

Brain MR Image Segmentation with Spatial Constrained K-mean Algorithm and Dual-Tree Complex Wavelet Transform

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Abstract In brain MR images, the noise and low-contrast significantly deteriorate the segmentation results. In this paper, we propose an automatic unsupervised segmentation method integrating dual-tree complex wavelet transform (DT-CWT) with K-mean algorithm for brain MR image. Firstly, a multi-dimensional feature vector is constructed based on the intensity, the low-frequency subband of DT-CWT and spatial position information. Then, a spatial constrained K-mean algorithm is presented as the segmentation system. The proposed method is validated by extensive experiments using both simulated and real T1-weighted MR images, and compared with the state-of-the-art algorithms.

Keywords Medical image segmentation · MR images · Dual-tree complex wavelet transform · K-mean algorithm

Introduction

Magnetic resonance imaging (MRI) is an important medical imaging technique for the early detection of abnormal changes in tissues and organs. In the analysis of MR images, segmentation of brain tissues plays a crucial role in three-dimensional volume visualization, quantitative morphometric analysis and structure function mapping for both scientific and clinical investigations.

However, automatic brain MR image segmentation is a complex and challenge task due to the complicated structure of brain.

Various methods have been applied for medical image segmentation, most notably thresholding [1], region-growing [2, 3], graph based [4], level set based [5], snake [6], clustering [7–10], and statistical methods. Clustering is the most popular method in medical image segmentation for its simplicity and efficiency, with expectation-maximization, K-mean, Fuzzy C-Means, and neural network algorithms being the typical methods.

Generally, using multi-spectral images (T1-, T2-, PD-weighted images) will usually generate segmentation results superior to those using single modality images [11]. In fact, extracting enough features from a single modality image, beyond simple pixel intensities, could make the segmentation based on it potentially comparable to a multi-modal approach [12]. In our work, we partition T1-weighted brain MR images into three main tissue types: white matter (WM), gray matter (GM), and cerebrospinal fluid (CSF), which is a topic of great importance.

In image segmentation, effective feature presentation could improve the final segmentation results. Wavelet theory provides a powerful framework to decompose images into different scales and orientations, and has been used in medical image processing [13]. The discrete wavelet transform (DWT) can provide multiple features of brain MR images [12]. However, since DWT is not shift invariant and has poor directional selectivity [14], a pseudo-Gibbs phenomena is exhibited in the neighborhood of singular points, alternating undershoot and overshoot of a specific target level [15].

In this paper, we introduce several features which are robust to shift and noise variation. Firstly, we use the original intensity-feature which retains the inherent information. Secondly, we exploit the dual-tree complex wavelet transform (DT-CWT) [14] to construct DT-CWT-feature, which can perfectly overcome the shortcoming of the discrete wavelet transform (DWT). Thirdly, we adopt spatial position (X, Y) to

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generate the position-feature which can capture complicated spatial layout of the individual tissues.

Based on the effective feature presentation, an automatic unsupervised segmentation method is presented for T1-weighted brain MR images with a high noise level and low contrast. Although the spatial feature is exploited in our method, we don't use any probability map to obtain the prior information. Therefore, registration processes are not required and the applicability of our method can be extended to diseased brains and neonatal brains.

The rest of this paper is organized as follows. Section 2 briefly describes the dual-tree complex wavelet transform. Our segmentation method is proposed in Section 3. In Section 4, experimental results are presented, followed by the conclusion in Section 5.

Preliminaries

In this section, we will briefly review the dual-tree complex wavelet transform (DT-CWT). DT-CWT was developed to overcome the shortcomings of DWT by Kingsbury [14]. It is a particularly suitable tool for feature extraction, as it is directionally selective, approximately shift invariant, limited redundant. Moreover, DT-CWT is efficient to detect the line- and curve-singularities (edges) which DWT is inefficient.

