Genome-Wide Association Study of Schizophrenia Using Bayesian Variable Selection Methods: Biological Insights and Practical Implications

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ABSTRACT
Schizophrenia is a severe mental disorder with substantial heritability. We conducted a reanalysis for the Molecular Genetics of Schizophrenia (MGS) dataset using Bayesian Variable Selection (BVS) method developed by Guan and Stephens in 2011. In the original publication, the MGS study identified a single locus at the major histocompatibility complex region that contributes to the development of schizophrenia. Using the exact same data of the MGS European ancestry case-control sample (2681 cases, 2653 controls), we identified 5 loci and some of these loci were the same as found in a later study with a much larger dataset of 150,000 subjects. We demonstrate that the BVS methods are powerful and capable of discovering association signals that otherwise would need a much larger sample size to discover. Our study has important implication that we can use the BVS methods to reanalyze published data sets to discover new risk variants for many diseases without new sample collection, ascertainment and genotyping.

12:00 Noon, Tuesday, October 30, 2018
47 College Street, Room 106B
11:45 AM - Lunch served outside Room 106B