Division of Biostatistics
Seminar Series Fall 2014

“Schizophrenias”: a translational person-centered analysis

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Friday, Oct 17, 2014, 12:30–1:30 pm
Graduate Program classroom, 3rd Floor in Shriner's Building
Coffee, water, and cookies will be provided

Abstract

Patients with mental disorders may receive the same diagnosis, yet share few symptoms in common, vary widely in severity, and respond differently to treatments. Genetic association studies of mental disorders were plagued by weak and inconsistent findings, largely due to clinical
and etiologic heterogeneity of cases when people were described only as having the disorder or not (cases vs. controls). Clinical classifications without regard for measured genotypic differences also failed to predict response to treatment. As a result, the APA’s official diagnostic manual (DSM-5) proposes to describe variation in a particular mental disorder along continuous dimensions; however, no one knows how to subdivide a mental disorder into evidence-based subtypes that have distinct genetic causes, symptoms, and treatments. Individual genes do not consistently cause a complex mental disorder; rather, it takes many genes operating in concert. In a recent multidisciplinary research effort, we developed a machine learning method termed PGMRA that allowed us to show for the first time, to the best of our knowledge, that schizophrenia can be subdivided into at least 8 heritable syndromes that differ in symptoms and severity of illness, each associated with different cluster of genes acting in concert. The sets of interacting genes identified convey an extremely high and consistent risk (70-100%) that replicates across 3 independent samples. The subjacent developmental and neurochemical pathways can lead to different schizophrenia syndromes. These results open the door for translational scientists to design effective personalized treatments for individuals founded on the basis of their illness. We will show results of a broader application that includes image analysis.