DT-CWT is implemented using two critically-sampled real DWTs in parallel, which utilize two trees of real filters to produce the real and imaginary parts of the complex coefficients. The odd and even length bi-orthogonal linear-phase filters are placed as shown to achieve the correct relative signal delays, so that the constructed complex wavelet is approximately analytic, which brings approximately magnitude/phase shift invariance of the wavelet coefficients. The two set of filters are also designed to give perfect reconstruction at each level and have some other good properties, including finite support and vanishing moments.

Similar to 2-D separable DWT, 2-D DT-CWT is implemented with the row-column implementation of 1-D DT-CWT. Differently, 2-D DT-CWT associates with six 2-D complex wavelet functions and produces six bandpass subbands of complex coefficients at each level, which are strongly oriented at angles of $75^\circ, 45^\circ, 15^\circ, -15^\circ, -45^\circ, -75^\circ$ respectively, as shown in Fig. 1.

The DT-CWT expansion of an image $f(x)$ can be represented by the translations and dilations version of six complex wavelet functions $\left\{ \psi_{j,k}^b \right\}_{j \leq J, k \in \mathbb{Z}^2}^{b \in B}$ and a complex scaling function $\left\{ \Phi_{J,k} \right\}_{k \in \mathbb{Z}^2}$ [16], that is,

$$f(x) = \sum_{k \in \mathbb{Z}^2} c_{J,k} \Phi_{J,k}(x) + \sum_{b \in B} \sum_{j \leq J} \sum_{k \in \mathbb{Z}^2} d_{j,k}^b \psi_{j,k}^b(x)$$

where $x=(x_1, x_2)$ denotes 2-D variable, $B = \{\pm 75^\circ, \pm 45^\circ, \pm 15^\circ\}$ denotes six subband directions, $c_{J,k}$ and $d_{j,k}^b$ refer to corresponding complex coefficients at the level- J low-frequency subband and the level- j high-frequency subbands.

Our proposed segmentation method

In this section, a detailed description about our proposed segmentation method is presented. In the preprocessing stage, the brain region is extracted and intensity inhomogeneities are corrected using the expectation-maximization segmentation (EMS) software¹ (based on [17]). Then, a multi-dimensional feature vector is extracted for each pixel. Finally, the segmentation system—spatial constrained K-mean algorithm is proposed for automatic T1-weighted brain MR image segmentation.

Features extraction

In this paper, we exploit T1-weighted MR images, and expand each pixel into a multi-dimensional feature vector, characterizing the image data beyond simple pixel intensities.

Spatial position-feature

The high complexity of spatial structure is an inherent part of the brain image. For the brain image segmentation, more features should be obtained from local spatial information. Generally, the intra variability of the intensity feature within a tissue (bias) is significantly less than the inter variability among different tissues in a local region. Appending spatial position-feature (X, Y) to a multi-dimensional feature vector could capture the complicated spatial layout of the individual tissues. In our method, we directly use spatial position information as the features, which is different from other methods [18] obtaining the spatial information from the templates or probability maps. So registration method is not needed in our method. In addition, incorporating with spatial position information, our algorithm builds the corresponding relationship between the cluster centroids and localized regions of brain MR image.

DT-CWT-feature

In order to generate the feature which is robust to shift and noise variation, we create the DT-CWT-feature from the low-frequency subband of the one-level DT-CWT. Integrated with the DT-CWT-feature, the segmentation result of our algorithm is better than that of wavelet transform with K-mean algorithm (named as WTK-mean), due to its properties of approximate

¹ <http://www.medicalimagecomputing.com/EMS/>



Fig. 1 A low-frequency subband and six high-frequency subbands which are oriented at 75°, 45°, 15°, -15°, -45°, -75° by the 3 level DT-CWT of the simulated brain MR image slice (z=86) shown on the left

shift invariance and good directional selectivity. The performance of our algorithm outperforms that of WTK-mean particularly with a high noise level, and we will discuss their comparison results in Section 4.2.

