complex and challenging task due to the intrinsic nature of the image. The brain image has a particularly complicated structure and it always contains artifacts such as noise, partial volume effects and intensity inhomogeneity.

There are a lot of methods available for MRI image segmentation [4] [5]. Niessen et al. roughly grouped these methods into three main categories: classification-based methods, region-based methods and boundary-based methods [8]. In [5], the same categories are also adopted by Liew, and a review of them is provided. Classification-based methods classify and label each pixel to a particular tissue class according to a certain criterion, including thresholding algorithm [9], statistical classification [3] and cluster algorithm [10]. The typical region-based methods are region growing technique [11] and watershed segmentation [12], which attempt to segment an image by identifying the various homogeneous regions that correspond to different objects in an image. Unlike above two categories, boundary-based methods rely on the gradient features near an object boundary as a guide for segmentation. Edge detection [13], deformable templates [14] and active contours [15] belong to this category. Just as pointed out in [5] and [8], the methods in the first two categories are limited by the difficulties due to intensity inhomogeneities, partial volume effects and susceptibility artifacts, while those in the last category suffer from spurious edges. Besides these three categories, there are also some other segmentation algorithms. Atlas guided approaches [16] [17] attempt to incorporate knowledge about brain anatomy into the segmentation process. Such knowledge-based a priori information, if applied appropriately, can significantly improve the accuracy of the final segmentation results. Machine learning approach such as artificial neural networks (ANNs) has also been used in MRI segmentation [18] [19]. J. De Bock[26] proposed a method using watershed algorithm and normalized cuts algorithm for image segmentation. They adopted a region adjacency graph when cut the graph which we did not.

In view of the problems mentioned above, plenty of approaches and their corresponding improvements have been proposed to ensure the accuracy and rapidity of image segmentation. But there is still much work to be done to overcome their drawbacks. Considering the abundant approaches,

Manuscript received July 4, 2008. This work was supported by the Training Fund of NENU'S Scientific Innovation Project (No. NENU-STC07018) and the Fund of Jilin Provincial Science & Technology Department (No. 20070322).

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it is difficult to present a totally new theory. However, attempts at utilizing knowledge on other domains, especially the Graph Theory, should be highly appreciated. In this paper we have proposed a novel segmentation method combining watershed algorithm and normalized cuts (CWNC) for MR brain images.

The rest of this paper is organized as follows. In Section 2, we present the standard watershed transform and normalized cuts algorithm. Our proposed algorithm is described in Section 3. Experimental and comparison results are presented in Section 4 and we conclude this paper in Section 5.

## II. WATERSHED TRANSFORM AND NORMALIZED CUTS

### A. Watershed Transform

The watershed transform is the method of choice for image segmentation in the field of mathematical morphology[20]. In geography, a watershed is the ridge that divides areas drained by different river systems. A catchment basin is the geographical area draining into a river or reservoir. The watershed transform applies these ideas to gray-scale image processing in a way that can be used to solve a variety of image segmentation problems. A gray-scale image is recognized as a topological surface, where the values of  $f(x, y)$  are interpreted as heights. We can visualize the image as the three-dimensional surface. If we imagine rain falling on this surface, it is clear that water would collect in the two areas labeled as catchment basins. Rain falling exactly on the labeled watershed ridge line would be equally likely to collect in either of the two catchment basins. The watershed transform finds the catchment basins and bridge lines in a gray-scale image. The gradient magnitude is used often to preprocess a gray-scale image prior to using the watershed transform for segmentation. The gradient magnitude image has high pixel values along object edges, and low pixel values everywhere else. Ideally, then, the watershed transform would result in watershed ridge lines along object edges. In this paper we employ the gradient watershed transform as initial segmentation.

