Exploring the Structure of the Thalamus with DTI

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Purpose: From atlas data that used histological staining it is known that the thalamus consists of several compartments or nuclear groups [1]. Significant individual differences in size and shape of the Thalamus render the comparison with cyto-architectonic atlas data difficult. Investigating the structure of the Thalamus on individual subject DTI data has become more and more popular in recent years. The role of the Thalamus as relay station that filters information going to the cortex is the reason for contrast within the Thalamus on DTI data which cannot be observed on standard anatomical images. Here, different methods for the segmentation of structures within the Thalamus are presented. Advantages and disadvantages of the individual methods are discussed.

Outline: Different types of DTI processing for the segmentation of structures within the Thalamus are presented: k-means clustering [2], level set methods [3], local diffusion classification [4], and connectivity analysis [5].

Wiegell and colleagues proposed to use clustering algorithms to identify individual nuclear groups within the Thalamus [2]. An example of their results is shown in Fig.1. They used k-means clustering to find nuclear groups with similar diffusion tensor profile. The similarity of the tensor is additionally weighted by spatial proximity. For this approach the number of clusters that should be found needs to be known prior to segmentation.

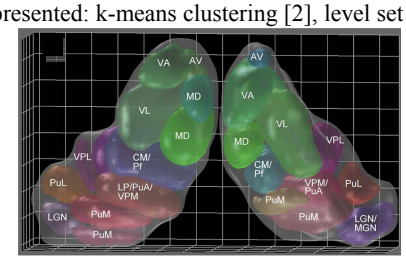

Figure 1: Surface renderings of the automatic segmentation [2]. The clusters are color coded by the principal eigenvector of the mean diffusion.

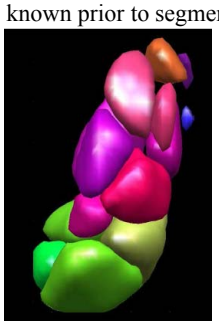

Figure 2: Surface renderings of the level set segmentation [3].

The approach proposed by Jonasson and colleagues [4] uses more advanced data driven similarity measures for local diffusion tensors. An example of their results is shown in Fig.2. Their level set technique is able to determine similarity without weighting of the special proximity. This allows the correct identification of more elongated structures, which tend to be split by k-means clustering. Jonasson and colleagues initialize their algorithm with the centroids of the nuclei determined by the k-means approach [2]. It therefore also finds 14 nuclear groups.

Both methods above require prior segmentation of the whole Thalamus because automatic segmentation with similarity measures needs to be spatially restricted to return reasonable results. Both methods also require tuning of the algorithm parameters. These parameters are determined heuristically and need adjustment for different data qualities. This makes the reproduction of their results difficult.

The method proposed by Unrath and colleagues does not use advanced similarity measures but classifies voxels according to the similarity of the local diffusion direction with a given set of reference directions [4]. This method is able to produce results that are reproducible in a large subject population without prior masking of the Thalamus as a whole. The classification uses only part of the Tensor and is therefore more susceptible to noise. The use of a fixed set of reference directions also requires a registration of subject data to a standard space. Errors in the registration will affect the segmentation results.

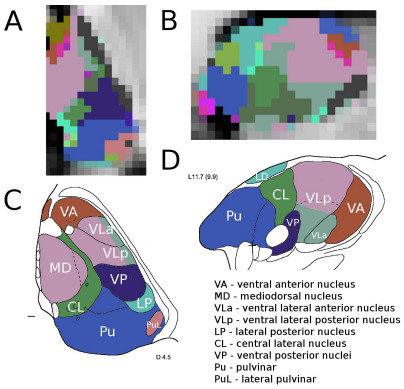

Figure 3: Segmentation results for the simple classification used in [4].

A completely different approach uses the connectivity of the voxels within the Thalamus to regions within the Thalamus [5]. Connectivity of the nuclear groups within the Thalamus was determined previously in invasive studies. The interpretation of the segmentation results is therefore straight forward. To determine the connectivity probabilistic fiber tracking is seeded in each voxel of the whole segmented Thalamus the voxel is classified according to the segmented cortical regions it is connected with. The number of regions that are detected in the Thalamus depends on the number of segmented cortical regions. The segmentation with this method depends to a large part on the quality of the fiber tracking results.

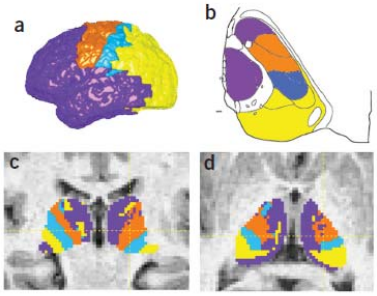

Figure 4: The segmentation results for four cortical regions [5].

Summary: There are a number of different approaches to determine sub-structures within the Thalamus on DTI data. Each method has advantages and disadvantages that need to be considered on selecting a tool for a specific study or task. Table 1 gives an overview over the methods. Fast rough results can be generated without advanced classification methods [4]. More detail in the segmentation, especially if you use prior knowledge can be gained with clustering methods [2,3]. If your focus is on the connectivity and you have enough time to perform fiber tracking use the connectivity based method [5].

	K-means clustering [2]	Level set [3]	Local diffusion classification [4]	Connectivity [5]
Segmented Thalamus	Needed	Needed		Needed
Segmented Cortical Regions				Needed
Weighting Parameter Tuning	Needed	Needed		
Tensor Information Used	Full Tensor	Full Tensor	EV1	Fibertracking*
Registration to Standard Space			Required	

Table 1: Features of the DTI based segmentation techniques. EV1 means the dominant diffusion orientation.
* The amount of tensor information used in the connectivity based method depends on the fiber tracking algorithm

References: [1] A. Morel, M. Magnin, and D. Jeanmonod. J. Comp. Neurol. 387:588-630, 1997. [2] M. R. Wiegell, D. S. Tuch, H. B. W. Larsson, and V. J. Wedeen. Neuroimage, 19:391–401, 2003. [3] L. Jonasson, P. Hagmann, C. Pollo, X. Bresson, C. Wilson, R. Meuli, and J.-P. Thiran. Signal Processing 87:309-321, 2007. [4] A. Unrath, U. Klose, W. Grodd, A. C. Ludolph, and J. Kassubek. Neurosci Lett, 434(3):322–327, 2008. [5] T. E. J. Behrens, M. W. Woolrich, M. Jenkinson, H. Johansen-Berg, R. G. Nunes, S. Clare, P. M. Matthews, J. M. Brandy, and S. M. Smith. Magn Reson Med, 50(5):1077–1088, 2003.