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Thalamus Segmentation from Diffusion Tensor Magnetic Resonance Imaging

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Abstract— **In this paper, we propose a semi-automatic thalamus and thalamus nuclei segmentation algorithm from Diffusion Tensor Magnetic Resonance Imaging (DT-MRI) based on the mean-shift algorithm. Comparing with existing thalamus segmentation algorithms which are mainly based on K-means algorithm, our mean-shift based algorithm is more flexible and adaptive. It does not assume a Gaussian distribution or a fixed number of clusters. Furthermore, the single parameter in the mean-shift based algorithm supports hierarchical clustering naturally.**

I. Introduction

Thalamus is the relay center for nerve impulses in the brain. It mediates communication among sensory, motor, and associative brain regions. Axons from almost every sensory system connect here as the last site before the information reaches the cerebral cortex. Information received from the diverse brain regions is passed on to the cortex through the thalamus. Anatomically, thalamus is the largest, most internal structures of the diencephalon consisting of dual lobe masses of gray matter. It is located at the rostral end of the mid brain on each side of the third ventricle. Each lobe is about 4 centimeters. Motor nuclei of the thalamus receive signals from the striatum and cerebellum and project into the motor and premotor areas of the cerebral cortex. The thalamus play a major role in the regulation of consciousness, alertness, arousal, and attention and is thus considered part of the limbic system.

Thalamus and thalamus nuclei segmentation have become more and more essential for a wide range of clinical and research applications. For example, thalamus changes in terms of volume and intensity are involved in a large number of diseases, such as schizophrenia, Parkinson's disease and multiple sclerosis, etc. Conventional imaging modalities such as Computerized Tomography (CT) or Magnetic Resonance Imaging (MRI) however, do not provide the necessary image contrast to differentiate the individual thalamic nuclei. On the other hand, a new non-invasive imaging modality Diffusion Tensor Magnetic Resonance Imaging (DT-MRI) can relate the image intensities to the relative mobility of tissue water molecules [1]. In DT-MRI, a tensor describing local water diffusion is calculated for each voxel from measurements of diffusion in several directions. Since water diffusion along neural fiber tracts of the brain is highly anisotropic, DT-MRI had been used to study the brain connectivity by extracting the fiber tracts from the brain white matter. Most recently, researchers have started to use DT-MRI for segmentation purposes. Wiegell et al. [6] were one of the first to segment thalamic nuclei directly from the DT-MRI data by using a k-means algorithm. Behrens et al. [2] proposed an algorithm to identify the thalamic nuclei by mapping the connections between the thalamus and the cortex. In [4] Jonasson et al. presented a method for segmenting the thalamus and its subnuclei by propagating a set of coupled level sets through a region based force defined from the similarity measure between the most representative tensor of each level sets and its neighboring voxels.

In this paper, we propose a semi-automatic thalamus and thalamus nuclei segmentation algorithm from Diffusion Tensor Magnetic Resonance Imaging (DT-MRI) based on the mean-shift algorithm [3]. Comparing with existing thalamus segmentation algorithms which are based on K-means algorithm [6] or use K-means as an initialization [4], our mean-shift based algorithm is more flexible and adaptive. It does not assume a Gaussian distribution or a fixed number of clusters. Furthermore, the single parameter in the mean-shift based algorithm supports hierarchical clustering naturally. We will briefly review the background on Diffusion Tensor Magnetic Resonance Imaging and Mean Shift Clustering in Section II. The main algorithm for thalamus and thalamus nuclei segmentation will be described in Section III. Finally the conclusion and some future work directions are discussed in Section IV.

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II. Background

A. Diffusion Tensor Imaging

Diffusion Tensor Magnetic Resonance Imaging (DT-MRI) is a recent MR imaging modality. In Diffusion Tensor MRI, a tensor describing local water diffusion is acquired for each voxel. The geometric nature of the diffusion tensors can quantitatively characterize the local structure in tissues such as bone, muscles, and white matter of the brain. A good review on DT-MRI can be found in [1] and [5].

In general, the symmetric 3x3 diffusion tensor D has six degrees of freedom (number of independent coefficients in a matrix representation). To estimate the tensor, then, at least six measurements (taken from different non-collinear gradient directions) are needed, in addition to the baseline image data S_0. Thus for each slice in the data set, seven images need to be collected with different diffusion weightings and gradient directions. Let S_0 represents the signal intensity in the absence of a diffusion-sensitizing field gradient and S_k the signal intensity in the presence of gradient $g_k = (g_{k_x}, g_{k_y}, g_{k_z}), k = 1, \ldots, 6$. the equation for the loss in signal intensity due to diffusion is given by the Stejskal-Tanner formula:

$$ln(S_k) = ln(S_0) - \gamma^2\delta^2(\Delta - \delta/3)g^T Dg, \qquad (1)$$

where γ is the gyromagnetic ratio of hydrogen H (protons), δ is the duration of the diffusion sensitizing gradient pulses and Δ is the time between the centers of the two pulses. The tensor D can then be computed by solving this system of six equations (Eq. (1)).

