1014-62-1059 **Ingileif Bryndis Hallgrimsdottir*** (`ingileif@stat.berkeley.edu`), Department of Statistics, University of Oxford, 1 South Parks Road, OX1 3TG Oxford, England. *Genetic linkage analysis.*

Most common diseases have a genetic component and many interacting genes play a role in the disease etiology. It is of great interest to identify these genes and genetic linkage analysis is concerned with exactly that, finding the chromosomal location (locus) of disease genes.

A k-locus model for disease is a k-dimensional subvariety of a $(3^k - 1)$-dimensional probability simplex. We have determined the algebraic invariants of these models with general characteristics for $k = 1$. For $k = 2$ we show that the algebraic invariants can be presented as determinants of 32×32 matrices of linear forms in 9 unknowns. In the special case of a multiplicative model, where there is no interaction between the two loci (genes), we determine the complete set of algebraic invariants that define it. By writing the likelihood ratio as a function of these invariants we can determine under what conditions a two-locus test has more power than a traditional one-locus test for linkage.

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