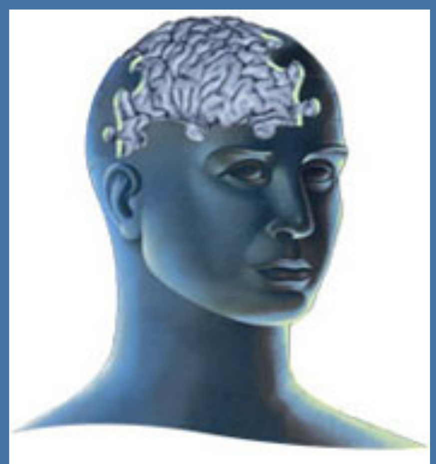
Software Tools for Anatomical ROI-based Connectivity Analysis



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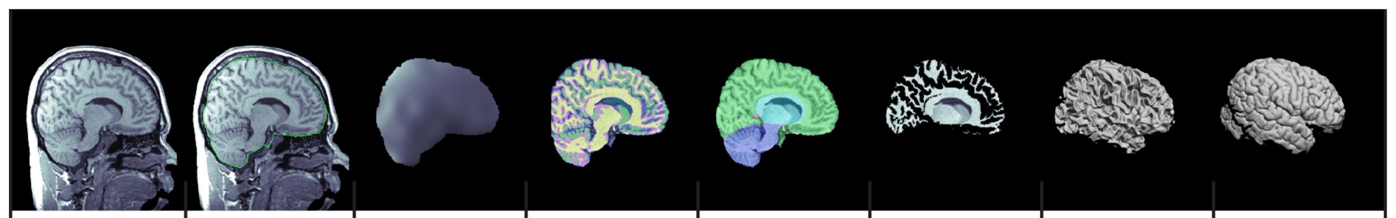
I. INTRODUCTION

- We describe BrainSuite13, a collection of software tools for jointly processing and visualizing structural and diffusion MRI of the brain.
- BrainSuite13 can combine the results of this structural and diffusion processing to generate connectivity maps of the brain based on a set of anatomical ROIs.
- These tools can be applied using scripts or through a graphical user interface (GUI) that provides sophisticated interactive processing and visualization capabilities.

II. METHODS

II.a. Software Implementation

- We developed the BrainSuite13 image processing software collection using C++ and compiled MATLAB code.
- The command line tools can be run on Windows, Mac, and Linux
- The graphical user interface is developed using C++, Qt, and OpenGL.
  - Provides interactive tools for displaying image slices, surface models, tensor glyphs, orientation distribution functions (ODFs), and streamline tractography.
  - Provides guided processing through extraction, registration, and labeling steps
  - Includes tools for delineating ROIs interactively.
- The interactive version is available for Windows and Mac (Linux release planned).



MRI	skull stripping	bias field correction	tissue classification	cerebrum identification	topology correction	tessellation	pial surface generation
	<2 sec	40s - 4 mins	<5 sec	<20 sec	<40 sec	<2 sec	<10 mins

Fig.1. The BrainSuite Cortical Extraction Sequence. This sequence can extract a set of inner and outer cortical surface meshes for a typical T1-weighted MRI in approximately 10-15 minutes (processed on an Intel 3.5GHz i7-3770).

II.b. SURFACE EXTRACTION

Whole-head human T1-weighted anatomical MRIs are processed using BrainSuite's automated cortical surface extraction sequence (see **Fig. 1**) [1].

- Produces inner and outer surface mesh models of the cerebral cortex.
- The GUI enables manual corrections to be applied at several stages if automated processing does not achieve sufficient quality for segmenting structures.

II.c. AUTOMATED LABELING OF NEUROANATOMICAL ROIS

The cortical mesh models are registered spatially to a labeled single subject anatomical brain atlas.

Neuroanatomical Atlas

- Based on a T1-weighted MRI with corresponding cortical surface mesh representations generated using the BrainSuite software.
- The atlas comprises surface and volume data that were delineated manually by an expert neuroanatomist into 98 anatomical ROIs (see **Fig. 2**).