B. Mean Shift Clustering

Mean shift is a powerful general purpose technique for clustering scattered data [3]. Instead of assuming a fixed number of clusters as is common with other clustering methods (K-means, EM), mean shift extracts the modes of the density function. We will brief review the mean shift algorithm in the following. For a complete description of mean shift, please refer to the original paper [3].

Given an arbitrary set of n points $\chi = x_1, \ldots, x_n$ in the d-dimensional Euclidean space R^d. The multivariate kernel density estimate obtained with kernel $K(x)$ and window radius h, computed in the point x is defined as:

$$\hat{f}(x) = \frac{1}{nh^d}\sum_{i=1}^{n} K(\frac{x - x_i}{h}), \qquad (2)$$

where $K(x)$ is the spherically symmetric kernel function satisfying

$$K(x) \geq 0, \qquad \int_{R^d} K(x)dx = 1 \qquad (3)$$

and h is a smoothing parameter called the bandwidth.

Assume now that we are interested in subdividing scattered data χ into a set of clusters. It is natural to consider the points where $\hat{f}$ defined by Eq. (2) has local maxima as centers of the clusters. The simplest method to find the local maxima of the $\hat{f}$ is to compute the gradient of $\hat{f}$ and use a hill-climbing process to map each input point to its local maxima (i.e. mode) defined by $\hat{f}$. These resulting modes can then be used to select cluster shapes using basins of attraction, and can have very nontrivial shapes–unlike k-means clustering where points are simply assigned to the nearest cluster center. The single bandwidth parameter h, allows the number of clusters to be chosen in terms of a length scale in the input point space.

From Eq. (2) and Eq. (3) we can compute the gradient of $\hat{f}$:

$$\nabla\hat{f}(x) = \frac{2c}{nh^{d+2}}\sum_{i=1}^{n} g(||\frac{x - x_i}{h}||^2)m(x), \qquad (4)$$

where $g(x) = -k'(x)$. $m(x)$ is the mean shift vector and is given by

$$m(x) = \frac{\sum_{i=1}^{n} x_i g(||\frac{x-x_i}{h}||^2)}{\sum_{i=1}^{n} g(||\frac{x-x_i}{h}||^2)} - x, \qquad (5)$$

i.e., the difference between the weighted mean, using the kernel g for weights, and x, the center of the kernel (window). The general mean shift clustering procedure consists of the following two steps:

1) Initialize: y_0= x;
2) Update by hill climbing: $y_{j+1} = y_j + m(y_j)$ until convergence.

In the case when each point x_i in the data set χ has two components of different nature, i.e. $x_i = (p_i, q_i)$: $p_i \in P, q_i \in Q$, the mean shift algorithm can be extended with separable kernels:

$$\hat{f}(x) = \frac{1}{nh_1{}^{d_1}h_2{}^{d_2}}\sum_{i=1}^{n} K_1(\frac{p - p_i}{h_1})K_2(\frac{q - q_i}{h_2}). \qquad (6)$$

III. Thalamus and Thalamus Nuclei Segmentation

In this section, we will describe our framework for thalamus and thalamus nuclei segmentation from DT-MRI data based on the previously described mean shift algorithm. Since there are two different domains of similarity–tensor and spatial in the DT-MRI image data, we employ the extended mean shift algorithm with separable kernels as defined by Eq. (6). In particular, K_1 is the kernel in the tensor domain with parameter h_1, K_2 is the kernel in the tensor domain with parameter h_2.

In the tensor domain, we choose a distance metric based on the Frobenius norm:

$$d(D_{x_1}, D_{x_2}) = \sqrt{Trace((D_{x_1} - D_{x_2})(D_{x_1} - D_{x_2})^T)}$$

and a normal kernel profile, D_{x_1}, D_{x_2} are the tensor matrices at voxel x_1, x_2, respectively. The bandwidth parameter h_1 was set as 1, however the algorithm did not seem to be very sensitive to different choices of h_1.

In the spatial domain, the kernel function $K_2(x)$ is chosen to be the normal kernel with the Euclidian distance metric. The spatial bandwidth parameter h_2 chosen will determine the scale of features detected, so different values may be desired based on the data set quality, features of interest, etc. In our experiment, we found that consistent thalamus segmentation results can be obtained by setting the bandwidth parameter h_2 in the x, y, z dimensions as 5, 5, 2, respectively. For thalamus nuclei segmentation, a relatively smaller bandwidth such as 3, 3, 1 seems to work quite well. The non-uniform scale of the parameter in the z dimension is due to the low resolution of the image data in the z dimension.

