# Population based Probabilistic Neural Tracts Atlas of Human Brain

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## *Introduction*

Diffusion MRI is the technique that helps map the white matter connectivity within the human brain non-invasively and has been applied to understand the brain development, brain functions, and clinical diseases [1]. In order to study the variations of neural connections between subjects, the extraction and selection of neural tracts have been adapted in most of the studies [2]. However, it is hard to identify the valid neural trajectories, especially under the interference of the individual variability. In this study, a probabilistic connectivity atlas was developed by the tract-based transformation which was used to map the tracts from individual space to MNI152 space [3]. The white matter tractography was based on FACT (fiber assignment by continuous tracking) and saved as a file type [4]. The T1-weighted image (T1WI) of each subject was mapped to MNI152 brain images via the affine linear registration. The same transformation matrix was then applied to the neural bundles mapping. By calculating the transferred neural bundles, the probabilistic tract atlas was regarded as a new template which can provide the correct location of neural bundles in MNI152 coordinate.

## *Materials and Methods*

***Magnetic Resonance Imaging:*** All MR data (n=10) were acquired at 1.5T MR system (Excite II; GE Medical Systems, Milwaukee, Wis, USA) with an 8 channels head coil. DTI was performed using single-shot spin-echo echo planar imaging sequence with TR/TE = 17000/68.9 ms, FOV=26x26 $cm^2$, slice thickness=2.2mm, matrix=128x128, noncollinear diffusion directions=13, b=900 $s/mm^2$, and NEX=6. T1WI were acquired using 3D FSPGE pulse sequence with matrix size=256×256, axial slice thickness of 1.5 mm, and the same FOV as DTI.

***Data processing:*** Fiber tracking was carried out by the FACT algorithm with fractional anisotropy (FA) threshold of 0.2 and angular threshold of 60 degrees. T1WI were co-registered to non-diffusion weighted T2 image with SPM2 to acquire the same coordinate as neural tracts. With FLIRT linear registration compiled in FSL library 3.3 (Oxford, UK), the transformation matrices were obtained by registering the co-registered T1WI with the reference MNI152 image. These transformation matrices were then applied to the neural tracts into MNI152 space. Finally, the transformed tracts were collected and mapped into the MNI152 coordinate to generate a probabilistic connectivity atlas. Fig.1 illustrated the flowchart of tract-based transformation. The interface of fiber tracking, transformation, and visualization was developed with Borland C++ Builder 6 and OpenGL API.

## *Results*

With collecting each tract from 49 subjects, the probabilistic tract atlas was mapped into MNI152 template. All tracts were performed in DTI tractography from the same defined ROI. The cingulum and superior longitudinal fasciculus (SLF) were demonstrated as the examples of neural atlas. In Fig.2, the cingulum was shown in coronal view with the MNI152 background. Fig.3 showed SLF in sagittal view with T1WI background in MNI152 space. The tracts could be segmented from the averaged neural structures to determine a probabilistic tract atlas.

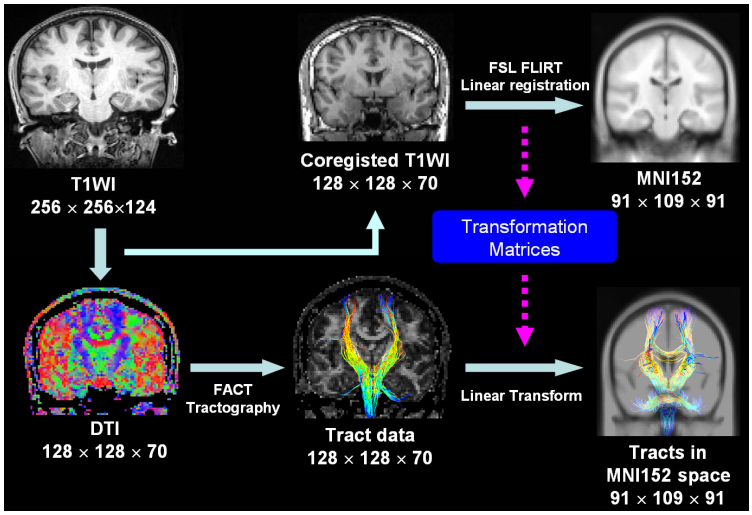


Figure 1: The transformation flowchart of the tract-based probabilistic atlas.

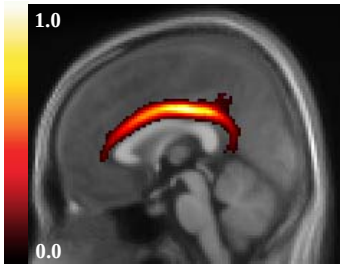


Figure 2: A probabilistic atlas were developed with the tract-based transformation, The probabilistic map of the cingulum from 49 subjects were identified in MNI space. The color of tracts is the probability scale from 0 (darkness) to 1 (brightness).

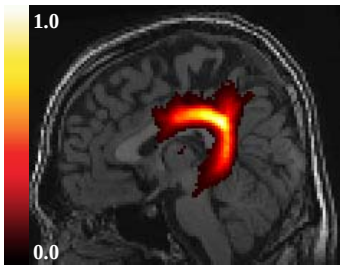


Figure 3: The probabilistic tract of SLF was mapped to T1-weighted image in MNI coordinates.

## *Discussions*

The probabilistic tract atlas was presented in this study. The extracted cingulum and SLF was demonstrated by the tract-based transformation. According to the results, the distribution of the neural tracts can be revealed by the statistic analysis of group data. The drawbacks of individual differences or imaging noises can be minimized according to the high probabilistic pathway selection. In this way, the precise trajectories could be located from the tract-based template. It can facilitate further studies on neural connectivity, brain mapping, and diffusion indices analysis for clinical applications. To have more reliable performance, more healthy subjects will be recruited in the next step.

## *Acknowledgement*

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## *References*

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