

Investigating community detection algorithms and their capacity as markers of brain diseases

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In this paper, we present the workflow for evaluation of brain functional connectivity with different community detection algorithms, and their strengths to discriminate between health and brain disease. We further analyze the computational complexity of particular pipeline steps aiming to provide guidelines for both its execution on computing infrastructure and further optimization efforts.

The human brain consists of 10^{11} neurons interconnected with approximately 10^{14} connections creating large complex structure. This anatomical connectivity is a substrate for brain function which we can both measure and model on various scales. The goal of current research is understanding the brain as a system and its behavior as whole, i.e. identifying the spatiotemporal structure of brain function. This large-scale functional connectivity of neuronal populations is defined as statistical relations between neural activities of distinct brain cortical regions and is usually measured by fMRI (functional magnetic resonance imaging), EEG or MEG (electro/magneto-encephalography). The very promising tool is to model the system as a network using network science methodology, drawing inspiration from previous applications in research areas such as economics, transportation, communication or immunology.

The network analysis models complex system as a set of discrete units and describes interactions between them, and provides ways to measure the importance of nodes and detects communities, by diverse metrics (properties) describes topology and whole-system events or can be used to model the growth of the system in size. Primarily, network analysis is a data-driven technique and is an excellent tool to study real systems and to understand them. It requires interdisciplinary and big data processing approaches.

Neuroscience community puts great effort into finding a potential marker of disease that would be noninvasive, easy to establish and stable. In this paper, we evaluate strengths of community detection methods to differentiate between networks of healthy and diseased subjects on the example of MCI-AD and AD (Mild Cognitive Impairment and Alzheimer's Disease) as illnesses known to influence network topology. We apply discriminant analysis including parameter sweeps of methods for data preprocessing to quantify the ability of community detection algorithms to distinguish between patient and control and thus evaluate each one of them as a promising or inconclusive marker of a disease. The pipeline consists of a relatively large number of subsequent steps. We provide the analysis of the computational complexity which will guide further optimization efforts. Since we're dealing with large amounts of data we use computing infrastructure of MetaCentrum, CESNET, Czech Republic, to be able to analyze the data.

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