Hence, for each pixel p , a multi-dimensional feature vector is constructed as the input vector of our algorithm. It has several components: original intensity-feature I_p , DT-CWT-feature D_p , and spatial position-feature $S_p=[X_p, Y_p]$, denoted by $f_p=[I_p, D_p, S_p]$.

Segmentation system

Spatial constrained K-mean algorithm

K-Means algorithm is an unsupervised clustering algorithm that classifies the input data points into multiple classes based on their inherent distance from each other. The algorithm assumes that the data features form a vector space and tries to find natural clustering in them. The points are clustered around centroids $c_i, i=1, \dots, K$ which are obtained by minimizing the objective

$$D = \sum_{i=1}^K \sum_{p_j \in C_i} \|f_{p_j} - c_i\|^2$$

where there are K clusters $C_i, i=1, 2, \dots, K$. f_{p_j} is the feature vector of pixel p_j , and c_i is the centroid of all the pixels $p_j \in C_i$.

K-mean algorithm is often suitable for biomedical image segmentation since the number of clusters (K) is usually known for images of particular regions of human anatomy. In biomedical applications, the spatially varying intensity change of a biomedical structure is usually caused by inhomogeneity in the process of image acquisition, such as the inhomogeneous distribution of the magnetic field gradient in MR imaging.

In our work, appending spatial position-feature to the multi-dimensional feature vector could make pixels clustered into the same centroid belonging to the same local region. In experiments, we set K according to the size of MR brain image. The algorithm is composed of the following steps:

- Initial step: Initialize the centroids with K random vectors $c_i^{(1)}=[c_{iI}^{(1)}, c_{iD}^{(1)}, c_{iS}^{(1)}], i=1, 2, \dots, K$.
- Repeat the following steps until the clustering results of all the pixels do not change anymore.
 - Assignment step: Assign each pixel to the closest centroid by $c_i^{(t)} = \{p_j : \|f_{p_j} - c_i^{(t)}\|^2 \leq \|f_{p_j} - c_m^{(t)}\|^2 \forall m, 1 \leq m \leq K\}$, where t is the iterative time.

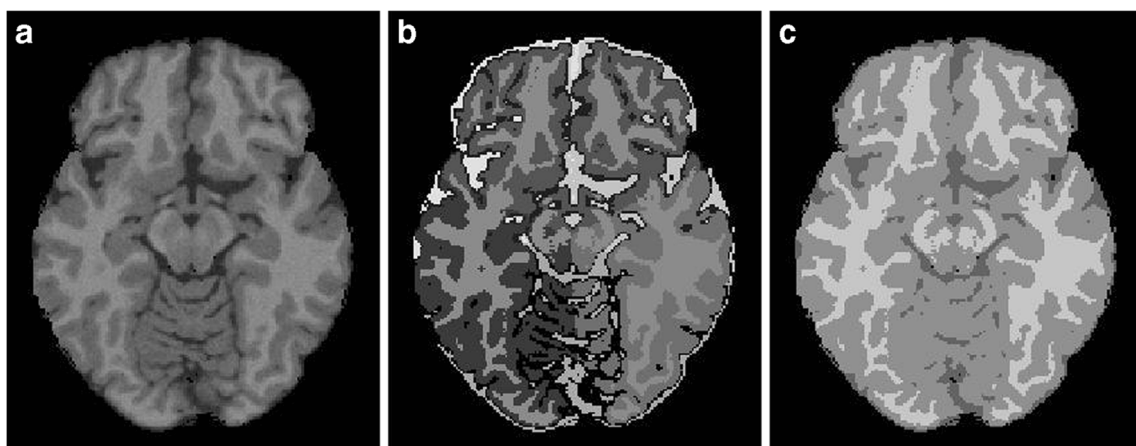


Fig. 2 A simulated schematic representation about spatial constrained K-mean algorithm on simulated brain MR slice (z=59) with 3% noise level and 0% intensity inhomogeneity. **a** Original image slice. **b** The result

after clustering with spatial constrained K-mean algorithm, where we label the pixels clustered to same centroid with same intensity. **c** The segmentation result with our method