Figure 1 shows a 2D slice view of the mean-shift based segmentation result at both the thalamus as well as the thalamus nuclei level. More specifically, Figure 1 (a) is the segmentation result by using a 5 by 5 by 2 bandwidth, while Figure 1 (b) is the segmentation result obtained by a 3 by 3 by 1 bandwidth. From Figure 1 (a), we can clearly see the anterior and posterior parts of the thalamus. More detailed nuclei structures can be seen in Figure 1 (b), which is quite close to the histological atlas of the human thalamus with nuclei outlined by black lines [2]. Note that, the initial thalamus segmentation is conducted interactively, i.e. the user need to identify the two clusters (anterior and posterior of the thalamus) from other clusters. Since the thalamus is bounded by relatively homogenous structures such as the fiber tract and CSF, this step can be done quite easily. The initially segmented thalamus will then serve as the mask for the subsequent thalamus nuclei segmentation, which will be conducted automatically with a smaller bandwidth parameter. A 3D rendering of the thalamus nuclei segmentation result is shown in Figure 2.

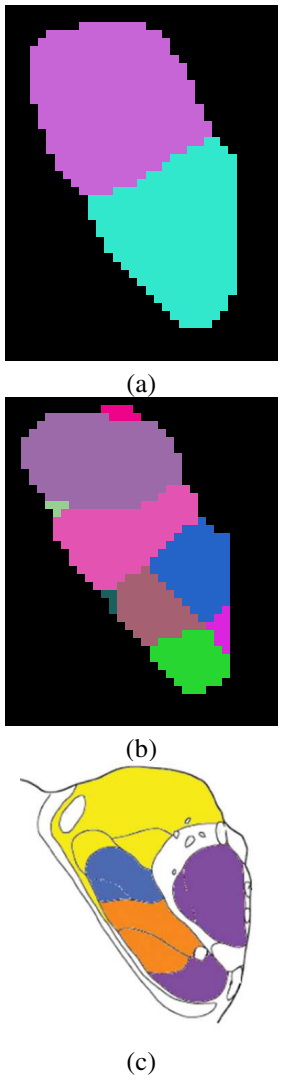

Fig. 1. Mean-shift based thalamus and thalamus nuclei segmentation results. (a) The segmented anterior and posterior parts of the thalamus by setting the bandwidth parameter h_2 as 5 by 5 by 2. (b) The segmented thalamus nuclei by setting the bandwidth parameter h_1 as 3 by 3 by 1. (c) The histological atlas of the human thalamus with nuclei outlined by black lines (Image courtesy of Behrens et al. [2]).

IV. Discussion

The main contribution of the paper is the application of the powerful mean shift clustering algorithm for thalamus segmentation from the DT-MRI data. Comparing with existing thalamus segmentation algorithms ([6], [4]) which are based on K-means algorithm, our mean shift based algorithm has several potential advantages; (1) Since the mean shift algorithm is based on non-parametric density estimation, it does not assume the data is always Gaussian, hence it is more generic and flexible. (2) Unlike K-means algorithm, the mean-shift algorithm does not assume a fix number of clusters, hence it is more adaptive to the diversity of the dataset. (3) There is only one parameter in the mean shift based algorithm, the bandwidth parameter, which controls the scale of the features detected, (4) and by setting the bandwidth parameter from large to small, mean shift naturally supports hierarchical clustering, as have been shown in this paper on thalamus and thalamus nuclei segmentation.

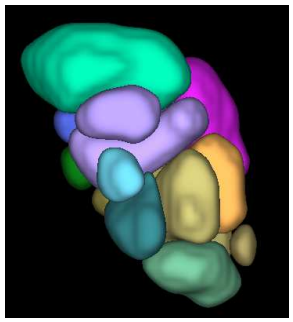

Fig. 2. A 3D view of the thalamus nuclei segmentation results.

There are two main directions to further improve the thalamus segmentation results; (1) Currently, the thalamus segmentation is conducted semi-automatically, i.e. the user has to pick the two distinct clusters (anterior and posterior parts of the thalamus) from other neighboring clusters such as the fiber tracts and CSF. Although this is quite easy to do, it would be even better if the thalamus can be automatically segmented; Moreover, a post-processing active-contour based diffusion step (as is done in [4]) might be able to further smooth the nuclei boundary obtained from the clustering algorithm. The diffusion operation may also be able to remove those very small clusters as can be seen from Figure 1 (b). (2) We would like to work closely with domain specialists such as neurobiologists to verify and validate the segmentation results, and to identify the thalamus nuclei structures. The collaboration with domain specialists will also help us to choose the best bandwidth parameter for the mean shift algorithm to create clinically most meaningful segmentation results.

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