A Statistical Method for Advancing Neuroimaging Genetics

Xuan Bi and Heping Zhang

Analyzing neuroimaging and genomic data is critical to the understanding of brain function. With the advent of modern technology, it has become feasible to collect both neuroimaging and genomic data from large-scale studies, such as the Philadelphia Neurodevelopmental Cohort (PNC) and the Pediatric Imaging, Neurocognition, and Genomics Study (PING). Utilization of such big data becomes a bottleneck that desperately needs to be resolved. In particular, insufficient work has been done through incorporating neuroimaging and genomic data simultaneously, which is known to be challenging and complex. Such analysis includes large volumes of complex information (e.g., multi-modality imaging, genetic, neurocognitive, and clinical), which is an emerging need and more daunting than analyzing typical neuroimaging data or genomic data. We develop an innovative and advanced statistical method that can better define the phenotypes by considering both neuroimaging and clinical data and can better combine generic variants. This strategy will maximize the power to identify genetic variants that have the biological implications through brain function and improve the quality of genetic studies over those based on the use of clinical diagnosis alone as the phenotypes.