Towards Completing and Annotating the Human Connectome With CGNN: Connectome Generation Neural Network

Jordan, Dean (School: International Academy)

The human brain is the most complex object in the universe, with over 86 billion neurons, each containing ~10,000 synapses. Determining the structure of the human brain in its entirety can provide a novel understanding of the neocortex in addition to a significantly deepened understanding of the brain as a driver of biological function. Standard methods of in-vivo and in-vitro connectome segmentation utilize electron microscopy on a series of two-dimensional imaging slices, employing existing learnable computational methods and extensive manual oversight to combine the slices into a three-dimensional connectome. However, while excellent in spatial and temporal resolution, these methods are highly ineffective for human connectome segmentation, with Drosophila being the largest organism with a segmented connectome. Hence, human connectome segmentation remains one of the most important open problems in neuroscience. This study develops CGNN, a machine learning tool for segmenting volumes of the human connectome via standard full-brain imaging techniques. CGNN is structured as a pipeline model whereby a series of independently-functioning neural networks generate and analyze domain knowledge to create an abstract representation of a connectome, which is then refined into a coordinate-bound, three-dimensional structure. CGNN consistently predicts personalized partial connectomes of the human brain with remarkably high accuracy. Furthermore, using neuro-symbolic programming and large language models, CGNN predicts unique hierarchical atlases for each predicted connectome volume, infers specific anatomical features, and enables further scientific experimentation. Thus, CGNN represents a limited solution to an open problem with numerous applications throughout neuroengineering.

Awards Won:
Second Award of $2,400