

Probabilistic Gray and White Matter MRI Atlas of Human Brain

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Introduction

Probabilistic human brain atlases (1) retain the variability of different subjects and are more representative than individual atlases. Existing probabilistic atlases were derived from T₁-weighted MRI images and are used to delineate morphology of overall brain, cortex, and subcortical nuclei. However, detail within the white matter is largely absent from these atlases. Diffusion tensor imaging has been widely used to reveal the white matter anatomy, including individual tracts. A probabilistic atlas of white matter anatomy was previously generated using diffusion tensor data from 28 subjects and transformed to MNI-152 coordinates (2). In the present work, we automatically segmented the cerebral cortex, cerebellar cortex, ventricles, and major subcortical nuclei and parcellated cerebral cortex into gyri from the same 28 subjects. Transformation matrices were obtained by mapping T₁ weighted image of each subject to MNI-152 coordinates using a 12 mode affine transformation. These matrices were then applied to the segmented structures and parcellated gyri. A comprehensive probabilistic human brain atlas is generated by summing the transformed data from each segmented structure or parcellated gyri.

Methods

Data acquisition: *in vivo* adult human data (n=28) were acquired using a 1.5 T Philips Gyroscan NT system. A single-shot EPI sequence with the SENSE parallel imaging scheme (SENSitivity Encoding, reduction factor R = 2.5) was used for DTI data acquisition. DWI parameters were: FOV=240/240/125mm, in plane imaging matrix = 96×96 (zero-filled to 256×256 with in plane pixel size = 0.9375×0.9375mm), axial slices thickness = 2.5 mm, parallel to the anterior-posterior commissure line, 30 independent diffusion weighted directions with b-value = 700 sec/mm², 5 additional images with minimal diffusion weighting (b= 33 sec/mm²). Coregistered magnetization-prepared rapid gradient echo (MPRAGE) images of the same resolution were also recorded for anatomical guidance. **Tensor fitting and DTI tractography:** DTI tensor fitting starts with raw DWI images after intra-subject AIR registration. The six independent elements of the 3×3 diffusion tensor were calculated using multivariate linear fitting. Fiber tracking was based on a linear line propagation model (FACT) with FA threshold 0.2 and angle threshold 40°. The same regions of interests (ROI) as those used in the literature (3) were adopted for fiber tracing of major white matter tracts. **Brain tissue segmentation:** Skull stripping was performed on T₁ weighted images with semi-automatic methods. TOADS (Topology-preserving Anatomy-Driven Segmentation) (4) was used for segmentation of brain structures based on skull stripped T₁ weighted images. **Cortical gyral parcellation:** With the ICBM atlas as source image and subject image as target image, an RBF (radial basis function) based registration method was used to acquire the transformation matrix. This transformation matrix was then applied to the ICBM gyral label to get the subject gyral parcellation.

Results

Segmentation of single subject: Fig. 1 shows images of DTI colormap (Fig 1a), co-registered skull stripped T₁ weighted image (Fig. 1b) and segmented structures (Fig. 1c-h) of a single subject. Figs 1a-g are in the same axial slice and Fig. 1h shows the cerebellar cortex in a coronal slice. With segmentation, individual structures of the brain are extracted and their morphologies are clearly revealed. **Probabilistic gray and white matter atlas:** Figs.2a shows the averaged DTI colormap of 28 subjects. As an example of white matter tract, averaged inferior fronto-occipital fasciculus (IFO) from 28 subjects is demonstrated in Fig. 2b. Figs. 3 (a), (b), (c) and (d) display the averaged gray matter, white matter, ventricle and integrated gray/white matter, respectively. From Figs 2 and 3, averaged atlases record individual variability and can always evolve with data of more normal subjects added in. With segmentation of neural structures based on T₁ weighted images and DTI based tractography, major gray and white matter structures in the brain can be separated and averaged to delineate their probabilistic morphology. **Probabilistic cerebral cortical gyri:** 27 cortical gyri were parcellated for each subject. Fig. 4 shows the probabilistic superior, middle and inferior frontal and precentral gyri overlaid on the same axial slice of MNI-152 atlas. The proposed probabilistic atlas represents cerebral cortex at gyral level, white matter at tract level and also includes ventricles, subcortical nuclei and cerebellar cortex. Thus, comprehensive brain morphological information is included.

