Software Tools for Anatomical ROI-based Connectivity Analysis

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Introduction

We describe a collection of software tools for jointly processing and visualizing structural and diffusion MRI of the brain. The results of the structural and diffusion processing are combined to generate a connectivity map of the brain based on a set of anatomical ROIs . These tools can be applied using scripts or through a user interface that provides sophisticated interactive processing and visualization capabilities (see Fig. 1).

Methods

We developed the BrainSuite image processing software using C++ and compiled MATLAB code. The user interface is developed using C++, Qt, and OpenGL. The software can be run on Windows, Macintosh, and Linux computers.

Structural Image Processing: Whole-head human T1-weighted anatomical MRIs are processed using automated image processing software [1] to generate mesh models of the cortical surface. These mesh models are registered spatially to a single subject anatomical brain atlas. We constructed this atlas based on a T1-weighted MRI with corresponding cortical surface mesh representations generated using the same software. The surface and volume atlas data were delineated manually by an expert neuroanatomist who identified anatomical regions of interest (35 ROIs per hemisphere). We perform the registration using a combined surface/volume registration procedure [2,3]. This procedure first employs a curvature-based surface registration process to align the cortical surface features of the subject and the atlas, which is then used to initialize a volumetric alignment, which is refined using elastic image registration. This produces an alignment of the cortical features in the surface space, with a corresponding alignment of the volumetric data. The labels from the atlas are then transferred to the surface and volume of the subject data, producing a structural segmentation of the subject MRI into the delineated ROIs. The structural image processing modules enable various attributes to be measured and compared, including cortical thickness and ROI volumes. The surface and volume labels are useful for analysis of functional, structural, and parametric images.

Diffusion Image Processing: Diffusion weighted images are first distortion-corrected using constrained non-rigid registration to the undistorted T1-weighted anatomical image [4]. The diffusion signal is then quantified by fitting a diffusion tensor imaging model and/or applying the Funk-Radon Transform [5] or the Funk-Radon and Cosine Transform [6] to estimate white matter fiber orientations. Models of fiber tracts are computed using a deterministic method.

Connectivity Analysis and Visualization: For each pair of ROIs, the number of tracts passing through both ROIs is counted to produce a connectivity matrix. The matrix is normalized by the maximum element. This matrix structure is represented visually using a circular plot, in which the connectivity strength is indicated by the weight and color of the arc connecting the ROIs on the plot. The connectivity graph is synchronized with the 3D display, enabling users to select regions of interest and visualize the corresponding connected fibers.
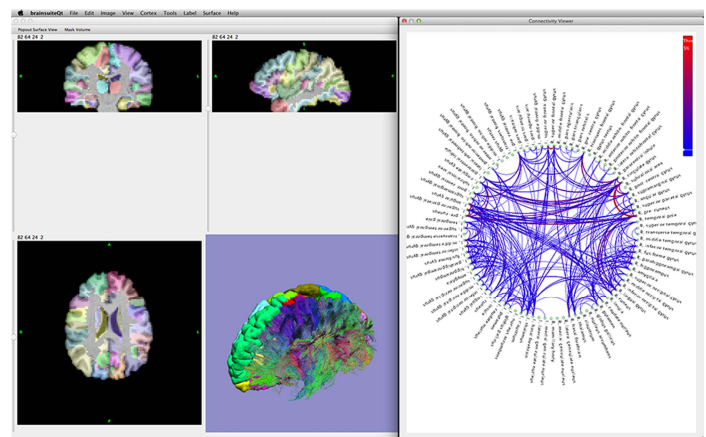

Fig. 1: An example labeling produced using our method. The surface was extracted and labeled automatically, and the connectivity of the corresponding tracts was assessed using the volumetric labeled ROIs. The connectivity matrix is represented in an interactive plot (right), which allows users to filter the fiber tracts according to regions of interest.

Results

Figure 1 shows an example of the user interface with a labeled T1-weighted MRI, along with the extracted surface model and aligned fiber tracts computed from rigidly aligned diffusion data. The interactive connectivity analysis graph, computed from the intersection of the fiber tracts and the labeled ROIs, is also shown. For more information or to download the software, please see: http://brainsuite.loni.ucla.edu.

References

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