### B. Normalized Cuts

Normalized cuts algorithm [21] is an approach for solving the perceptual grouping problem in vision. Rather than focusing on local features and their consistencies in the image data, the approach aims at extracting the global impression of an image. It treated image segmentation as a graph partitioning problem. The normalized cuts criterion measures both the total dissimilarity between the different groups as well as the total similarity within the groups. It showed that an efficient computational technique based on a generalized eigenvalue problem can be used to optimize this criterion. The method used the eigenvectors and eigenvalues of a matrix derived from the pairwise similarities of pixels. The normalized cuts algorithm consists of the following steps:

1. Given an image or image sequence, set up a weighted graph  $G = (V, E)$  and set the weight on the edge connecting

two nodes to be a measure of the similarity between the two nodes.

2. Solve  $(D - W)x = \lambda Dx$  for eigenvectors with the smallest eigenvalues.

3. Use the eigenvector with the second smallest eigenvalue to bipartition the graph.

4. Decide if the current partition should be subdivided and recursively repartition the segmented parts if necessary.

## III. CWNC ALGORITHM

Spectral methods use the eigenvectors and eigenvalues of a matrix derived from the pairwise similarities of pixels. The problem of image segmentation based on pairwise similarities can be formulated as a graph partitioning problem in the following way: consider the weighted undirected graph  $G = (V, E, W)$  where each node  $v_i \in V$  corresponds to a locally extracted image features, e.g. pixels and the edges in  $E$  connect pairs of nodes. A weight  $w_{ij}$  is associated with each edge based on some property of the pixels that it connects (e.g., the difference in intensity, location or some other local attribute). Let  $\Psi = \{V_i\}_{i=1}^k$  be a multi-class disjoint partition of  $V$  such as  $V = \cup_{i=1}^k V_i$  and  $V_i \cap V_j = \Phi, i \neq j$ . Image segmentation is reduced to the problem of partitioning the set  $V$  into disjoint non-empty sets of nodes  $(V_1, \dots, V_k)$ , such similarity among nodes in  $V_i$  is high and similarity across  $V_i$  and  $V_j$  is low. Normalized cuts [21] considered each pixel of the image as the node  $v_i$  in the graph, and the weights on the edge which were represented by the similarity matrix, the size of the similarity matrix is  $n$  by  $n$  ( $n$  is the number of pixels in the image). The solution in measuring the goodness of the image partitioning is the minimization of the normalized cuts as a generalized eigenvalue problem. The running time of the algorithm is  $O(mn)$ , where  $n$  is the number of pixels and  $m$  is the number of steps Lanczos[22] takes to converge. On the  $100 \times 200$  test image, the normalized cuts algorithm takes about 2 minutes on Intel Pentium 2.40GHz machines. In order to lessen the computation time, we need to reduce the size of the similarity matrix.

In this paper we replace the individual pixels by micro segments in order to reduce the number of nodes in the graph. However, it is very important that the atomic regions will already yield a meaningful segmentation. Watershed segmentation is a classical and effective method for image segmentation in grey scale mathematical morphology that meets these requirements. The method, in a wide perspective, has been applied into biomedical applications [23].

### A. Initial Segmentation

Watershed transform was employed as the initial segmentation because it yield a meaningful segmentation result. First, we obtain the gradient image of the MRI, which has high pixel values along the edges, and low pixel values everywhere else that will remove the local minima. And then we apply the gradient watershed transform[20] on the gradient magnitude image. After segmentation, the small regions are regarded as atomic regions. They are homogeneous and the

edges contained in the image also correspond to segment boundaries. Fig. 1 shows the initial segmentation result.

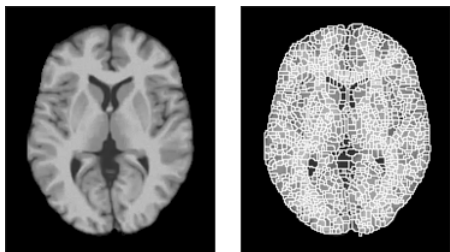


Fig. 1. Initial segmentation using watershed transform. (a) Original image. (b) After watershed transform.

