In-vivo Visualization of the Human Basal Ganglia Structure and Connectivity using High Resolution 7T MRI

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Introduction: Accurate localization of the basal ganglia (BG), surrounding structures of the midbrain such as the thalamus, and their anatomical connectivity patterns, is critical for clinical applications such as deep brain stimulation (DBS), and for improving our understanding of the changes in structural connectivity that lead to movement disorders. Insufficient resolution and/or contrast of standard imaging techniques and significant anatomical variability currently preclude the direct in-vivo visualization of the targets and connections of interest. Utilizing the advantages of high-field (7T) combined with an array of acquisition schemes, we have developed an imaging protocol and analysis pipeline, to generate a comprehensive, subject-specific, 3D model of the BG region and their connectivity pattern. We have successfully resolved and visualized several key fiber pathways such as the pallidothalamic and nigrostriatal tracts, and were able to **quantify** the probability of these connections with the rest of the basal ganglia. Finally, we successfully parcellate the BG structures based on their connectivity profile with other deep brain areas.

Method: Five healthy subjects were scanned on a 7T Siemens Avanto magnet using a 16-channel transmit/receive head coil and the following protocol: T1 MPRAGE and PD, 1 mm isotropic; axial and coronal high resolution T2s using a turbo spin echo sequence, 0.4x0.4x2 mm^3; axial and coronal Susceptibility-Weighted Imaging (SWI) using a 3D flow compensated gradient echo sequence, 0.4x0.4x1 mm^3; Diffusion-weighted imaging (DWI) using a single refocused 2D single shot spin echo EPI sequence, 1.5 mm isotropic, 128 direction at b=1500 s/mm^2 and 15 B0. DWI was corrected for eddy current distortions, motion and susceptibility distortions using FSL [1]. Fractional anisotropy (FA) maps were used to delineate the thalamus, putamen and caudate nucleus in both hemispheres. SWI and T2 images were used to delineate the internal and external segments of the globus pallidus, the substantia nigra and the subthalamic nucleus [2]. Masks were subsequently resampled into the DWI native space and visualy validated for accuracy in order to perform probabilistic tractography (Fig. 1). FSL's *bedpostx* and *probtrackx* were respectively used to model crossing fibers at each voxel (using a 3-fiber model) and estimate connectivity distributions between every pairs of masks.

Results & Discussion: Pathways were defined as the set of voxels exhibiting a probability of connection between both endpoints to be at least 10% of the maximum value of the probability map (Fig. 2). We are able to reliably identify major pathways of the basal ganglia circuits. Moreover, we quantify the probability of these connections for each structure with the rest of the basal ganglia (Fig. 4) and use this information to parcellate nuclei into distinct subregions (Fig. 3). This was achieved by labeling a voxel as connected to a certain structure if its probability of connection is at least 50% of the maximum value of the corresponding probability map. We present here, for the first time, a comprehensive 3D model based on the delineation, visualization and quantification in-vivo of the human basal ganglia, their structure and anatomical connectivity.

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References: [1] http://www.fmrib.ox.ac.uk/fsl [2] A. Abosch, E. Yacoub, K. Ugurbil, and N. Harel, An assessment of current brain targets for deep brain stimulation surgery using susceptibility-weighted imaging at 7T, Neurosurgery 67 (6), 2010

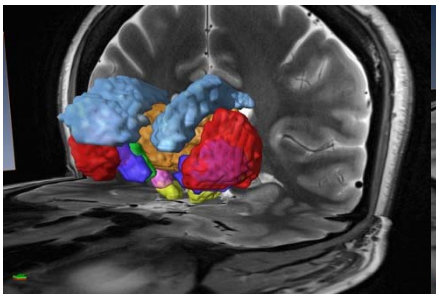

Fig. 1 - ROIs definition

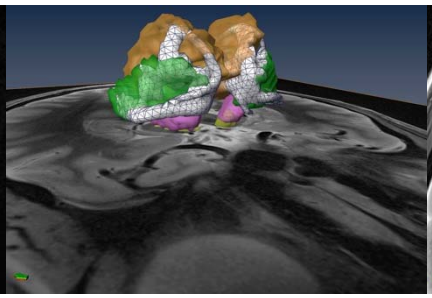

Fig. 2 - Pallidothalamic tract (wireframe)

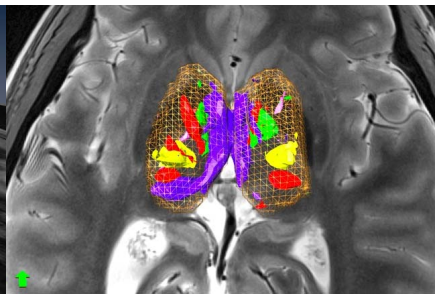

Fig. 3 - Thalamus parcellation

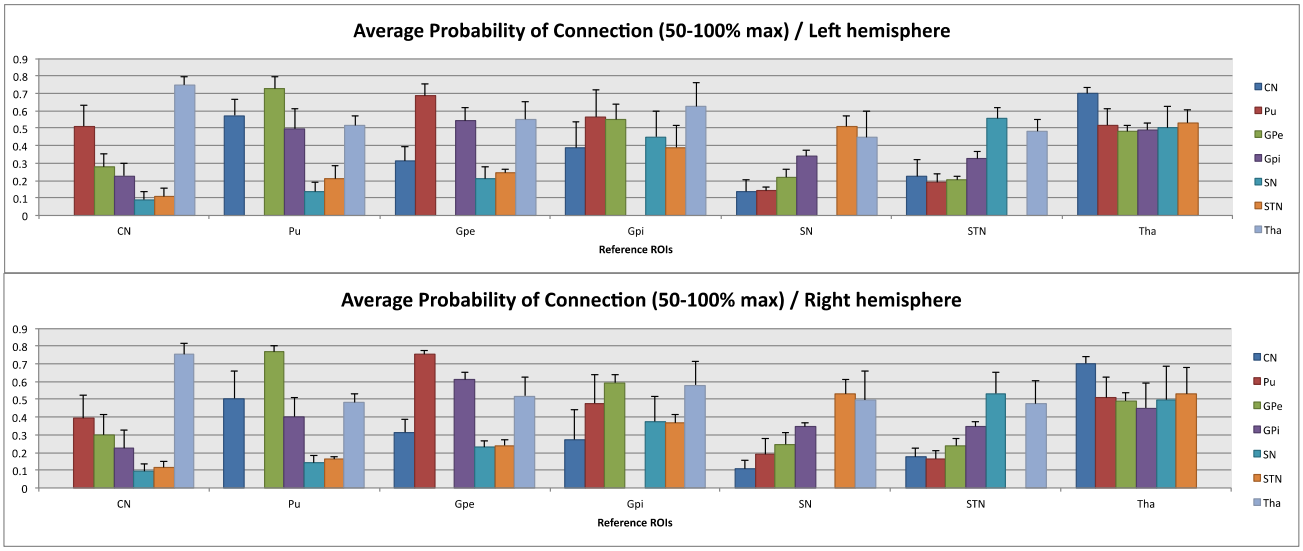

Fig. 4 – Average probability of connection and standard deviation for the basal ganglia and thalamus (N=5)