Revealing brain network communities with empirical mode decomposition and k-modes clustering

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INTRODUCTION

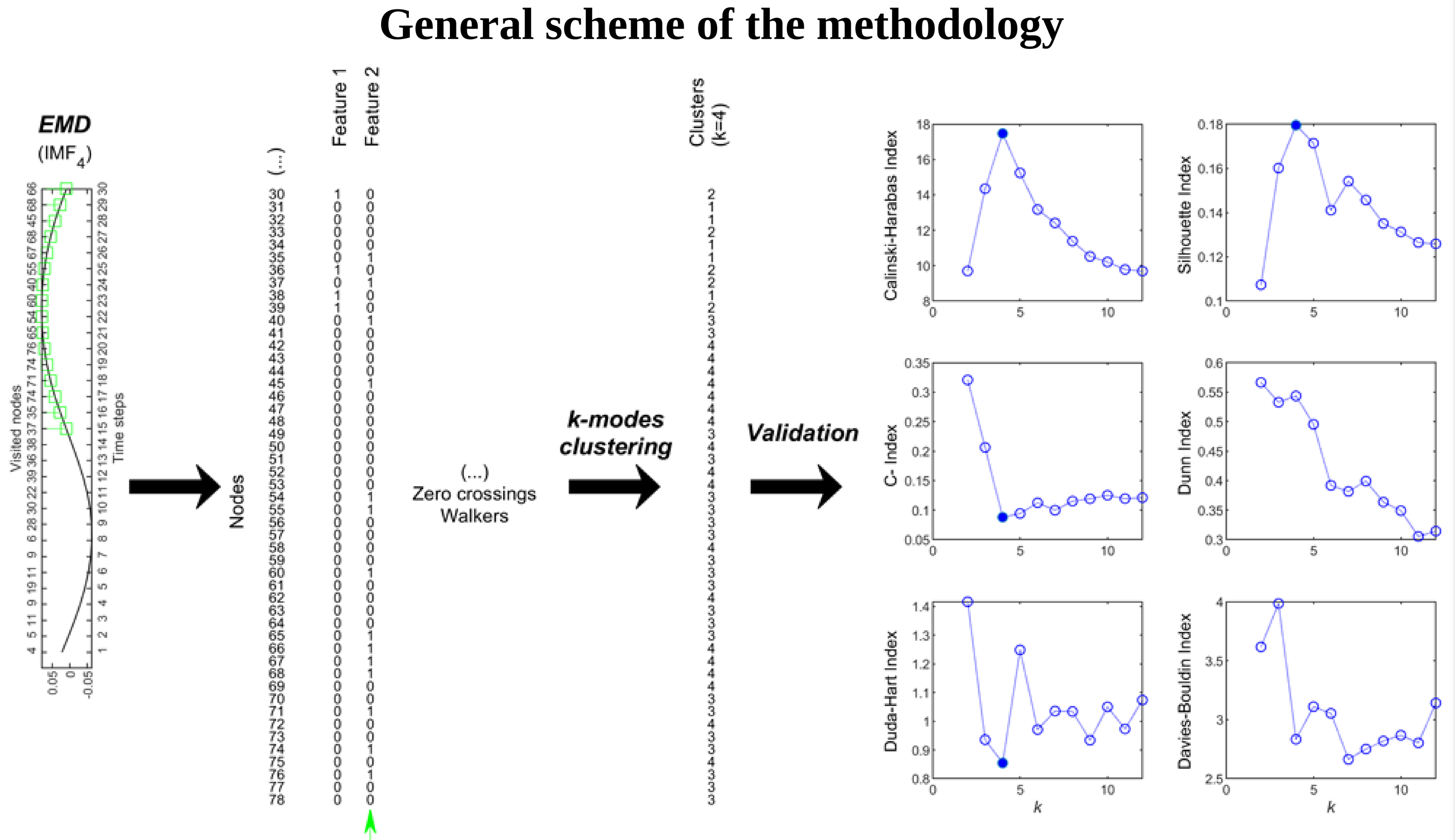
Effective community detection in the brain is critical for gaining insights into the processes of functional segregation and integration of information [1]. Works aiming at unveiling community structure generally build on the maximization of a modularity function [2]. These methods present deficiencies including being parameter-dependent and biased towards breaking down large communities [3]. We introduce an approach based on the analysis of a signal reflecting the information flow in the brain network. The signal's decomposition into intrinsic modes yields robust, quasi-parameter-free community finding at different scales.

