Note on how cerebral functional connectivity encodes structural constraints of the human brain

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1 Introduction

Neuroimaging techniques allow to get different kind of information on the brain. For example, Diffusion Tensor Imaging (DTI) is a measure of the density of fibers and their orientation at a certain point in the brain whereas functional Magnetic Resonance Imaging (fMRI) and Positron Emission Tomography (PET) measure the level of *cerebral activity*. Techniques that essentially measure the same trait such as fMRI and PET have different spatial and temporal resolutions but can be used in a complementary analysis of that trait [1].
It seems natural that it is more difficult to use data measuring different traits such as fMRI and DTI in a unifying framework. Model based analyses [2] have allowed to draw some connections between structural and functional information (DTI and fMRI data, respectively) but the way structural properties constrain cerebral activity remains poorly understood.
In this work we represent both functional and structural data by *graphs* because they allow to encode and detect important properties of neuronal data [3]. In order to detect the communities at different scales we use the general concept of *stability*, a measure of the quality of a partition that also includes a measure of robustness of the results through the notion of *variation of information* [4].

2 Methods

We denote by $\mathbf{X}_{(m,T)}$ the resting state fMRI signal, with m the number of voxels and T the number of time samples. The m time courses are first band-pass filtered in order to extract only the neuronal contribution. We then consider the correlation matrix of this cleaned fMRI signal as the functional adjacency matrix $\mathbf{A}_T^f$.
The structural adjacency matrix $\mathbf{A}_T^s$ is obtained by log-rescaling DTI data to an acceptable range of values (see [2] for details).
Stability is denoted by $r(t)$ where t is a resolution parameter and our formulation of stability is the following :

$$r(t) = \max_H r_f(t,H) + \lambda(t) r_s(t,H) \quad (1)$$

where H is a given partition of the graph, r_f (r_s) is the stability of the partition H at the resolution t based on the functional (structural) adjacency matrix $\mathbf{A}_T^f$ ($\mathbf{A}_T^s$). λ is a weighting parameter to balance functional and structural stability contributions.

3 Ongoing work

A first part of the work is to compare the large-scale networks that are deduced from this graphical approach to networks that are obtained using classical techniques such as independent component analysis [1]. The correspondence between those results can be considered as a quality measure but the robustness (measured by the variation of information) of the network that is extracted using our approach has the advantage of being a quality measure by itself and hence we can confront those two criteria.
A second key question is to study the role of the weighting parameter λ. In particular we want to answer the following questions :

- How does λ influences the correspondence between the networks deduced from our approach and the classical component analysis approach, when keeping λ constant across different scales ($\lambda(t) = \bar{\lambda}$).
- What happens if the weighting parameter is not constant across time scales?
- Is the matching between the networks different at different scales and hence is functional connectivity encoding different structural constraints at different resolutions ?

References

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