Surface/Volume Registration (SVReg)

- Registration is performed using a combined surface/volume procedure [2].
  - First employs a curvature-based surface registration process to align the cortical surface features of the subject and the atlas.
  - Surface registration is used to initialize a volumetric alignment.
  - Volumetric alignment is refined using elastic image registration.
  - 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 transferred to the surface and volume of the subject data, producing a segmentation of the subject MRI into the delineated ROIs.
- The ROI boundaries on the cortical surfaces are refined locally at the mid-cortical surface using geodesic curvature flow [3], such that the boundaries conform to the bottoms of the sulcal valleys.
- The structural image processing modules enable various attributes to be measured and compared, e.g., cortical thickness and ROI volumes.
- The surface and volume labels are useful for analysis of functional, structural, and parametric images.
- Registration, labeling, and refinement stages can be performed in ~40 minutes for a typical MRI (processed on an Intel 3.5GHz i7-3770).

ACKNOWLEDGEMENTS

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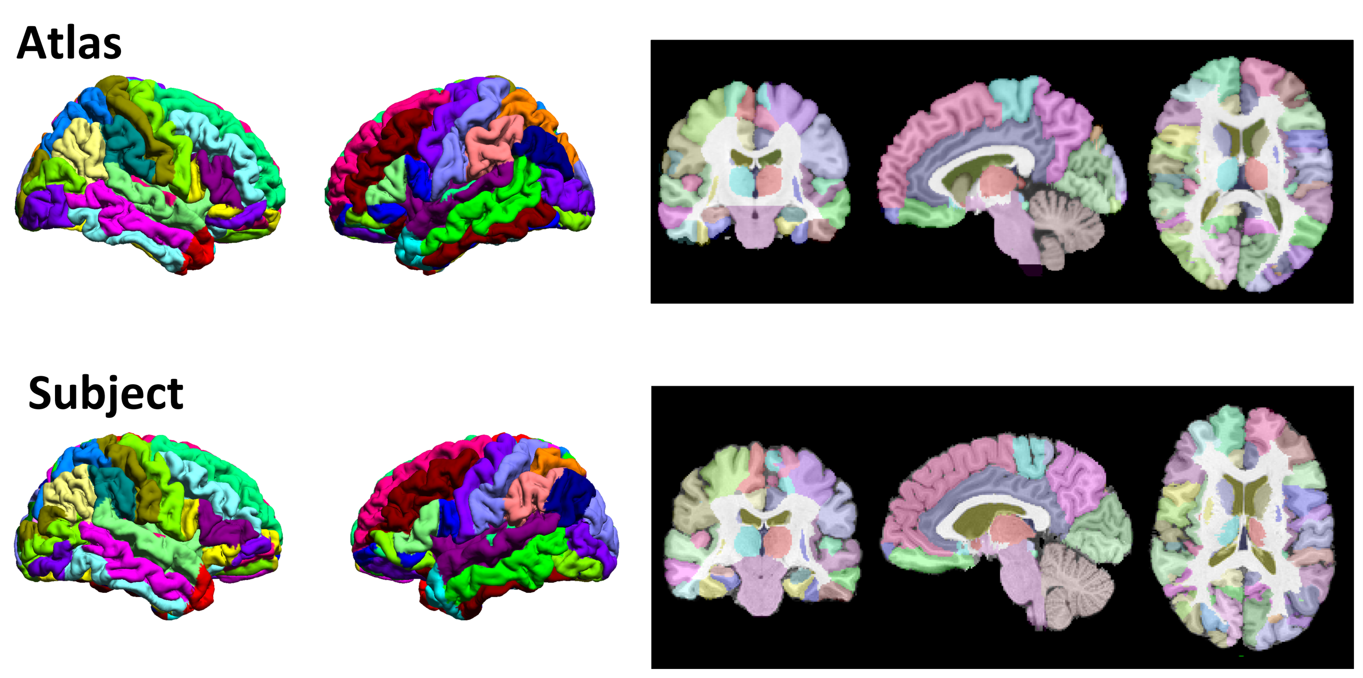

Fig.2. BrainSuite13 ROI Labeling (top) Surface and volume views of the BrainSuite13 anatomical atlas, delineated into anatomical regions of interest. (bottom) Similar views of an automatically labeled subject dataset.

II.d. DIFFUSION IMAGE PROCESSING

Distortion Correction

BrainSuite13 provides two methods for correcting distortion induced by B0 inhomogeneity in diffusion weighted images (either can be used for correction):

- Registration-based: uses a constrained non-rigid registration (see **Fig. 3**) to the undistorted T1-weighted anatomical image [4] (does not require fieldmap).
- Fieldmap-based: uses a fieldmap collected during the diffusion MRI session to correct for distortion.