METHODS

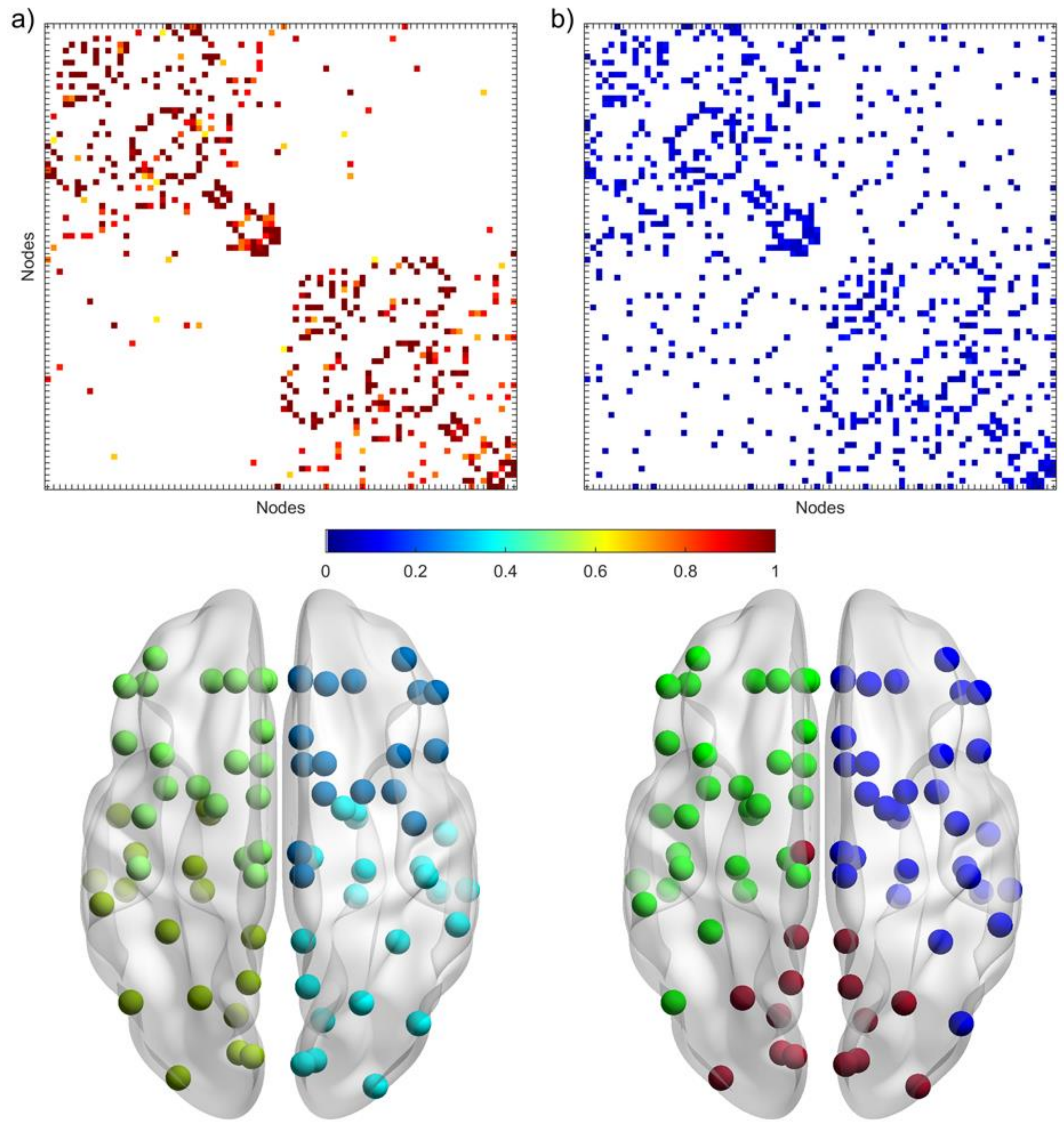
We release a high number of random walkers over the brain network. The evolution of the walker is described in terms of the fraction of walkers that a given one finds at each node [4]. The activity of the walkers is separated into oscillatory modes through empirical mode decomposition [5]. This allows the unveiling of a hierarchical organization. Intuitively, a walker would spend considerable times in large communities, which is seen in slow oscillatory modes –and vice versa. Finally, we employ the *k*-modes clustering algorithm [6], with clustering features that group nodes seen between zero crossings of the oscillatory mode. The correct number of clusters is elucidated through different adapted metrics [7].

An average healthy human brain anatomical network was constructed and analyzed (http://www.psy.cmu.edu/~coaxlab/data.html) [8,9], as well as the simulated functional connectivity of a set of Kuramoto oscillators [10] existing over the anatomical network. The community structure in the parcellated connectome of the human brain resting-state fMRI (https://www.fmrib.ox.ac.uk/datasets/HCP-CCA/) was also explored.