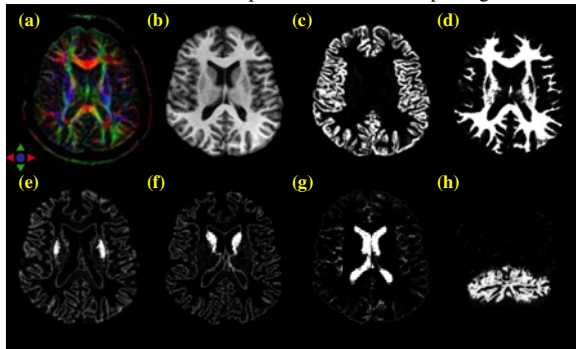


Fig 1 (up): DTI colormap (a), T₁ weighted image (b) and segmented structures of a single subject (c-h).

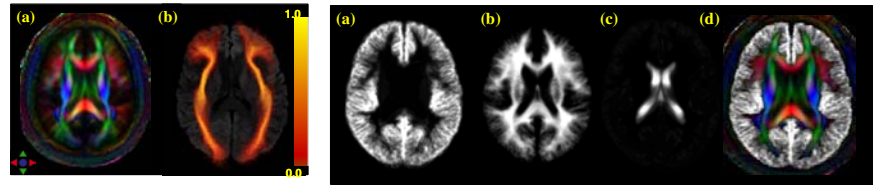


Fig 2: Probabilistic DTI colormap (a) and IFO tract (b). Color bar indicates the probability.

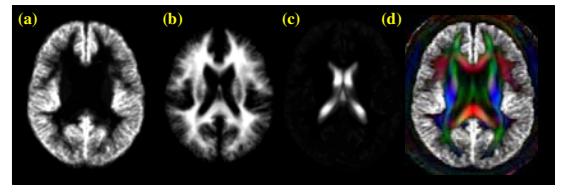


Fig 3: Probabilistic gray matter (a), white matter (b), ventricle (c) and integrated gray and white matter (d). Gray scale intensity indicates the probability.

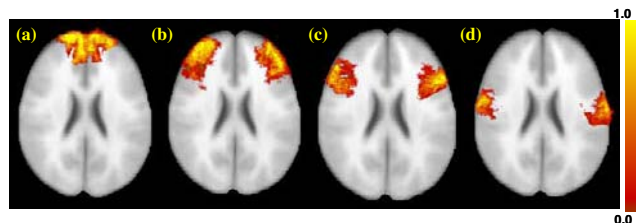


Fig. 4 (right): Probabilistic superior frontal (a), middle frontal (b), inferior frontal (c) and precentral gyri (d).

Discussion

This abstract presents some preliminary results of the probabilistic gray and white matter atlas. Different from most currently available probabilistic MRI atlas based on T₁/T₂ weighted images, the proposed atlas is a comprehensive atlas as it includes cortical gyri, major neural structures and fiber bundles in both gray and white matter. Data of more normal subjects will be added in the probabilistic atlas.

References: [1] Mazziotta, J.C. et al (1995). A probabilistic atlas of the human brain: Theory and rationale for its development. *NeuroImage* 2, 89. [2] Hua, K. et al (2006). Tract probability map in stereotaxic spaces and analysis of asymmetry. *ISMRM* 1084. [3] Wakana, S. et al (2004). Fiber tract-based atlas of human white matter anatomy. *Radiology* 230, 77. [4] Bazin, P.L. and Pham, D (2006). TOADS: Topology-preserving, anatomy-driven segmentation. *Proc IEEE Symp Biomed Imaging*.

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