Extracting Connectomic Profiles from Group Resting State fMRI Data using Dictionary Learning

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Introduction Functional networks of human brain derived from resting state fMRI (rsfMRI) data have drawn increasing interest in both research and clinical applications. Although there are multiple studies on the generation of functional networks [1, 2], quantitative characterization of connectomic profiles for distinct functional regions has been rare in literature, likely due to difficulty imposed by the well-recognized anatomical variability across individuals. This abstract presents our recent effort towards connectomic profile characterization for distinct cortical regions, taking into account anatomical variability.

Methods A 198-subject dataset released by Yufeng Zang in the 1000 Functional Connectomes Project (FCP) was used for this study. Five of them were excluded from our analysis due to poor image quality. Our analysis framework includes the following steps: (1) map the preprocessed rsfMRI data (by FCP pipeline) onto the generated central cortical surfaces (based on pial and white matter surfaces by FreeSurfer); (2) parcellation of the bilateral cortical surfaces into 200 distinct regions, respectively, by normalized cut [3], according to regional BOLD signal homogeneity. Since it is almost impossible to achieve voxel-by-voxel correspondence across subjects, region-based correspondence should have superior performance; (3) to find the connectomic profile of a template cortical region, and to further alleviate the influence of imperfect image registration, we applied an over complete dictionary learning algorithm [4] to a group of connectivity patterns (in matrix form $X^{k \times n}$, $k = 400$, and $n = 193$) of this region:

$$\min_{D \in C, \alpha \in \mathfrak{R}^{k \times n}} \frac{1}{2} \sum_{i=1}^{n} \| x_i - D\alpha_i \|_2^2 \quad s.t. \quad \| \alpha_i \|_0 \le \lambda \; ; \; \text{and} \; C = \{ D \in \mathfrak{R}^{k \times p}, \&\& \; \forall j \in [1, p], \; (1-\beta) \| dj \|_2^2 + \beta \| dj \|_1 \le 1 \}$$

, which contains sparsity constraints on both the dictionary D and the loadings α. The dictionary element corresponding to the maximal summation of loadings was considered as the profile of this cortical region; (4) Affinity Propagation (AP) clustering [5] of resultant connectomic profiles of the entire cortex generated functional networks and their corresponding network profiles.

Results Figure 1A and 1B depict examples of connectomic profiles for a cortical region, posterior cingulate cortex or PCC, and default mode network or DMN, respectively. As highlighted by orange arrows in Fig. 1A, the learned connectomic profile of PCC closely follows its raw connectivity pattern, e.g., high positive intensity of the profile corresponds to strong positive connectivity while high negative intensity corresponds to
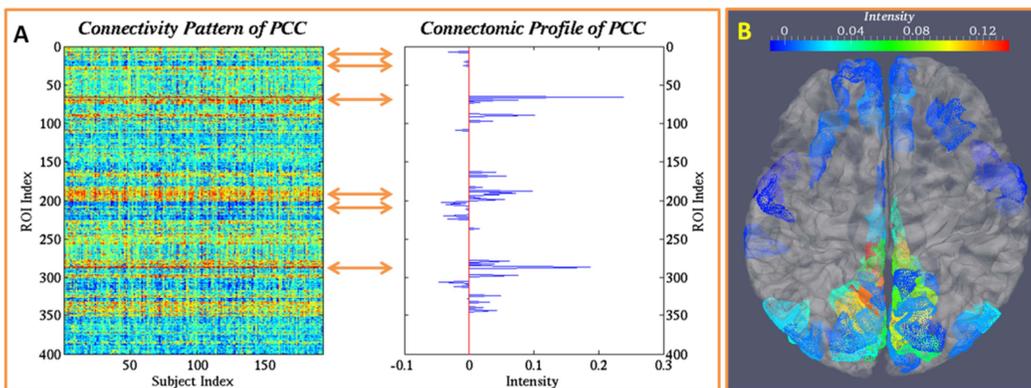

Fig. 1: Examples of connectomic profiles for PCC (A), and DMN (B).

strong negative connectivity. AP clustering of all resultant 400 connectomic profiles for the entire cortex generated 43 resting-state functional networks, and Fig. 1B shows the profile representation of DMN. As can be seen, bilateral PCCs have the strongest connectivity in DMN, bilateral anterior cingulate cortices and inferior parietal lobules have moderate connectivity, and superior temporal cortices demonstrate negative connectivity.

Discussion and Conclusion Our results indicate that connectomic profiles can accurately characterize connectivity patterns, and can be used for the identification of distinct cortical regions or functional networks. Unlike existing group ICA approaches that heavily rely on spatial smoothing and brain registration techniques, the framework described here utilized two measures, cortical parcellation by BOLD signal homogeneity and over complete dictionary learning, to account for the anatomical variability across individuals. Another particular feature of the present framework is that it not only creates profiles for networks but also for distinct functional regions, facilitating building statistical models for these profiles and pinpointing disrupted regions in pathological/psychiatric brain disorder datasets.

References

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