**Medical Image Computing**

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**Paper Name: Supervised Multi-topology Network**

**Cross-diffusion for Population-driven Brain**

**Network Atlas Estimation**

Questions/Answers

**Q1: How to visualise brain anatomy using graphs?**

Graph theory provides a theoretic framework to represent the whole brain as a brain network and analyzing its topology. This network has associations and connections between various regions and subregions in the brain and can be defined as a graph G (V, E) , where nodes (V) may represent voxels or ROIs.For example, the Automated Anatomical Labeling (AAL) atlas divides the whole brain into 116 distinct brain structures (90 cortical and subcortical regions and 26 cerebellar regions).For each region, the representative time course in each region was obtained by averaging the time series across all voxels in the region. Then, the weight of each edge (e ∈ E) in the brain network was computed based on the correlation coefficient between time series from all pairs of regions.

**Q2: How to use topological measurements to determine important regions?**

Recent research has shown that graph theory based complex network analysis provides a powerful framework for examining the topological properties of brain networks, where nodes represent brain regions, and edges represent the functional connections between brain regions .Topological properties of brain networks can be derived at the large-scale of the whole brain, i.e. metrics on the entire graph; at the intermediate scale of several regions of the brain. It follows that the selection of the topological metrics is an important step that requires great attention. Depending on the nature of the neuroimaging experiment, the functional connections, and the thresholding method, some graph indices can result in being more appropriate than other ones.

**Q3: How to distinguish between a healthy and a non-healthy brain?**

Graph matching is an essential step for inference and classification analyses on brain graphs. Graph matching is the process of finding a correspondence between the nodes and the edges of two or more graphs that satisfies some (more or less stringent) constraints ensuring that similar substructures in one graph are mapped to similar substructures in the others. In realistic applications, the matching is done by comparing the model graph which is stored in a file and an input graph that is given at the run time.