Assessing Thought Disordered Behavior Using Finite Mixture Models

Charity Morgan
University of Alabama at Birmingham

ABSTRACT

Schizophrenia is a genetically complex mental illness in that multiple genes are thought to be involved and the mode of transmission is not Mendelian. Recent research has focused on studying the clinically well first-degree relatives of schizophrenic patients, some of whom may be non-penetrant carriers of schizophrenia genes. A number of traits that are associated with schizophrenia and that aggregate in relatives of schizophrenics at a rate much higher than that of the clinical disorder have been identified. These traits, provisionally identified endophenotypes, may be alternative manifestations of schizophrenia genes that are more penetrant than schizophrenia itself. The presence of alternative manifestations may help to identify healthy relatives who have inherited one or more of the genes that increases susceptibility for schizophrenia. One of these traits is thought disorder with "schizophrenic" features. In the first part of this talk, we apply finite mixture models to a sample of normal controls and clinically unaffected first-degree relatives of schizophrenic patients as a first step towards using these potential alternative manifestations of schizophrenia genes to uncover more information about the heritability of the disorder.

We note that in order to justify the use of the previous model, which assumes independent observations, we fit this model to a subsample of the original data. In the second part of this talk, we demonstrate that the original model is not appropriate for the full data set and we develop a hierarchical model that can accommodate correlated data. We demonstrate the efficacy of this model and provide further evidence for the addition of thought disorder with schizophrenic features to the schizophrenia phenotype.