### B. CWNC

First we use the watershed transform to divide the MRI into regions, and treat each atomic region as the node in the graph and connecting each pair of nodes by an edge. The goal is to construct a weighted undirected graph and then cut the graph into different parts. Given a partition of nodes of a graph  $V$ ,  $N = |V|$ . The weight on the edge should reflect the likelihood that the two regions belong to one object. Using just the mean brightness value of each region and their spatial location, we can define the graph edge weight connecting the two nodes  $i$  and  $j$  as:

$$w_{ij} = e^{-\frac{\|F_{(i)} - F_{(j)}\|_2^2}{\sigma_I^2}} * S_{ij},$$

if region  $i$  is the neighbor of the region  $j$ , or region  $j$  is the neighbor of the region  $i$ , then  $S_{ij} = 1$ , otherwise  $S_{ij} = 0$ .  $F_{(i)}$  is the mean intensity of region  $i$ .

$W$  is the similarity matrix defined above with  $W(i, j) = w_{ij}$ . When the similarity matrix  $W$  is constructed, Solve for the eigenvectors with the smallest eigenvalues of the generalized eigensystem:

$$D^{-\frac{1}{2}}(D - W)D^{-\frac{1}{2}}x = \lambda x,$$

where  $D$  is an  $N * N$  diagonal matrix with  $d$  on its diagonal,  $d(i) = \sum_j w(i, j)$  is the total connection from node  $i$  to all other nodes.

Since  $W$  is sparse, and also the size of the similarity matrix is small (just the square of the number of the regions), so the matrix-vector computation is only  $O(n)$ . Once the eigenvectors are computed, we can partition the graph into pieces using the second smallest eigenvector. After the graph is broken into pieces, we can recursively run our algorithm on the partitioned parts.

In summary, our proposed algorithm (CWNC) consists of the following steps:

1. Initial segment the MR image into atomic regions with watershed transform.
2. Compute the mean of each atomic region.
3. Given a set of nodes, set up a weighted graph  $G = (V, E)$ , compute the weight on each edge by:

$$w_{ij} = e^{-\frac{\|F_{(i)} - F_{(j)}\|_2^2}{\sigma_I^2}} * S_{ij},$$

and summarize the information into  $W$  and  $D$ .

4. Solve for the eigenvectors with the eigenvalues of the generalized eigensystem:

$$D^{-\frac{1}{2}}(D - W)D^{-\frac{1}{2}}x = \lambda x.$$

5. Partition the graph into pieces using the eigenvectors.

## IV. EXPERIMENTAL RESULTS ANALYSIS AND COMPARISON

The proposed algorithm was implemented in Matlab on a PC with Intel Pentium 4 2.40GHz processor and 512M RAM and tested on the simulated and real MR images which were gained from the McConell Brain Imaging Center at the Montreal Neurological Institute, McGill University[25]. Because the ground truth of segmentation for real MRI brain images is not usually available, it is impossible to evaluate the segmentation performance quantitatively. However, Brainweb provides simulated brain database which includes a set of realistic MRI data volumes produced by an MRI simulator. Fuzzy c-means (FCM) algorithms with spatial constraints (FCM\_S) have been proven effective for MR image segmentation. The two different methods FCM and its extension FCM\_S methods are used in our experiments for comparison.

In this section, we present the methods on 2-D brain images and the extracranial tissues such as skull, meninges and blood vessels have been removed from all images prior to applying any segmentation algorithm. The number of tissue classes in the segmentation is set to three, which corresponds to gray matter (GM), white matter (WM) and cerebrospinal fluid (CSF). Background pixels are ignored in our experiment.

We first evaluate the visual performance on simulated MR phantom. Fig. 2 demonstrate the comparison of the result between FCM, FCM\_S and our proposed algorithm. Fig. 2(b) is the simulated image corrupted by 5% noise and 20% intensity inhomogeneities. The result Fig. 2(e) of our method is similar to the true tissue classification Fig. 2(a). FCM and FCM\_S however, show the misclassification and speckling in the present of noise in Fig. 2(c) and Fig. 2(d). Another experiment on simulated MR phantom is shown in Fig. 3.

