Connectome

A connectome is a comprehensive map of neural connections in the brain, and may be thought of as its “wiring diagram”. More broadly, a connectome would include the mapping of all neural connections within an organism's nervous system.

The production and study of connectomes, known as connectomics, may range in scale from a detailed map of the full set of neurons and synapses within part or all of the nervous system of an organism to a macro scale description of the functional and structural connectivity between all cortical areas and subcortical structures. The term “connectome” is used primarily in scientific efforts to capture, map, and understand the organization of neural interactions within the brain.

Research has successfully constructed the full connectome of one animal: the roundworm C. elegans (White et al., 1986, Varshney et al., 2011. Partial connectomes of a mouse retina and mouse primary visual cortex have also been successfully constructed. Bock et al.'s complete 12 TB data set is publicly available at Open Connectome Project.

The ultimate goal of connectomics is to map the human brain. This effort is pursued by the Human Connectome Project, sponsored by the National Institutes of Health, whose focus is to build a network map of the human brain in healthy, living adults.

Brain mapping has entered a new era focusing on complex network connectivity. Central to this is the search for the connectome or the brains 'wiring diagram'. Graph theory analysis of the connectome allows understanding of the importance of regions to network function, and the consequences of their impairment or excision.

Resting state functional magnetic resonance imaging data were acquired using multi-echo, echo planar imaging pre-operatively from five participants each with a right temporal-parietal-occipital glioblastoma. Complex networks analysis was initiated by parcellating the brain into anatomically regions amongst which connections were identified by retaining the most significant correlations between the respective wavelet decomposed time-series.

Key characteristics of complex networks described in healthy controls were preserved in these patients, including ubiquitous small world organization. An exponentially truncated power law fit to the degree distribution predicted findings of general network robustness to injury but with a core of hubs exhibiting disproportionate vulnerability. Tumours produced a consistent reduction in local and long-range connectivity with distinct patterns of connection loss depending on lesion location.

Connectome analysis is a feasible and novel approach to brain mapping in individual patients with brain tumours. Applications to pre-surgical planning include identifying regions critical to network function that should be preserved and visualising connections at risk from tumour resection. In the future one could use such data to model functional plasticity and recovery of cognitive deficits 1).

Resting-state and task-based functional connectivity matrices, or connectomes, are powerful predictors of individual differences in phenotypic measures. However, most of the current state-of-the-art algorithms only build predictive models based on a single connectome for each individual. This approach neglects the complementary information contained in connectomes from different sources and reduces prediction performance. In order to combine different task connectomes into a single predictive model in a principled way, we propose a novel prediction framework, termed multidimensional connectome-based predictive modeling. Two specific algorithms are developed and implemented under this framework. Using two large open-source datasets with multiple tasks-the Human Connectome Project and the Philadelphia Neurodevelopmental Cohort, we validate and compare our framework against performing connectome-based predictive modeling (CPM) on each task connectome independently, CPM on a general functional connectivity matrix created by averaging together all task connectomes for an individual, and CPM with a naïve extension to multiple connectomes where each edge for each task is selected independently. Our framework exhibits superior performance in prediction compared with the other competing methods. We found that different tasks contribute differentially to the final predictive model, suggesting that the battery of tasks used in prediction is an important consideration. This work makes two major contributions: First, two methods for combining multiple connectomes from different task conditions in one predictive model are demonstrated; Second, we show that these models outperform a previously validated single connectome-based predictive model 2).

Connectome-guided resection

Connectome-guided resection

1) Hart MG, Price SJ, Suckling J. Connectome analysis for pre-operative brain mapping in neurosurgery. Br J Neurosurg. 2016 Jul 22:1-12. [Epub ahead of print] PubMed PMID: 27447756.

2) Gao S, Greene AS, Constable RT, Scheinost D. Combining multiple connectomes improves predictive modeling of phenotypic measures. Neuroimage. 2019 Jul 20:116038. doi: 10.1016/j.neuroimage.2019.116038. [Epub ahead of print] PubMed PMID: 31336188.