

Skeptical Connectivity: Time for Something Completely Different

Organizers:

Victor Solo

University of New South Wales, Australia; MGH-Martinos Center for Biomedical Imaging, Harvard Medical School, Boston, MA, United States

DuBois Bowman

Columbia University, New York, NY, United States

The advent of high quality data from the human connectome project has given additional impetus to the study of brain connectivity; already a subject of intense interest for at least a decade. But existing approaches seem to have reached some kind of stasis. Typical analyses proceed as follows: summarise a set of cortical parcels by representative time series; thus compute a correlation matrix; then apply some kind of threshold to it; then draw some network related conclusions perhaps using graph analysis. Certainly, recently some more sophisticated methods have come into play such as: sparsity; a lumbering recognition that partial correlation should replace correlation; the recent concern with time-variant connectivity. But signs that all is not well are emerging: the big data aspect has largely been ignored i.e. the fact that the correlations are enormously noisy so that embarrassingly spurious results (e.g. in the small world network domain) have been 'obtained'. And very importantly the compelling potential to find biomarkers for disease has not so far eventuated. Clearly something new is needed.

In this workshop we pursue three angles. Firstly there is huge data wastage in reducing each parcel to a single time series. So we will exhibit a new multivariate conditional mutual information-based method that uses all the data. Secondly new methods are emerging in the physics/sociology/applied mathematics/statistics network sciences and we will highlight two of them. We will illustrate the use of emerging network methods from statistics and sociology based on so-called block models. We will also illustrate the use of the powerful new tool of topological data analysis for network comparison. Without the use of all the data; without the use of more sophisticated methods of network science we cannot hope to realise the potential of biomarker discovery. Attendees will come away from the workshop with a clear understanding of the problems with current methods of brain connectivity analysis. They will gain a basic understanding of three powerful new approaches which tackle brain connectivity from very different directions while overcoming the weaknesses of current methods.

Discovering network structure with flexible, multi-subject stochastic block models

Thomas Nichols, Warwick University, Warwick, United Kingdom

Mapping heritability of large-scale brain network via persistent homology

Moo Chung, University of Wisconsin, Madison, WI, United States

Multivariate Mutual Information Finds the Secrets of Resting-State Functional Brain Networks

Victor Solo, University of New South Wales, Australia; MGH-Martinos Center for Biomedical Imaging, Harvard Medical School, Boston, MA, United States

