

An Analysis Tool for Quantification of Diffusion Tensor MRI Data

Hae-Jeong Park^{1,2,3}, Martha E. Shenton³, Carl-Fredrik Westin²

¹Division of Nuclear Medicine, Dept. of Diagnostic Radiology, Yonsei University, College of Medicine, Shinchon-dong, Seodaemun-gu, Seoul 120-749, Korea
parkhj@yumc.yonsei.ac.kr

²Laboratory of Mathematics in Imaging, Dept. of Radiology, Brigham and Women's Hospital, Harvard Medical School, 75 Francis Str. Boston, MA 02115, USA
westin@bwh.harvard.edu

³Clinical Neuroscience Division, Laboratory of Neuroscience, Boston VA Health Care System-Brockton Division, Dept. of Psychiatry, Harvard Medical School, Boston, MA 02115, USA
martha_shenton@hms.harvard.edu

Abstract. A software tool for analyzing Diffusion Tensor MRI (DT-MRI) data is presented. The tool includes methods for segmentation of white matter for automatic definition of seed points for fiber tractography, and methods for 2D slice visualization using different types of tensor glyphs and color-coding schemes.

1 Introduction

DT-MRI is rapidly gaining clinical importance but tools for exploring and analyzing data from DT-MRI are still not widely available. In this paper, we introduce a diffusion tensor analysis tool developed with the aim of meeting current demands in both research and clinical applications.

2 Methods

This software tool, DoDTI, is implemented in Matlab (Mathworks Inc., USA), which is available for a wide range of platforms. The basic features of this tool are:

1) 2D slice visualization of DT-MRI data with several types of tensor glyphs and coloring schemes displayed on a background of fractional anisotropy, T2-weighted MRI data, or the apparent diffusion coefficient (ADC).

2) Automated or semi-automated methods for whole brain tractography where seed-points and stopping criteria may be assigned, either from automated segmentation using SPM2, or in a user-configurable manner. The tractography algorithm is based on a 4th order Runge-kutta integration solver with a choice of several regularization schemes to better handle crossing fiber bundles.

3) 3D visualization of fiber bundles using streamlines or streamtubes with optional, orthogonal, gray-level reference images superimposed. In addition, parcellations of gray matter can be used for classifying fiber bundles with specific colors.

4) Selection of fiber bundles based on user-defined criteria, such as a combination of the length of a fiber, maximal angle difference, and minimum distance between end points of a fiber. Manually or semi-automatically drawn regions of interest (ROIs) can be used for the selection of fibers of interest intersecting those ROIs. Visualization of fiber bundles with renderings of ROIs is available for better understanding of the fiber connection between ROIs.

5) Information about the properties of fiber bundles of interest, such as the mean fractional anisotropy along the fiber, can be calculated, which is useful for further evaluation of white matter abnormality.

6) Integration of functional MRI activation maps derived using SPM2 can be used as ROIs to enable the exploration of brain function or functional abnormality in relation with anatomical connectivity.

3 Conclusion

The software tool DoDTI has been developed to provide analysis and quantification of DT-MRI data and includes methods for visualization and automated methods for fiber tractography. More information and directions on how to download this tool can be found at the following URL: <http://neuroimage.yonsei.ac.kr/dodti>.

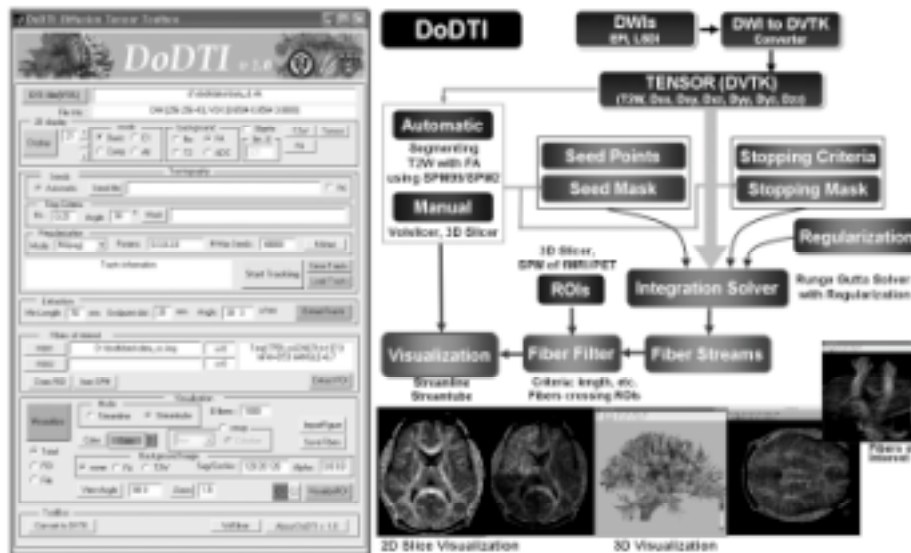


Fig. 1. Analysis flow of DoDTI