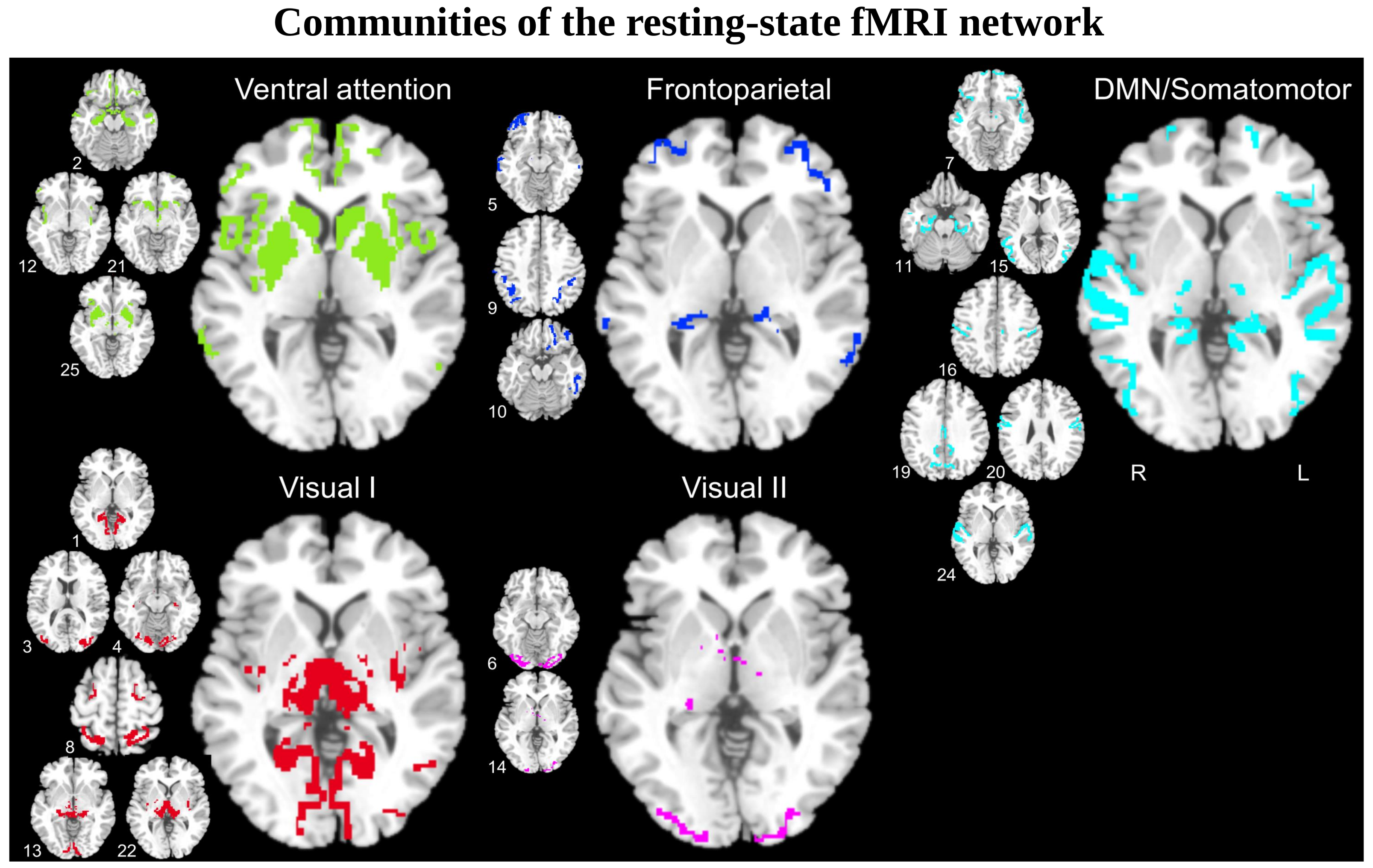
General scheme of the methodology



Communities of the anatomical and simulated functional networks



Communities of the resting-state fMRI network



RESULTS

We obtained two organizational levels of the anatomical connectivity matrix. The highest of the two consisted of two communities, the left and right hemisphere of the brain. Running the clustering algorithm with the features of the fourth fastest mode yielded a structure of subdivisions. This four-community organization is practically symmetrical except for three regions. The two communities to the top are mainly part of the frontal lobe, the cingulate cortex and the basal ganglia. On the other hand, those shown toward the bottom generally correspond with parietal, occipital and temporal areas. In the case of the synthetic functional network, two communities belonged to the left (nodes colored in blue) or right (in green) hemisphere. A third community consisted of fifteen inter-hemispherical regions, including all the occipital areas and others that also process visual stimuli.

In the resting-state fMRI connectome, five communities with a high degree of correspondence with well-established functional sub-systems [11] were identified. Allowing the overlapping nature of resting-state functional connectivity in the algorithm can yield further improvements.

CONCLUSIONS

- The observed partitions include specialized communities seemingly given by physical proximity and shared function. The detection of these communities supports the notion of functional integration and segregation.
- Our results stimulate the research of hierarchical community organization in terms of temporal scales of information flow.
- A specific set of codes containing a demonstration on how to concatenate the method pipeline is offered at https://www.soterolab.com/software.

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