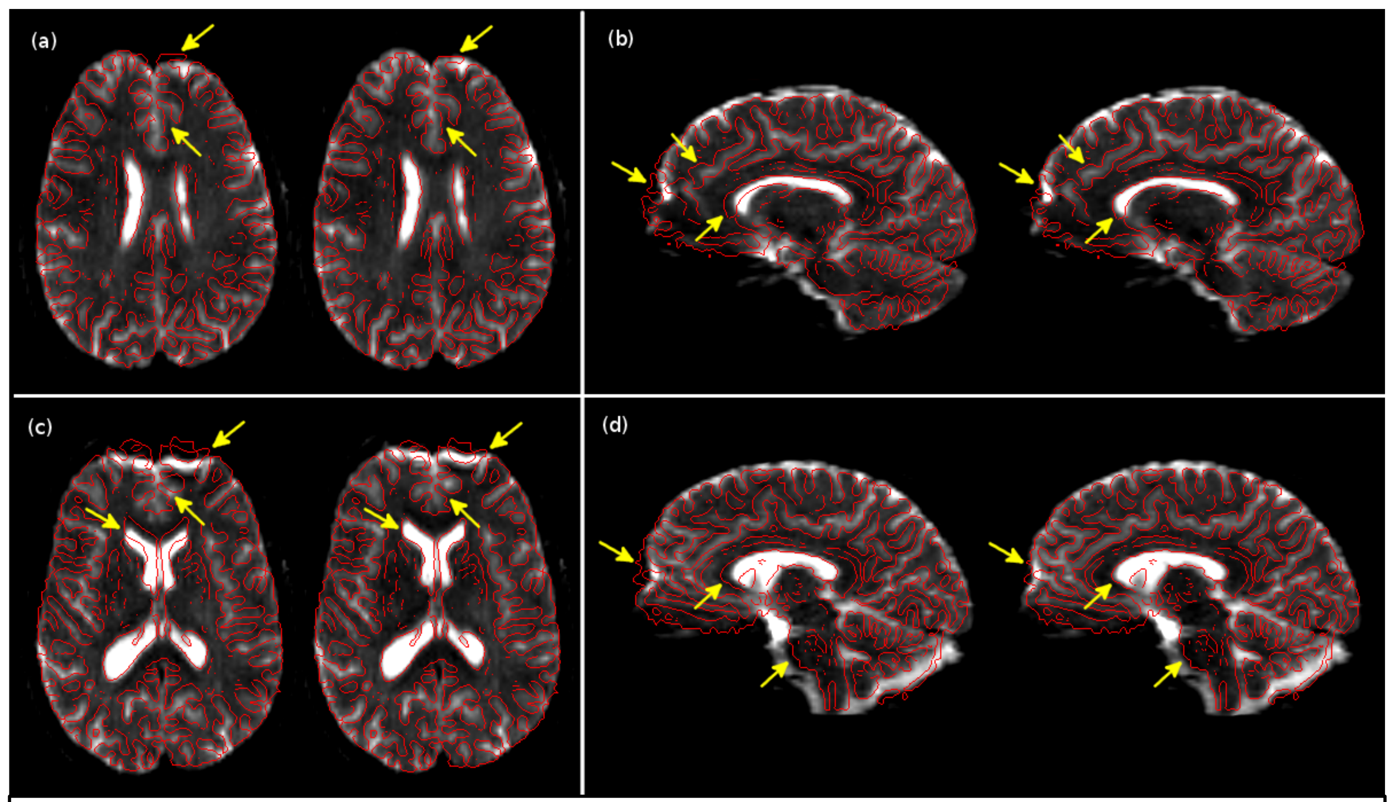

Fig. 3. Registration based distortion correction (without fieldmap) via the BrainSuite Diffusion Pipeline (BDP). Each sub-figure shows (left) distorted and (right) corrected b=0 image, overlaid with the edge-map (red outline) generated from the T1-weighted image. Arrows indicate areas of significant correction.

Tensor and ODF Estimation

- After coregistering the diffusion weighted images and the T1-weighted image, tensors and ODFs are estimated in the structural T1 image space (see **Fig. 4**).
- The BrainSuite Diffusion Pipeline can quantify the diffusion signal in three ways:
  - Fitting a diffusion tensor imaging (DTI) model.
  - Applying the Funk-Radon Transform (FRT) [5].
  - Applying the Funk-Radon and Cosine Transform (FRACT) [6-7].
- The Funk-Radon and Cosine Transform is a new linear transform-based ODF estimation method that generalizes the FRT.
  - FRACT can provide higher angular resolution and/or robustness to noise and modeling errors than existing state-of-the-art ODF estimation methods.
  - To learn more about FRACT, please attend the presentation of **Abstract #771** by **Justin Haldar** at 4PM Thursday in "Fibers and Tractography".

