

STANFORD UNIVERSITY
DEPARTMENT OF STATISTICS
DEPARTMENTAL SEMINAR

4:15 p.m., Tuesday, January 31, 2006
Sequoia Hall Room 200
(Cookies at 3:45 in 1st Floor Lounge)

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**MCMC Linkage Analysis for Two Genes and
a Polygenic Component on General Pedigrees**

Linkage analysis involves statistical inference about the location of genes influencing a trait, using trait and genetic marker data collected on families. We describe a new approach, implemented in a computer program, for parametric linkage analysis with a quantitative trait model having one or two genes and a polygenic component, which models additional familial correlation from other unlinked genes. Competing programs use simpler models: one gene, one gene plus a polygenic component, or a crude approximation to the two gene model. Using simple models when they are incorrect, as for complex traits that are influenced by multiple genes, can bias estimates and reduce power to detect linkage. Simulated examples, with various sizes of pedigrees, show that two-gene analysis correctly identifies the location of both genes, whereas other analyses based on simpler models fail to identify the location of genes with modest contributions.

We compute the likelihood with MCMC realization of segregation indicators at hypothesized gene locations conditional on marker data, summation over phased multilocus genotypes of founders, and peeling of the polygenic component. This is the first program for two genes and a polygenic component. It has no restriction on number of markers or complexity of pedigrees, facilitating use of more complex models with general pedigrees.

This is joint work with Elizabeth Thompson and Ellen Wijsman.