The superiority of our algorithm is also demonstrated on real MRI images. We then evaluate the visual performance on MR data. Fig. 4 shows the results from and FCM, FCM\_S and CWNC on a real image corrupted by intensity inhomogeneities.

We can see that FCM was unable to correctly classify the image, FCM\_S yielded a better result while CWNC gained a much better result by performing in a global way.

To measure the segmentation accuracy, we also apply the quantitative evaluation of performance by defining the misclassification ratio (MR), which is given by:

$$MR = \frac{\text{number of misclassified pixels}}{\text{total number of pixels}}$$

As the table I demonstrated, the MR columns show that as the percentage of noise is increased, the errors for all the

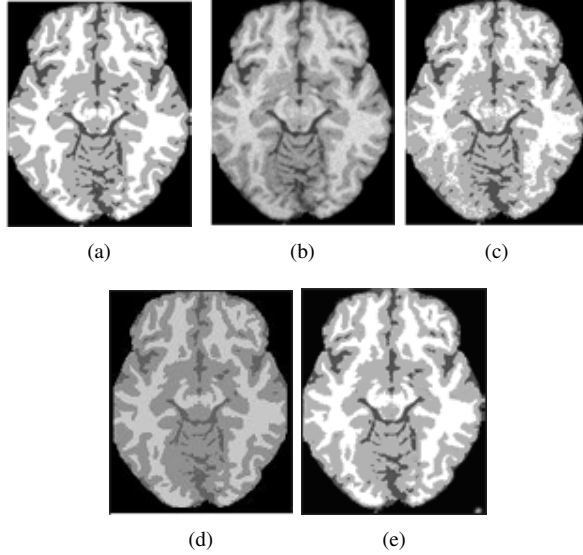


Fig. 2. Simulated MR phantom results: (a) True tissue classification. (b) Simulated MR image corrupted by 5% noise and 20% intensity inhomogeneities. (c) Result of FCM segmentation. (d) Result of FCM-S segmentation. (e) Result of our proposed method. Parameter setting:  $\sigma_I = 0.07$ .

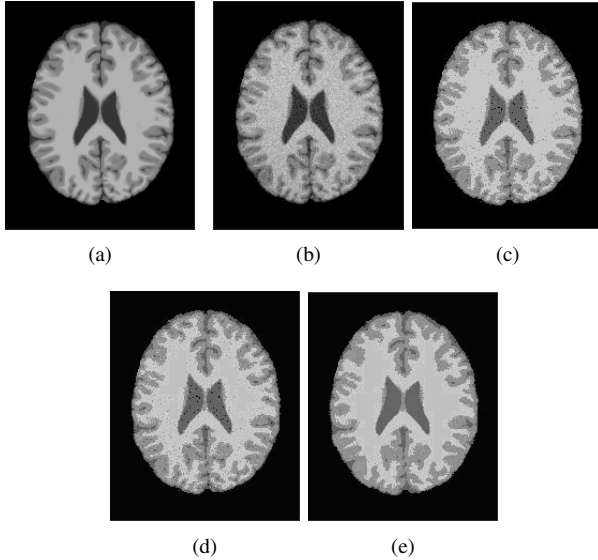


Fig. 3. Simulated MR phantom results: (a) True tissue classification. (b) Simulated MR image corrupted by 7% noise and 20% intensity inhomogeneities. (c) Result of FCM segmentation. (d) Result of FCM-S segmentation. (e) Result of our proposed method. Parameter setting:  $\sigma_I = 0.05$ .

methods also increase. Our method, however, is much more robust to increased inhomogeneity and noise than the other two methods.

Three different indices (false positive ratio  $\gamma_{pf}$ , false negative ratio  $\gamma_{fn}$ , and similarity index  $\rho$  [24]) are exploited for each of three brain tissues as quantitative measures to validate the accuracy and reliability of our method.

