

STANFORD UNIVERSITY
DEPARTMENT OF STATISTICS
Joint Statistics/Biostatistics Seminar

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A Latent Variable Model of Segregation Analysis for Ordinal Traits

Many health conditions including cancer and psychiatric disorders are believed to have a complex genetic basis, and genes and environmental factors are likely to interact one another in the presence and severity of these conditions. Assessing familial aggregation and inheritability of diseases is a classic topic of genetic epidemiology, which is commonly referred to as segregation analysis. While it is routine to conduct such analyses for quantitative and dichotomous traits, there do not exist methods and software that accommodate ordinal traits. To this end, we propose a latent variable model by extending the work of Zhang and Merikangas (1999) who examined binary traits. The advantage of this latent variable model is its flexibility to include environmental factors (usually represented by covariates) and its potential to allow gene-environment interactions. The model building employs the EM algorithm for maximization and a peeling algorithm for computational efficiency. The statistical inference can be made based on the asymptotic theory, a permutation procedure as well as simulation studies. At the end, I will use this model to analyze the familial transmission of alcoholism.

This is a joint work with Rui Feng, Hongtu Zhu, and Kathleen Merikangas.