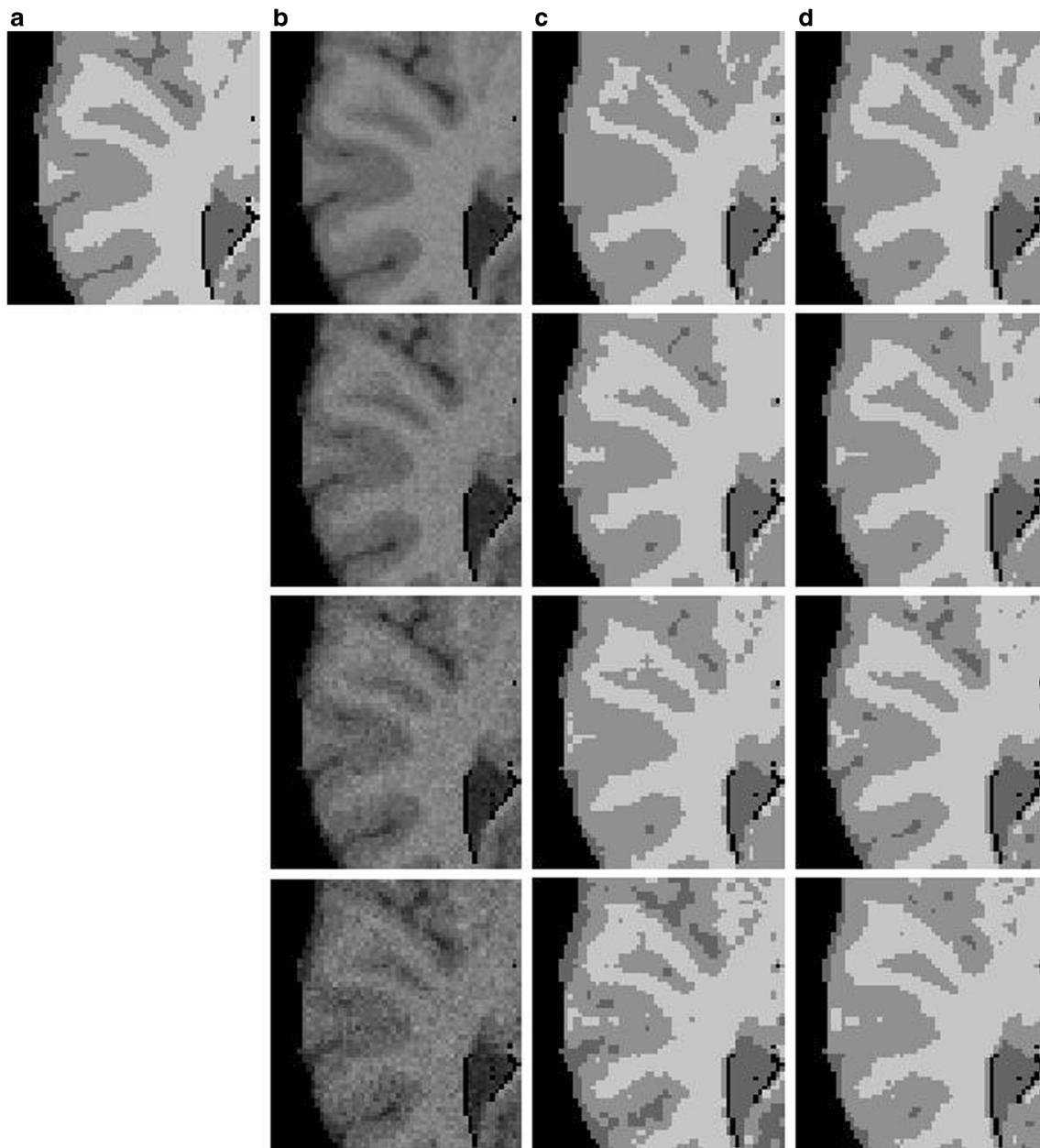


Fig. 3 Comparing the segmentation results of simulated T1-weighted MR slice 78 with different noise levels and 0 % intensity inhomogeneity using WT-K-mean and our algorithm. Upper row: 3 % noise level.