For a given brain tissue  $i$ ,  $i = 1, 2, 3$  for CSF, GM and WM respectively, suppose that  $A_i$  and  $B_i$  represent the sets of voxels labeled into  $i$  by the "ground truth" and by our method

TABLE I  
MISCLASSIFICATION RATIO (MR) FOR SIMULATED MR RESULTS

Method	3%N20%	5%N20%I	7%N20%I
FCM	5.579%	7.856%	11.347%
FCM-S	4.878%	5.986%	7.562%
CWNC	4.254%	5.014%	6.295%

respectively.  $|A_i|$  denotes the number of voxels in  $A_i$ . The widely-used false positive ratio  $\gamma_{pf}$ , representing the error due to the misclassification in a brain tissue  $i$ , is defined as  $\gamma_{pf} = (|B_i| - |A_i \cap B_i|)/|A_i|$ . Likewise, the false negative ratio  $\gamma_{fn}$ , representing the error due to the loss of desired voxels of  $i$ , is defined as  $\gamma_{fn} = (|A_i| - |A_i \cap B_i|)/|A_i|$ . The similarity index  $\rho$  is an intuitive and plain index to consider the matching volume/area between  $A_i$  and  $B_i$ , defined as  $\rho = 2|A_i \cap B_i|/(|A_i| + |B_i|)$ .  $\rho$  is sensitive to discrepancies in shape, location, and size;  $\rho > 0.7$  indicates an excellent similarity [24]. The validation results of Fig. 2 are shown in Table II.

TABLE II  
SIMILARITY INDICES FOR DIFFERENT METHODS IN FIG. 2.

Method	Indices	CSF	GM	WM
FCM	$r_{fp}$	18.81	8.98	11.87
	$r_{fn}$	11.88	12.76	7.45
	$\rho$	85.17	87.25	91.29
FCM-S	$r_{fp}$	12.37	10.11	9.28
	$r_{fn}$	11.34	11.11	8.25
	$\rho$	88.20	89.34	91.28
CWNC	$r_{fp}$	5.35	1.52	5.51
	$r_{fn}$	2.38	5.69	0.77
	$\rho$	96.19	96.24	96.81

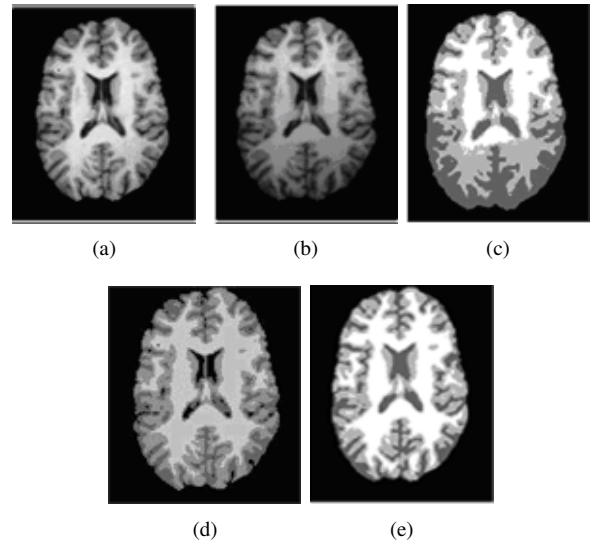


Fig. 4. FCM, FCM-S and CWNC segmentation in the case of intensity inhomogeneities: (a) Original image. (b) Corrupted image of (a). (c) FCM segmentation. (d) FCM-S segmentation. (e) CWNC segmentation. Parameter setting:  $\sigma_I = 0.03$ .

## V. CONCLUSIONS

In this paper, we proposed a simple and effective algorithm for automatic tissue classification. This method has been applied to the segmentation of MR brain structures with intensity inhomogeneities and noise. The experimental results are promising and outperform the standard fuzzy C-means and its extension FCM\_S. And the computational time of our proposed method is much smaller than other algorithms. We acknowledge that the result is preliminary and more researches are required in the future. And future works will focus on the preservation of useful details while removing the intensity inhomogeneities and noise.

## VI. ACKNOWLEDGMENTS

The authors would like to thank all the members of PAMI for providing great help and cogency advice. The authors would also like to express sincere appreciation to the reviewers for their comments.

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