Automated identification of the human thalamic nuclei using local white-matter properties.

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We introduce a method for automatic segmentation of the thalamic nuclei. The method uses diffusion-weighted MR images to subdivide the thalamus in a predefined set of nuclei. The method relies on two basic assumptions. First, it assumes that white-matter fascicles’ orientation is homogeneous within each thalamic nucleus (Wiegell et al., 1999). Second, it assumes that nuclei are spatially homogeneous (Wiegell et al., 2003). Based on these assumptions thalamic nuclei are segmented by a weighted combination of local tensor information (Basser et al., 1994) and spatial coordinates.

The method avoids manual intervention by computing in each subject the dissimilarity (Pekalska and Duin, 2005) among voxels in the thalamic region. Dissimilarity represents the difference of each voxel from the rest of the voxels along each dimension; spatial position and diffusion tensor. We use multidimensional scaling (Bronstein et al., 2005) to produce a compact encoding of the dissimilarity information. This reduces processing time for the clustering algorithm. Finally, we use k-means clustering (Hartigan and Wong, 1979) to automatically segment the thalamic nuclei.

We tested the method on 15 human brains (Dougherty, et al., 2007). Thalamic segmentation shows high-level of inter-subjects reliability. The algorithm can identify most of the Thalamic nuclei. A different number of target nuclei can be requested; four to seventeen (Morel et al., 1994). We show a hierarchical organization of the Thalamic nuclei. Larger nuclei –obtained when requesting a low number of nuclei– are ulteriorly subdivided into smaller nuclei as the number of requested nuclei increases.

Recently there have been a number of attempts to automatically segment the thalamus (Broser et al., 2011, Mang et al., 2012). The proposed automatic segmentation algorithm is scalable, which means that it can combine different types of MR measurements, such as T1, T2 contrasts. The method is based on standard data analysis and processing tools (FreeSurfer, mrDiffusion and Matlab) and is freely available to the neuroscientific community.

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References:


