Towards understanding connectivity network within biomedical images

S. Shailja

The development of noninvasive neuroimaging and electrophysiological techniques has enabled scientists to expand the brain connectomics research. "Connectomics" aims at elucidating the wiring of brain networks with cellular resolution. Such data are indispensable for realistic modeling of brain circuitry and function. An important part of this research is to construct structural and functional connectivity networks of the human brain. The study of complex brain networks will not only promote the construction of the human brain connectome but also deepen our understanding of the important topological properties caused by brain disorders. Therefore, analysing these brain networks can provide important guidance for early diagnosis and treatment of brain disorders. As a computer vision researcher who is motivated to improve the health of communities, I am interested in contributing to this critical need.

Throughout my research career, I have been involved in developing AI algorithms to deduce elusive information using imaging data. Based on my experience, I believe the rise of graph theoretical analysis of brain networks are opening many new possibilities to study brain disorders. However, existing graph analysis approaches for connectomes do not exploit the richness of the imaging data that are available and hence cannot yet be generalized. For example, across different brain parcellation schemes, inconsistent results have been observed even for common graph metrics. It is clear that the current methods[1] do not adapt to the complexity of brain imaging data and primarily apply general network theory performance metrics not specific to the brain. I am interested in bridging this gap between graph-theoretic algorithms and brain image analysis.
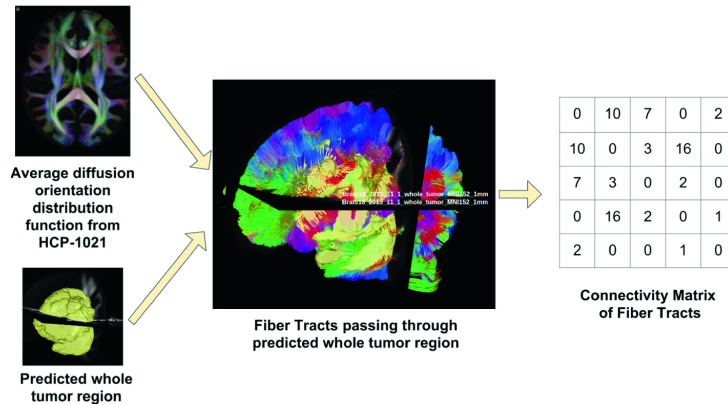

Figure 1: Workflow for building a connectivity matrix for each subject. The fiber tracts are created by DSI Studio (http://dsi-studio.labsolver.org/), and ITK-SNAP is used for visualizing the 3D MR images and 3D labels.

Before delving into brain connectivity analysis, I started my research career in computer vision for autonomous robots. I nurtured my ability to pursue proposed research work by developing central concepts of graph theory and image analysis in multiple degrees. At vision research laboratory at

---

[1]J. Wang, X. Zuo, and Y. He, "Graph-based network analysis of resting-state functional mri,"Frontiers in systems neuroscience, 2010.

UCSB, I further developed the required intuitions and concepts through different projects leveraging graph networks in the biomedical images. The biomedicine domain is increasingly turning into a data-intensive field that requires deep learning tools for analysis. However, the widespread use of such models is limited by the notion that they are 'black box' algorithms whose performance and robustness is difficult to characterize analytically. This is exacerbated by the fact that neural network models are by construction disconnected from the mechanistic aspects of the physical system. For biomedical applications, a mapping of physical parameters onto the learning models is crucial to provide insights. During my PhD research up until this point, I have aimed to develop methods and models to not just achieve high performance on singular benchmark metrics but also provide practical insights to the biologists. For example, in our recently published paper on brain tumor segmentation[2] and tractographic feature extraction[3] from structural MRIs, we presented a novel use of tractographic features as shown in Figure 1. It conveys how these features describe potential neural disruptions of different brain regions due to the brain tumor. I believe that biological insight along these lines are of utmost importance as it has potential to aid in the treatment of brain tumor patients.

The overall goal of my thesis is to develop theoretical concepts and algorithms to analyze the brain network using tractographic features. In particular, I propose the following tasks: 1) The commonly used two dimensional brain connectivity matrix loses the geometrical attributes of the connections and the image properties of the MRI. We will develop an AI-based algorithm to represent the brain network as a multidimensional graph to embed geometrical information of white matter. 2) We will adopt modern techniques involving pattern analysis, convolutional neural network (CNN) to measure the predictive power of brain regions in predicting labels, and generative models to measure informativeness of a label in generating brain regions. We will align these models with graph theoretical concepts that could transform our understanding of complex properties in the human brain networks. 3) We plan to develop a systematic approach to construct different graph metrics tailored to the human brain connectome for efficient computation and comparison across different subjects. Our approach will incorporate graph metrics that emerge out of desired biological/disease properties. We will develop methods to quantify the similarity/differences between connectivity matrices under various disease conditions. 4) By focusing the study on the ongoing collaborative research in our lab, we aim to elucidate the characteristics of brain connectivity matrix as well as the similarity index. Among the ongoing research in Vision Research Lab at UCSB, I find its applications in synapse classification for *Ciona*, Normal Pressure Hydrocephalus (NPH) detection, Alzheimer's disease analysis, and study of women health in pre-and post-menopause stage.

---

[2]P.-Y. Kao, S. Shailja et al. "Improving patch-based convolutional neural networks for mri brain tumor segmentationby leveraging location information," Frontiers in Neuroscience, 2020

[3]P.-Y. Kao, T. Ngo, et al. "Brain tumor segmentation andtractographic feature extraction from structural mr images for overall survival prediction," in International MICCAI Brain lesion Workshop, 2018.