Second row: 5 % noise level. Third row: 7 % noise level. Forth row: 9 % noise level. Columns: **a** ground-truth, **b** original image, **c** WTK-mean algorithm, **d** our algorithm

- Update step: Calculate the new centroids of the new clusters by $c_i^{(t+1)} = \frac{1}{|C_i|} \sum_{p_j \in C_i^{(t)}} f_{p_j}$

Figure 2 presents a simulated schematic representation about spatial constrained K-mean algorithm on simulated brain MR slice ($z=59$) with 3 % noise level and 0 % intensity inhomogeneity, where we mark the pixels clustered to the same centroid with the same random intensity in Fig. 2b. So, each tissue is represented with multiple clusters, and each cluster corresponds to a localized region of a certain brain tissue. In a

local region, the intra variability of the intensity feature with a tissue (intensity inhomogeneities) is generally less than the inter variability among different tissues. Therefore, intensity inhomogeneities to some extent could be overcome.

Labeling the clustering centers

After clustering with spatial constrained K-mean algorithm, each tissue is represented with multiple clusters. A cluster i (denoted by C_i) has a centroid $c_i = [c_{ib}, c_{id}, c_{is}]$ corresponding to the input feature vector $f_p = [I_p, D_p, S_p]$, and the cluster related

to the same tissue have approximate centroid values on c_{iI} and c_{iD} . In our work, we adopt the centroid value c_{iD} to estimate the tissue label of cluster i , which could suppress the noise effect compared with the value c_{iI} .

To automatic labeling clusters with the tissue class, Bayesian clustering method is used $\text{label}(C_i) = \arg \max_{j \in \{1,2,3\}} p(\text{tissue } j|C_i)$, where $p(\text{tissue } j|C_i)$ is the posterior probability of cluster C_i belonging to tissue j (CSF, GM and WM). So each cluster is labeled by one tissue class, which provides the final segmentation map. We apply the expectation-maximization (EM) algorithm to calculate the posterior probabilities of clusters belonging to each tissue class in an unsupervised manner. Fig. 2c is the segmentation result of the source image (Fig. 2a) with our method.

The EM algorithm iterates between computing the posterior probabilities $p(\text{tissue } j|C_i)$ and estimating the mean u_j , variance σ_j^2 , prior probability π_j as follows:

- Initialize the mean u_j , variance σ_j^2 , cardinal N_j of each tissue $j \in \{1,2,3\}$ by K-means clustering method and prior probability $\pi_j = N_j/N$ (N is the total number of the clusters).
- E-step: compute the posterior probability of cluster i belonging to tissue j by Bayes formula

$$p(\text{tissue } j|C_i) = \frac{\pi_j p(C_i|\text{tissue } j)}{\sum_{k=1}^3 \pi_k p(C_i|\text{tissue } k)}, j = 1, 2, 3.$$

We assume that the probability density function follows Gaussian distribution, that is, $p(C_i|\text{tissue } j)$ has the form

$$p(C_i|\text{tissue } j(u_j, \sigma_j)) = \frac{1}{\sqrt{2\pi}\sigma_j} \exp\left[-\frac{(c_{iD}-u_j)^2}{2\sigma_j^2}\right], j = 1, 2, 3,$$

where u_j and σ_j^2 are the mean and variance of the clusters related to tissue j .

