INVESTIGATING THE ANATOMICAL SUBSTRATE OF FUNCTIONAL NETWORKS OBTAINED AT REST: A COMBINED FMRI AND FIBER TRACKING APPROACH

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Introduction

Knowledge of the link between anatomical fiber connections and functional brain regions is essential to an integrated understanding of the organization of the human nervous system. The pathways involved in specific functions could thereby be inferred and hypotheses about brain networks formulated and tested. Systematic investigations of neuronal connectivity and of large-scale interregional pathways in the mammalian cerebral cortex have demonstrated that the topology of the brain is neither entirely random nor entirely regular [1]. Recent advances in fMRI allow to extract sets of functionally dependent brain regions constituting networks [2]. However, to our knowledge, few studies have addressed the relationship between functional networks and the underlying anatomy, mainly due to limitations of white matter fiber tracking methods [3]. Some studies have examined the anatomical substrate of specific functional regions like the primary motor cortex [4]. But these studies remain limited due to the complexity of functional networks. We present an original investigation of the anatomo-functional connectivity in the human brain, which reflects the dual challenge of extracting specialized information and revealing its integration. We use a robust probabilistic fiber tracking method that allows to consider a large number of regions simultaneously.

Materials and methods

Resting state fMRI data and DTI images were acquired from thirteen healthy volunteers with the 3T Siemens Trio scanner of the *Centre de Recherche de l'Institut Universitaire de Gériatrie de Montréal* (Canada). FMRI acquisition parameters were: FOV=224 mm; 160 volumes of 42 contiguous slices; 3.5 mm isotropic voxels; (TE; TR)=(30; 2500) ms; flip angle: 90°. Group representative functional networks were identified from fMRI data using methods involving Independent Component Analysis [2,6] and a set of regions of interest (ROI) was manually defined from each network. A functional connectivity index (fCI) was defined as the functional correlation computed between all pairs of ROIs. DTI acquisition parameters were: FOV=256 mm; 52 slices; 2 mm isotropic voxels; (TE; TR)=(97; 8200) ms; Nex=4; 12 independent directions; b-value=1000 s.mm^{-2}. To reveal the anatomical structure of the networks, we used a probabilistic white matter fiber tracking method [7], which consists of formulating the uncertainty on diffusion data *via* a Bayesian framework. The method was used to track all possible connections between all pairs of the ROIs defined above. An anatomical connectivity index (aCI) was defined as the mean number of fibers connecting two given ROIs. The two connectivity indices were averaged across the ROIs of each network to obtain anatomical and functional connectivity indices at the network scale. A Multidimensional Scaling (MDS) analysis was then used to measure the organization of the networks according to these observed anatomical and functional connectivities.

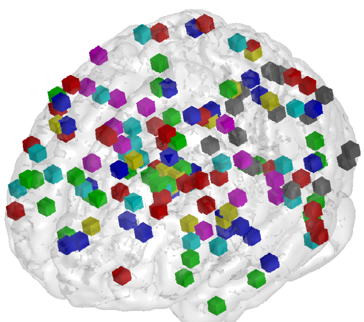

Fig. 2: Functional networks. See color code in the text.

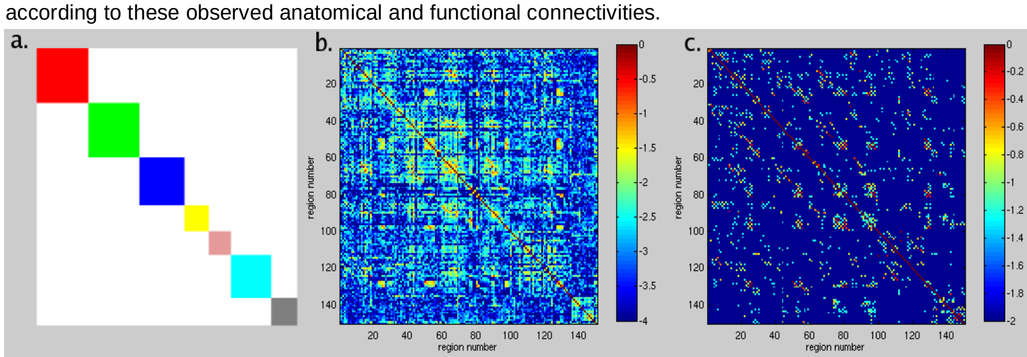

Fig. 1: (a) Matrix organization of the functional networks and their ROIs (color code in the text), (b) functional and (c) anatomical connectivity matrix (logarithmic scale).

Results

Seven networks were extracted (Fig. 1 & 2(a)): dorsal and ventral attentional (red & cyan), language (green), default mode (dark blue), mesolimbic (yellow), motor (pink) and visual (grey) networks, corresponding to 150 ROIs in total. Functional (Fig. 2(b)) and anatomical (Fig. 2(c)) connectivity matrices display the connectivity indices fCI and aCI for each pair of ROIs, suggesting that a relationship exists between functional and anatomical connectivity; indeed, several ROIs are clustered in a similar fashion in both representations. The MDS plot (Fig. 3) shows the global organisation of the networks and suggests that the underlying structure of the functional connectivity is close to that of the anatomical connectivity.

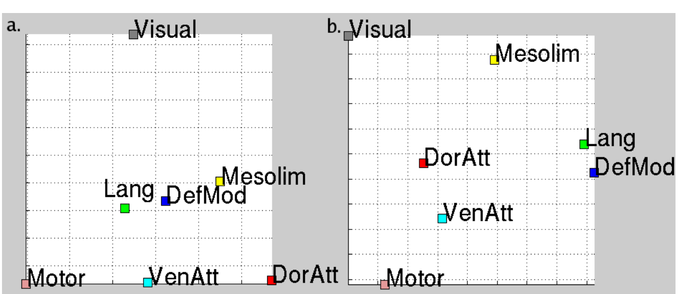

Fig. 3: (a) Functional and (b) anatomical MDS representations.

Conclusions

These preliminary results support the existence of an underlying anatomical substrate for the functional networks. These results are in agreement with the literature and previous findings in animals [4,8], which suggest that different functional networks are also separated in terms of anatomy. Probabilistic tracking accurately described anatomical connectivity, yielding to an anatomical index that proved to behave similarly to the functional connectivity index. Work in progress addresses the issue of fiber quantification, for a more precise characterization of anatomo-functional connectivity.

References

[1] D.J. Felleman and D.C. Van Essen. *Cerebral Cortex.* 1991; 1:1-47. [2] F. Esposito and al. *NeuroImage.* 2005; 25:193-205. [3] S. Mori and J. Zhang. *Neuron.* 2006; 51:527:539. [4] M. Guye and al. *NeuroImage.* 2003; 19:1349-1360. [5] A.T. Toosy and al. *NeuroImage.* 2003; 21:1452-1463. [6] J.S. Damoiseaux and al. *PNAS.* 2006; 103:13848-13853. [7] T.E.J. Behrens and al. *NeuroImage.* 2007; 34:144-155. [8] J. L. Vincent and al. *Nature.* 2007; 447:83-86.