Segmentation of Thalamic Nuclei using a Modified k-Means Clustering Algorithm and High Resolution Quantitative Magnetic Resonance Imaging

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Introduction: Patient outcome in minimally invasive stereotactic neurosurgical procedures depends on the ability to accurately locate the desired functional region in the deep brain while avoiding the surrounding anatomy. Currently, electrophysiological exploration and histological atlases are required to define the surgical target within the thalamus due to the lack of contrast within this region in conventional MR images. Due to individual variability in the size and location of the nuclei, generic atlases may be highly inaccurate. Here we introduce a method for segmenting the individual thalamic nuclei using high resolution quantitative MRI, providing improved target visualization and decreasing the reliance on generic anatomical atlases.

Methods: Whole brain T1 and T2 maps were acquired from 4 healthy volunteers using the DESPOT1 and DESPOT2 quantitative imaging methods[1]. Specific imaging parameters were: DESPOT1: TR/TE = 11.7ms/2.4ms, α = 4°,15°, BW = 15.6kHz. DESPOT2: TR/TE = 11.7ms/2.4ms, α = 15°,55°, BW = 62.5kHz. FOV and matrix size was 25cm x 25cm x 13cm and 256 x 256 x 128. Total imaging time was ~17 minutes for each volunteer. The maps were non-linearly registered[2] to a standardized brain[3] in Talairach space[4] and the left thalamus was manually segmented. The 3D centre-of-mass (COM) coordinates of the primary thalamic nuclei (obtained from an anatomical atlas[5]) were mapped onto the T1 and T2 maps and used as seeds for an automated segmentation algorithm. A genetic algorithm based segmentation algorithm incorporating aspects of the k-means clustering algorithm[6] was to divide the thalamus into distinct regions by minimizing the total T1 and T2 variance within each region.

Results: Figure 1 shows the starting COM points superimposed on a volunteer's T1 map. 3D results from the superior and lateral aspects of the four thalamic segmentations are shown in Fig.2. Strong similarity is observed between the 4 results, an expected consequence of registering the datasets to the same common template. Comparison of slices from one segmentation result with slices from a representative anatomical atlas are shown in Fig.3 and reveals good correspondence in nuclei size, shape and location. Comparison of segmentation and atlas COM coordinates reveals an average absolute Euclidean distance difference of 3.3mm across all nuclei and the four volunteers. The mean absolute Euclidean distance difference in the anteroposterior, mediolateral and dorsoventral directions were 1.7mm, 2.2mm and 1.3mm.

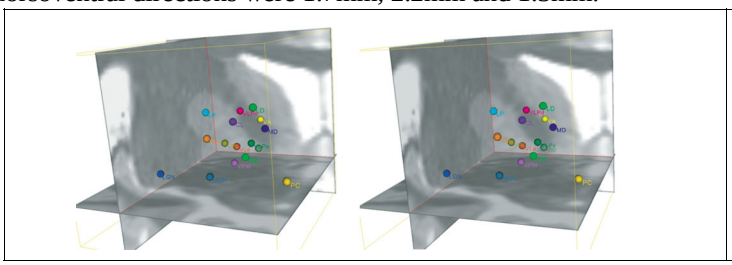

Figure 1: COM points for each of the primary thalamic nuclear divisions superimposed on a volunteer's T1 map. Data is presented as a stereo-pair.

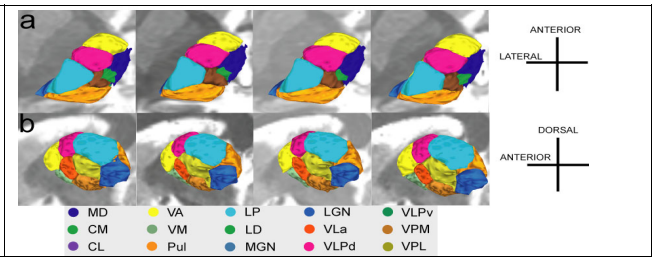

Figure 2: Segmentation results of all four volunteers from

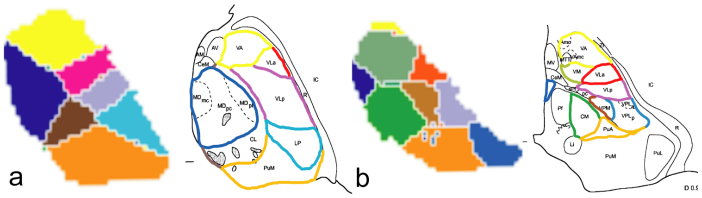

Figure 3: Comparison of automatic segmentation results with equivalent sections from the Moral histological atlas. Colour coding has been used to identify consistent nuclei between the two results. Close agreement is seen between the two results

Discussion and Conclusions: The results presented here demonstrate the first attempt to automatically segment the major nuclei of the thalamus on the basis of their T1 and T2 relaxation times. Strong agreement is seen between COM coordinates calculated from the four individual segmentations and coordinates obtained from a classic histological atlas, with a mean distance difference of 3.3mm. Visual comparison of the segmentation results with the histological atlas also demonstrates good agreement in size, shape and location of the nuclear divisions. These promising results point to the potential utility of this approach in surgical planning and image-guidance for stereotactic functional deep brain procedures.

References: [1] Deoni SCL et al. MRM 49:515-526, 2003, [2] Collins DL et al. J Comp Assist Tomogr 18:192-205, 1994, [3] Holmes CJ et al. J Comp Assist Tomogr 22:324-333, 1998, [4] Talairach J et al. Masson & Cie, Paris, 1957, [5] Morel A et al. J Comp Neurol, 387:588-630, 1997 [6] Hartigan JA & Wong MA Appl Statist 28:100-108, 1979.