Abstract:
Genetic studies completed over the past decade have identified numerous genetic variants contributing to common psychiatric traits. However, despite high overall trait heritability of diseases such as bipolar disorder, risk variants identified thus far explain a relatively small proportion of variation in these traits. Furthermore, recent studies have demonstrated a very high level of polygenicity underlying many psychiatric conditions, which poses considerable challenges for risk gene identification and risk prediction. These observations reveal the difficulties facing the implementation of precision medicine in psychiatry. The high polygenicity of psychiatric traits is believed to be driven partly by a high degree of underlying clinical and genetic heterogeneity. In this talk I will give examples of analyses that take into account phenotypic heterogeneity to identify genetic risk factors for complex psychiatric traits and to learn about their genetic architecture. I will also discuss the need for development of statistical methods that can address genetic heterogeneity in studies of complex traits, both in the search for contributing risk factors and in risk prediction.