

Robust subdivision of the thalamus in children based on probability-distribution-functions calculated from probabilistic tractography.

P. J. Broser¹, F. Vargha-Khadem², and C. A. Clark³

¹Imaging and Biophysics Unit, UCL Institute of Child Health, London, London, United Kingdom, ²Developmental Cognitive Neuroscience Unit, UCL Institute of Child Health, ³Imaging and Biophysics Unit, UCL Institute of Child Health, London, United Kingdom

Introduction

It has been shown that a meaningful subdivision of the thalamus can be achieved at the group level by estimating the most likely cortical target by using probabilistic tractography [1]. Probabilistic tractography is a technique that estimates the likelihood of connection between two points in the brain by sampling the distribution of greatest diffusion directions in each voxel of the brain image. In this study a new method of normalizing and analyzing the data from the probabilistic tractography algorithm was developed. This method relies on anatomical evidence that every cortical area receives input from the thalamus. Therefore the probability of finding one path from the thalamus to any cortical mask is one. The new method normalizes the number of paths in each thalamic voxel by the total number of paths from every thalamic voxel to the given cortical mask. Each cortical mask is then analyzed independently from the others. The normalization thus generates distributions of probability of connectivity which can be analyzed on an individual basis. The method was applied to the imaging data of a cohort of children acquired for a separate study. A center-of-mass analysis was then used to illustrate the inter-individual robustness of this new method.

Methods

Subjects: 43 healthy children (22 girls and 21 boys) with age ranging from 8 to 13 (10.5 ± 1.5 years) were studied from whom informed consent was obtained.

MRI data acquisition: Diffusion tensor imaging (DTI) data were obtained along 20 non-collinear directions, with b values of 0 and 1000 s mm^{-2} on a 1.5 T Siemens Avanto scanner using to a double refocused spin echo EPI sequence. The acquisition was repeated 3 times and the resulting volumes were composed of 45 contiguous 2.5 mm slices (averaged for two acquisitions with TE = 89 ms) with reconstructed voxel size 2.5 mm isotropic. A T1-weighted 3D FLASH structural image was acquired using 176 contiguous sagittal slices, a $256 \times 224 \text{ mm}$ field of view and $1 \times 1 \times 1 \text{ mm}$ image resolution.

Tractography: probtrackx tool from the FMRIB Software Library was used to perform probabilistic tractography. The following parameters were used: curvature threshold = 0.2, maximum number of steps = 2000, Number of samples = 5000 and a step length of 0.5mm. Each voxel in the thalamus was used as a seed to draw samples from the connectivity distribution. For each voxel in the thalamus the number of samples that passed into each of the cortical masks was calculated.

Distributions of probability of connectivity: The data images containing the number of paths from each thalamic voxel to each given cortical mask were transferred from native diffusion-weighted MRI space into MNI space using nearest neighbor interpolation [2]. For each individual mask the total number of samples from each voxel in the thalamus into the given cortical mask (i) was calculated:

$$Total_i = \sum_{x \in \text{ThalamusMNI space}} S_i(x) \quad \text{with } S_i(x) : \text{Number of Samples from Voxel } x \text{ to Cortical Mask } i.$$

The number of samples in each voxel was divided by the total number of samples: $F_i(x) = S_i(x) / Total_i$

So the resulting number in every voxel reflects the fraction of this voxel to the total number of samples:
$$\sum_{x \in \text{ThalamusMNI space}} F_i(x) = 1$$

The $F_i(x)$ therefore represent a probability distribution function. Their magnitude reflects the relative probability to find a path to the cortical mask.

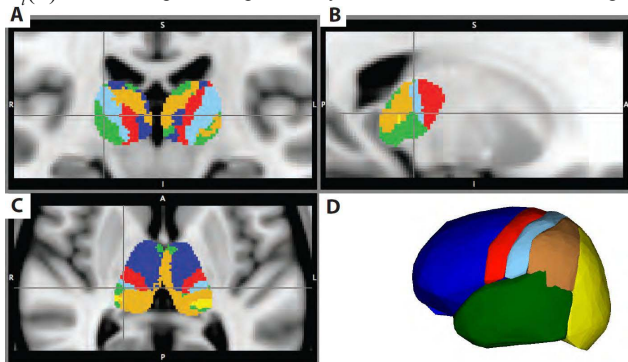


Figure 1: Structural parcellation of the thalamus using the “winner takes it all” method.

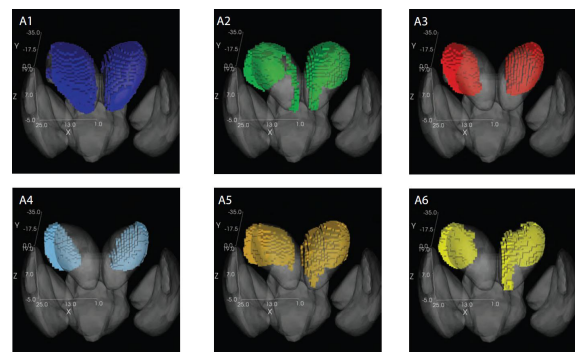


Figure 2: Comparison of the distribution of probability of connectivity images with the Mai anatomical atlas [4]

Results

Results from the ‘winner takes it all’ method [3] are shown in Figure 1 with the probability of connectivity images shown in Figure 2. Generally, lower standard deviations for thalamic volumes were found for the probability of connectivity compared with the ‘winner takes it all’ method. Thalamic substructure volumes in the paediatric cohort were similar to those found previously in adults and there was no evidence for a gender effect. The centre of mass analysis showed an average standard deviation of the mean position of the centre of mass $\pm 2 \text{ mm}$.

Discussion and conclusion

In summary, the method developed here is a suitable technique to analyze the substructures of the thalamus based on their likely cortical target in *individual* datasets. The data acquired for this study was processed to create a standard map of the thalamic substructures in children. The combination of the new method and the standard atlas offers the possibility to analyze the thalamus and its constituent substructures in individual data sets and might in future be used to further analyze changes in these substructures as a result of brain injury in children in much greater detail.

References

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