

Mapping the human connectome with Lausanne Neuroimaging Tools

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Purpose

Connectomics is the science that deals with the mapping of the human brain structural network and its analysis [1,2]. There is growing evidence that studying the nervous system as a network is going to be a major paradigm shift in neuroscience [3,4]. The advent of connectomics is enabled by major technological developments in terms of imaging hardware and software as well as the development of an appropriate mathematical framework derived from graph theory. Major initiatives are being taken to create an extensive connectome map of the human brain [www.humanconnectome.org] and there is growing interest in investigating major neurodegenerative diseases using that framework. With the aim to promote in the broadest scientific community the use of connectomics approaches, we have developed a freely available open-source framework in Python to map and analyze the human connectome from in-vivo MRI acquisitions. The purpose of the presentation is to explain how to use our tools that can be downloaded freely from the web: www.connectomics.org

Outline of Content

1) What are the “Lausanne Neuroimaging Tools for Connectomics” and where can I get them? 2) What is the human connectome? 3) What MRI acquisition do I need? 4) How do I process the data with the Connectome Mapping Toolkit (each step is explained)? 5) What is the Connectome File Format? 6) How do I visualize the mapped connectome with the ConnectomeViewer? 7) What analyses can I perform with the ConnectomeViewer? 8) How can I share my discoveries with others? 9) How can I contribute improving the tools?

Summary

Connectomics is a word expressing the paradigm shift occurring in neuroscience moving from a classic phrenologic view of spatially localized brain function to a more complex model where brain function is encoded in spatially distributed neuronal networks. Connectome science emerges from the conjunction of several major technological and scientific developments. With the aim of making connectomics as accessible as possible to the scientific community we present our set of freely available tools to map the human connectome and provide a stepwise explanation on how to proceed from a raw MRI acquisition up to the network analysis.

References

[1] Hagmann, PhD Thesis, EPFL 2005. [2] Sporns et al, PLoS CB 2005. [3] Hagmann et al, PLoS Bio 2008. [4] Biswal et al PNAS 2010.

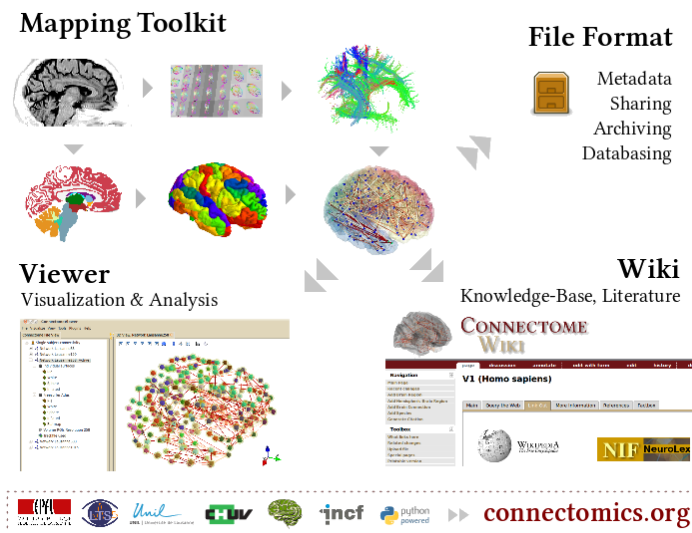


Fig 1: Connectomics.org front page.