Cortical parcellation with graph representation learning on resting-state fMRI

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ABSTRACT

Cortical parcellation, which partitions the cerebral cortex into a set of disjoint regions, facilitates interpreting and comparing neuroscientific discoveries as well as reducing computational complexities of analyzing high-dimensional neuroimaging data. It has a close relationship with graph learning as it can be formulated as a clustering/community detection problem. In recent years, a number of novel graph representation learning methods have emerged, such as DeepWalk (1). These methods have not yet been fully exploited in brain parcellation despite their applicability. The few publications that doapply graph representation learning to generate brain parcellations, such as (2), emphasize methodology and lack detailed comparisons with popular parcellation schemes.

We introduce a set of novel cortical parcellations that use a recently developed graph node embedding method NetMF (3) which approximates DeepWalk (4) as matrix factorization. We construct a graph using a set of spatial maps of brain networks derived from resting-state functional magnetic resonance imaging (rsfMRI) data. Each map represents a different large-scale brain network. The spatial maps were obtained using a combination of temporal alignment (BrainSync (5, 6)) and a 3-way tensor decomposition method (NASCAR (7, 8)), which avoids imposing biologically implausible constraints such as orthogonality (as with PCA) or independence (as with ICA). We applied this method to minimally preprocessed 3T rsfMRI data for 500 subjects from the Human Connectome Project (HCP) (9, 10). We compared our parcellation with a comprehensive list of commonly used atlases (e.g., Yeo (11), Schaefer (12)) in terms of resting-state functional connectivity (RSFC) homogeneity and alignment with task contrasts, evaluated using a weighted average of task variance with parcels. In the 100-parcel setting, our atlas possesses a similar delineation of motor and primary visual areas as the Schaefer atlas, but presents distinct divisions in a number of other regions (Fig. 1). Results show that our parcellation schemes outperform other commonly used atlases in terms of homogeneity measures (Fig. 2) and task alignment (Fig. 3) across almost all scales (number of parcels).

KEYWORDS

Cortical parcellation; Resting-state fMRI; Graph representation learning; Tensor decomposition

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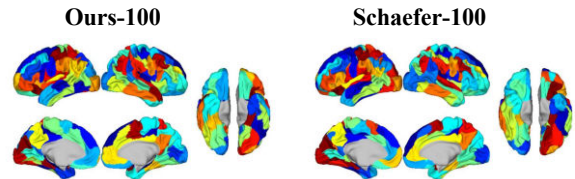6. A. A. Joshi, M. Chong, J. Li, S. Choi, R. M. Leahy, *NeuroImage*. **172**, 740–752 (2018).
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Fig. 1. Visualization of our atlas and Schaefer atlas. Both with 100 parcels.
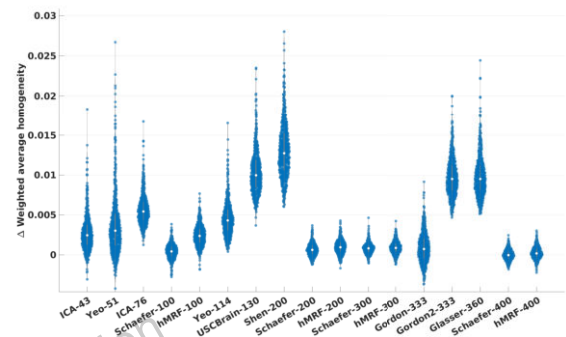

Fig. 2. Difference of RSFC homogeneity between ours and matched baseline atlas of each test subject in the HCP dataset. Each violin plot represents the pair-wise differences on 500 test subjects. Values greater than zero indicate that our parcellation is more homogeneous than the compared baseline.
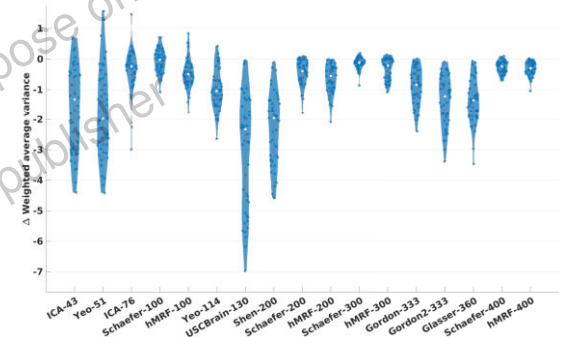

Fig. 3. Difference of task variance evaluated on 100 independent data sets from HCP. Each violin plot represents the pair-wise difference of the weighted contrast variance of our parcellation against the matched baseline parcellation for each of the 47 unique task contrasts. Values smaller than zero indicate our parcellation has higher agreement with the task contrasts than the baseline.