The University of Chicago

Department of Statistics

Seminar

Matthew Stephens

Department of Statistics, University of Washington

"Exploring Heterogeneity in Recombination Rates Across the Genome"

Monday, May 12, 2003 at 4:00 PM
133 Eckhart Hall, 5734 S. University Avenue

ABSTRACT

There has been a great deal of recent interest in the idea that patterns of genetic variation in humans exhibit a "block-like" structure, with high correlations between positions within blocks, and low correlation between blocks. There has also been much speculation, and occasionally experimental confirmation, that this structure is due, at least in part, to variation in local rates of recombination, and in particular to the presence of "recombination hotspots". However, current methods for investigating the link between recombination rates and patterns of variation in population data are limited: either they are computationally intractable for even rather small datasets, or they are unable to make quantitative statements about the strength of the evidence for the existence of a hotspot, or its magnitude if it does indeed exist. In this talk I describe a statistical method that comes some way towards addressing these deficiencies, and demonstrate its effectiveness on both simulated and real data.

4/23/03