ANALYSIS TOOLS FOR THE STUDY OF BRAIN CONNECTIVITY BASED ON DIFFUSION MRI[1]

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Introduction

Diffusion-Weighted Magnetic Resonance Imaging (dMRI) is the preferred technique for the non-invasive study of brain connectivity [1]. It relies upon the diffusion of water molecules to allow the reconstruction of the main brain anatomical bundles in vivo. Tractography datasets contain millions of 3D polylines, called "fibers" or streamlines, representing the main macroscopic structure of white matter (WM) neuronal fibers. Next, we describe several methods proposed for the analysis of this data.

Fiber clustering: These methods group fibers based on a similarity or distance metric. Exploratory algorithms aim to reduce the dimensionality of the data, remove noise and get a better representation of the main white matter structure.

White matter bundle atlases: Through the use of fiber clustering methods and anatomical data, it is possible to construct atlases of white matter fiber bundles, created from a population of subjects, with fascicles present in most of the subjects.

White matter bundle manual segmentation: The bundles can be extracted using Regions of Interest (ROIs) manually defined, using the anatomical description of the bundles, based on the ROIs that are connected or traversed by the bundles.

White matter automatic segmentation: These are automatic methods applied to identify bundles on a new subject tractography. They must include anatomical information, typically in the form of a ROI template and/or a bundle atlas.

Diffusion-based cortical parcellation: In order to get useful information for the description of the Human Brain Connectome, the cortical surface can be parcellated based on the connectivity given by tractography data. From the parcellation, connectivity matrices can be calculated and compared between populations.

Hypothesis

It is possible to develop high-quality and efficient tools to process large tractography datasets for the analysis of brain connectivity based on diffusion MRI

Objectives

- To develop methods for a better understanding and description of white matter structure
- To design and implement solutions with efficient use of memory and computing resources
- To develop effective algorithms to process complex and large tractography datasets

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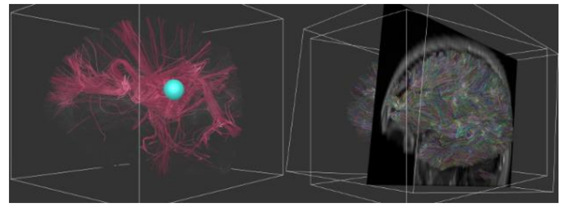
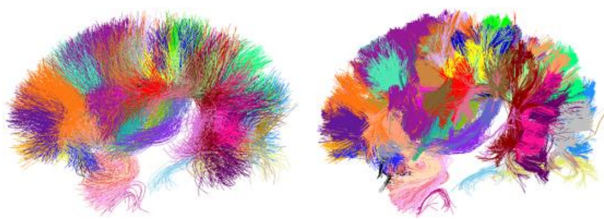
Results – proposed methods and perspectives

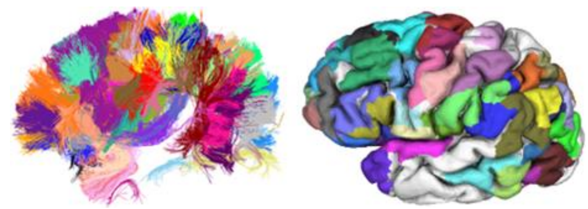
An efficient fiber clustering method based on fiber point distribution [2]



Interactive fiber visualization and manipulation tools [3].



An efficient segmentation method based on a multi-subject atlas [4,5]



A method that uses segmented short bundles to create a parcellation of the cortical mesh [6].

Those methods have been used to study several psychiatric disorders [7,8].

The developed methods and tools will be applied to the Human Brain Project (HCP) database, to contribute to a better description of human brain connectome.

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