- M-step: Update the prior probability π_i of tissue j , the mean u_j and variance σ_j^2 :

$$\pi_j = \frac{\sum_i p(\text{tissue } j|C_i)}{N}$$

$$u_j = \frac{\sum_i p(\text{tissue } j|C_i) c_{iD}}{\sum_i p(\text{tissue } j|C_i)}$$

$$\sigma_j^2 = \frac{\sum_i p(\text{tissue } j|C_i) (c_{iD}-u_j)^2}{\sum_i p(\text{tissue } j|C_i)}$$

Table 1 Comparing the segmentation results of six different algorithms provided by IBSR with our method using Tanimoto similarity index

Method	Source	GM		WM	
		Mean	Std.Dev.	Mean	Std.Dev.
Adaptive MAP	IBSR	0.56	0.13	0.57	0.18
Biased MAP	IBSR	0.56	0.17	0.56	0.21
Fuzzy c-means	IBSR	0.47	0.12	0.58	0.20
MAP	IBSR	0.55	0.16	0.55	0.21
Tree-structure k-means	IBSR	0.48	0.12	0.57	0.20
Maximum-Likelihood	IBSR	0.54	0.16	0.55	0.21
Our proposed method		0.70	0.04	0.63	0.05

Experimental results

Database and similarity indices

Two brain MR image databases are used in our experiments. One is simulated MR image database obtained from the BrainWeb Simulated Brain Database.² The other is the real MR database taken from the Center for Morphometrics Analysis, Massachusetts General Hospital Repository (IBSR).³ These databases all provide the ground truth for quantitative validation. The number of tissue classes for segmentation is set to three, which corresponds to CSF, GM and WM. Background pixels are ignored in the segmentation, and extracranial tissues are removed from all images prior to segmentation with the ground truth. We correct the intensity inhomogeneity using the expectation-maximization segmentation (EMS) software package (based on [17]). To quantify the overlap between the segmentation results and the ground truth for each tissue, Dice similarity index [19] and Tanimoto similarity index [20] are adopted in our experiments.

The efficiency of DT-CWT-feature

To illustrate the efficiency of DT-CWT-feature, we compare the segmentation results of WTK-mean (with db4 wavelet transform feature), referring to the ground truth. Figure 3 demonstrates segmentation results on a single slice ($z=78$) with varying noise levels and 0 % intensity inhomogeneity.

The segmentation results of WTK-mean are shown in the third column of Fig. 3. Although the noise could be suppressed by the db4 wavelet transform-feature in the low noise level, there are still some boundary regions of different tissues which are not partitioned accurately. Integrated with DT-

² <http://www.bic.mni.mcgill.ca/brainweb>

³ <http://www.cma.mgh.harvard.edu/ibsr>

CWT-feature, our algorithm could suppress the noise effect and obtain more robust segmentation results in the tissue boundary regions. The segmentation results of our algorithm are exhibited in the forth column of Fig. 3.

Comparing the performance of our algorithm with other methods on real MR data

20 normal T1-weighted real data sets from IBSR are taken to validate the efficiency of our proposed approach. These data sets contain varying levels of difficulty, with worst scans consisting of low contrast and large intensity inhomogeneities. Six different segmentation algorithms are provided as part of IBSR website for comparison, which are adaptive Map (amap), biased MAP (bmap), fuzzy c-means (fuzzy), maximum a posteriori probability (map), tree-structure k-mean (tskm), and maximum-likelihood (mlc) algorithm. The overlap metric used by the IBSR repository is Tanimoto coefficient. The comparison results using mean and standard deviation are shown in Table 1. Our algorithm produces better segmentation results than most of others.

Conclusions

In this paper, an automatic unsupervised segmentation method—spatial constrained K-mean algorithm is presented for T1-weighted brain MR images. Our algorithm adopts a multi-dimensional feature vector which consists of intensity-feature, DT-CWT-feature and spatial position-feature as the input vector. The DT-CWT-feature based on the low-frequency subband enhances the robust of our method to the shift and noise variation. The spatial position-feature enables to capture the complicated spatial layout of the individual tissues. It should be noted that our method does not use an atlas to obtain the prior information. Therefore, registration processes are not required and the applicability of our method can be extended to diseased brains and neonatal brains in the further research.

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