SOFTWARE DOWNLOAD

For more information or to download the software, please visit the BrainSuite website: http://brainsuite.loni.ucla.edu. Tutorials and sample data are also available on our website.

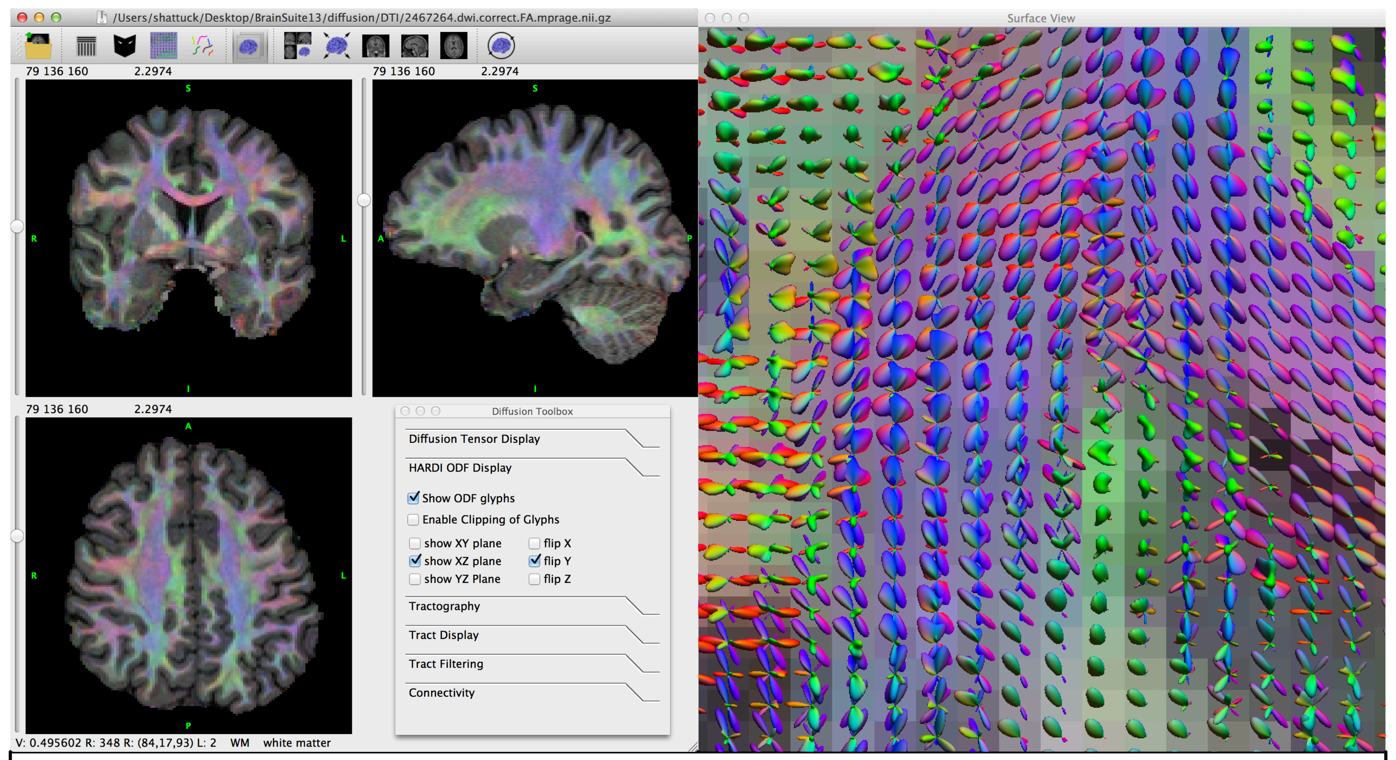

Fig. 4. Diffusion Imaging in BrainSuite13. (left) T1 image, overlaid with a color FA map computed from the coregistered, distortion-corrected diffusion images; and (right) 3D rendering of FRACT ODFs displayed with blended T1 and color FA image slices. The input imaging data are from the Beijing Enhanced dataset [8].

II.e. CONNECTIVITY ANALYSIS AND VISUALIZATION

- Diffusion streamlines are tracked using a deterministic method.
- For each pair of ROIs, the number of tracks passing through both ROIs is counted to produce a connectivity matrix, which is normalized by its 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 (see **Fig. 5**).
- The connectivity graph is synchronized with the 3D display, enabling users to select regions of interest and visualize the corresponding connected fiber tracks.

