Connectivity-based atlas of human brain white matter in ICBM-152 space.

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TARGET AUDUENCE: Researchers studying brain connectivity or using white matter segmentation.

PURPOSE: Digital human brain atlases consisting of MRI-based templates and semantic labels delineating different brain regions serve a critical role in neuroimaging, mainly facilitating spatial normalization and automated segmentation, for the purposes of voxel-wise, region-of-interest, and network analyses. As part of the IIT Human Brain Atlas project (www.nitrc.org/projects/iit2), we have recently developed, anatomical as well as state-of-the-art diffusion tensor[1] and high angular resolution diffusion imaging (HARDI) templates[2], as well as probabilistic gray matter (GM) labels[3] in ICBM-152 space. The purpose of this project was to construct the first probabilistic connectivity-based atlas of human brain white matter (WM) in ICBM-152 space.

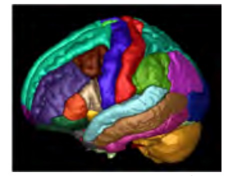

Figure 1. 3D view of the IIT gray matter atlas.

MATERIALS AND METHODS: White matter tractography protocol: Each GM label of the IIT Human Brain Atlas[3] (Desikan-Killiany labels) (Fig.1) was used as a seed and all other GM labels combined were used as targets for probabilistic tractography based on the HARDI template of the IIT atlas. For each GM label, *2000* fibers originated from each WM voxel of the WM-GM interface of that label. Probabilistic HARDI-based tractography was performed using the MRtrix software[4]. WM parcellation: First, probabilistic connectivity maps were generated for each pair of GM labels. Second, the "winner takes all" approach was applied on the tractography results to assign labels to WM based on: a) GM label connectivity (Fig.2A), b) lobar connectivity (Fig.2B), or c) categorization into commissural, association or projection fibers (Fig.2C). Third, to account for the limitation of the "winner takes all" approach when multiple fiber populations share the same voxels, multi-dimensional maps of WM were constructed, in which each WM voxel contains a list of the GM pairs that have the most probable connections crossing through it. Fourth, a well-established two ROIs approach[5] was used on the tractography results to segment major fiber bundles (Fig.3). GM network: The tractography results for each pair of GM labels were used to construct an 89 x 89 brain network (Fig.4). Evaluation: Connectivity-based segmentation of the corpus callosum and thalamus were used to evaluate the connectivity information of the atlas. 1000 fibers originated from each voxel of the corpus callosum in the mid-sagittal plane and each voxel of the thalamus, and the "winner takes all" approach was used to map connectivity of different segments of the two structures to cortical GM labels and lobes (Fig.5).

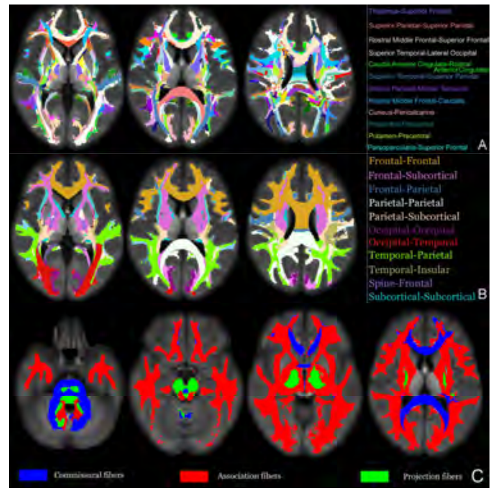

Figure 2. White matter parcellation based on connectivity of A) GM labels and B) lobes. C) Commissural, association and projection fibers. "Winner takes all" was used in all cases.

RESULTS & DISCUSSION: A WM connectivity-based atlas with varying levels of detail was generated in ICBM-152 space. On one end, thousands of probabilistic connectivity maps were generated for all the possible pairs of GM labels. Individual maps can be useful in studies of the connectivity of particular GM label pairs. An intermediate level of detail resulted from using the "winner takes all" approach to generate a single WM parcellation map based on GM label connectivity (Fig.2A). This is expected to be useful to most neuroimaging studies using a WM atlas. A lower level of detail was provided in the "winner takes all" WM parcellation based on lobar connectivity (Fig.2B), categorization into commissural, association or projection fibers (Fig.2C), or in the maps of major fiber bundles (Fig.3). The results of this work are in general agreement with previous literature and known brain anatomy (Figs.3,4,5). The symmetry across hemispheres further increases confidence in the results. However, to fully evaluate the anatomical validity of all the new information that has been generated through the combination of probabilistic tractography on the HARDI template and the Desikan Killiany GM labels of the IIT atlas, will require a considerable amount of time and effort combining MRI and histology. Finally, a major advantage of the generated framework is its flexibility, since one can repeat this work to generate WM atlases based on any set of anatomically or functionally defined GM labels located in the popular ICBM-152 space.

CONCLUSION: The generated WM atlas complements already available high-quality templates and gray matter atlas located in ICBM-152 space. The resulting set of tools is expected to support and enhance a number of neuroimaging efforts.

REFERENCES: [1] Zhang S, et al. Neuroimage 2011;54:974-984. [2] Varentsova et al., Neuroimage 2014;91:177-186. [3] Zhang S, Arfanakis K. ISMRM 2013, p.2129. [4] Tournier JD, et al. Int J Imag Syst Tecah 2012;22:53-66. [5] Wakana S, et al. Neuroimage 2007;36:630-644.

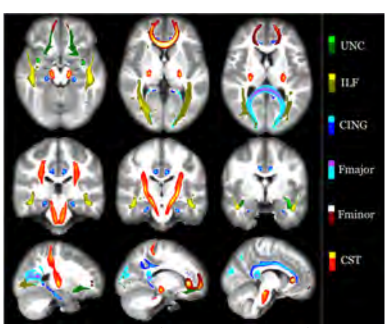

Figure 3. Confidence maps from the probabilistic segmentation of major bundles.

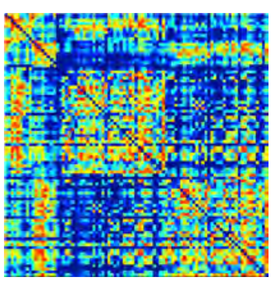

Figure 4. Connectivity matrix based on 89 GM labels (log of the number of fibers is shown).

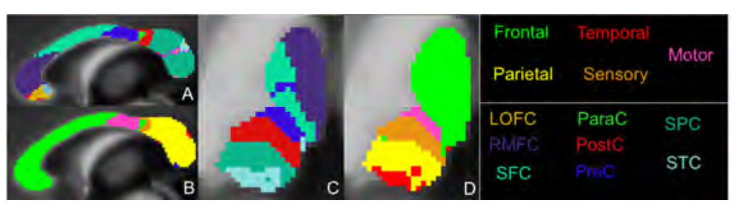

Figure 5. Connectivity-based segmentation of (A,B) corpus callosum and (C,D) thalamus. A and C show segmentation based on connectivity to cortical GM labels. B and D show segmentation based on connectivity to lobes. "Winner takes all" was used in all cases. (LOFC: lateral orbitofrontal cortex; RMFC: rostral middle frontal cortex; SFC: superior frontal cortex; ParaC: paracentral gyrus; PostC: postcentral gyrus; PreC: precentral gyrus; SPC: superior parietal cortex; STC: superior temporal cortex).