Probabilistic Atlas of the Connections between the basal ganglia and the cortex

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Introduction

The basal ganglia are topographically connected to cortical areas. These connections define motor, associative and limbic territories. These basal ganglia are therefore involved in motor as well as cognitive and behavioral functions. Dysfunction of basal ganglia territories leads to various neurological diseases that are specifically associated with each territory. In this abstract, we present the design of a surface probabilistic atlas of the connections between the basal ganglia and the interface between the white matter (WM) and the cortex. Such an atlas can be built on a population of healthy subjects as well as on a population of specific patients. Statistical tools can then be used to detect the regions with significant differences on the cortex that may correspond to underlying abnormalities of the striato-pallido-cortical connections. Such differences could yield new biomarkers of neurological pathologies.

Material and methods

In order to build a probabilistic atlas of the connections between the deep nuclei and the WM/cortex interface, T1-weighted data was used to segment both the basal ganglia and the cortex, while diffusion-weighted (DW) data was used to recover the fiber bundles connecting the deep nuclei to the cortex. Our study aimed at developing the methodology required to construct the probabilistic surface atlas of the cortico-striatal connections, and was conducted on a population of 10 healthy subjects that signed an informed consent. These subjects were part of TRACK-HD study.

Acquisition - Data were acquired on a Siemens Tim Trio 3T MRI system. Sequence parameters were as follows: **T1-weighted 3D MPRAGE** FOV=256mm, matrix 256x256, TE/TR=2.98ms/2.3s, TH=1.1mm, Phase FOV=93.8%, 160 slices per slab, RBW=240Hz/pixel; **Single-shot twice refocused spin-echo DW-EPI** FOV=256mm, TH=2mm, matrix 128x128, TE/TR=86ms/12s, GRAPPA 2, partial Fourier 6/8, 80 slices, RBW=1630Hz/pixel, b-value b=1000s/mm², 50 directions; DW data were corrected from susceptibility artifacts using a preliminary field map acquisitions with a fieldmap based reinterpolation and matched to the T1 data.

Deep nuclei segmentation: The basal ganglia were segmented from T1 volumes using a deformable model with regions in competition as described in [1]. Nuclei included the caudate nucleus, the putamen and the globus pallidus.

Tractography: A field of Orientation Distribution Functions (ODF) was computed from the DW data using the analytical QBall model described in [2]. A tractography was performed on the whole brain using a streamline deterministic algorithm constrained by the previous ODF field [3]. For each deep nucleus, the crossing fibers were isolated in order to compute the connectivity of that nucleus to the interface between the white matter and the cortex.

Surfacic coordinate system and subject template:For each subject, the WM/cortex interface was computed using FreeSurfer which allows a correspondence between the vertices of all the subjects thus providing a way to analyze the information on the surface in a common frame [4]. The interfaces of all the subjects were combined in order to construct an average surface for all the subjects on which the atlas will be elaborated.

Connectivity matrix: an occurrence matrix of the connections between each deep nucleus and each vertice of the WM/cortex interface was calculated for each subject, using the previous tractography results as well as the automatically delineated WM/cortex interface[5]. In order to take into account the uncertainty of tractography results, a Gaussian smoothing of the connectivity matrix was applied on the surface (σ=5mm).

Probabilistic atlas: Since a correspondence between the vertices of all the subjects exists, we have combined the connectivity information of all the subjects by adding their connectivity matrices and normalizing it for each deep nucleus. This process yields a final connectivity matrix which represents the probability of connection between the deep nuclei of all the subjects to each vertice. These probabilities were finally represented on the average surface for each pair of homologue nuclei, using a color intensity representing directly the probability. A red color is used for left nuclei and a green color is used for the right nuclei.

Results and discussion

Figure (1) depicts the 3D renderings of the deep nuclei obtained automatically on a single subject with its corresponding anatomical connectivity stemming from the tractography. The probabilistic surface atlases corresponding to the connectivities of each pair of deep nuclei are shown in figure (2). The caudate nuclei (2a) have a high connectivity rate to the anterior frontal lobes and rostral premotor areas. The putamen (2b) is connected to the motor and premotor areas as well as ventral frontal areas. Of note, the ventral limbic connections of the putamen and caudate nuclei (rostal medial and orbital frontal regions) were not analyzed separately and are visble in figure 2a and 2b. Little connections were evidenced for the globus pallidus as expected, as its connections mainly come from the striaturm.

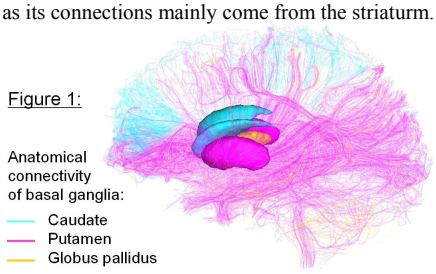
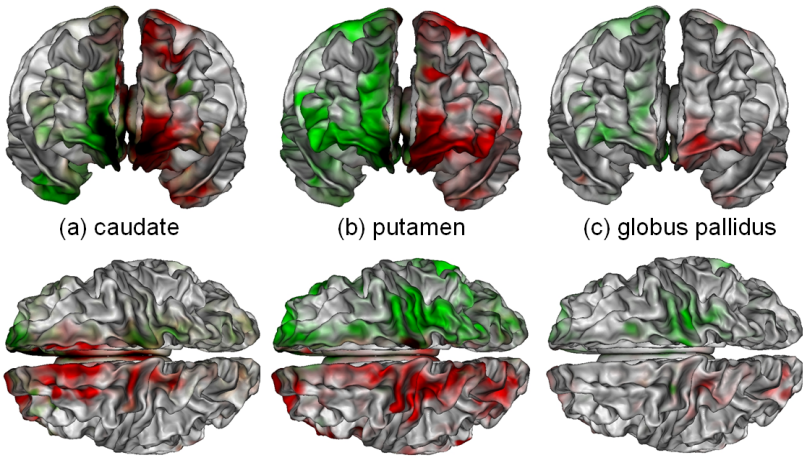


Figure 1:

Figure 2



Conclusion

We have built a probabilistic surface atlas of the connections between the basal ganglia and the cortex in good agreement with the descriptive anatomy found in the literature. Tractography methods will be improved to better capture connections with the lateral frontal cortex. This probabilistic atlas built from 10 healthy subjects allowed quantifying the amount of cortical connections for each nucleus on a population of healthy subjects. In its current status, the ventral limbic connections of the basal ganglia were not separated from connections of the caudate nucleus and the putamen. In the future, we will increase the size of the population to get a more robust probabilistic atlas, and we will individualize the ventral limbic areas of the basal ganglia. We will also build such atlases on population of patients, in order to perform comparisons, aiming at isolating specific markers of the various pathologies involving disorders of the deep nuclei, such as motor disorders, like Parkinsonian syndromes or Huntington disease.

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