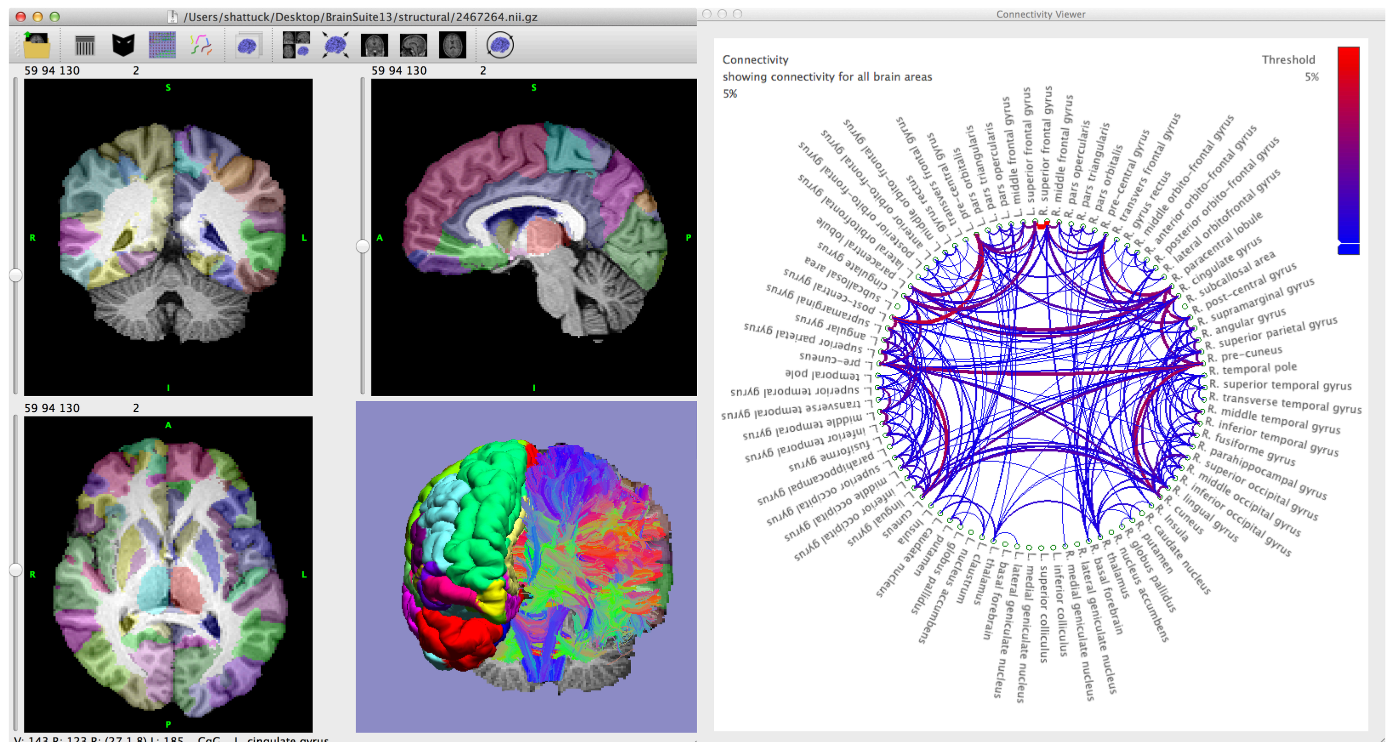

Fig. 5. Tractography and connectivity in BrainSuite13. (left) a T1-weighted MRI and extracted hemisphere surface with labeled ROIs, and a set of diffusion fiber tracks; (right) the interactive connectivity diagram, based on the same data shown in Fig. 4.

III. RESULTS AND CONCLUSION

- Our recently released software, BrainSuite13, provides integrated functionality for processing and visualizing structural and diffusion MRI.
- The results of BrainSuite13's segmentation, labeling, diffusion, and connectivity processing are shown in **Fig. 5.**
- BrainSuite13 features:
  - Fast processing times – less than 1 hour to extract, register, and label a T1 MRI.
  - Novel methods for correcting distortion in DWI.
  - Visualization capabilities for multiple types of data.
  - Powerful tools for exploring diffusion and connectivity information.
  - Flexibility for performing different types of analysis.

IV. REFERENCES

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