

April 19, 2005

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South Hall 5607F
(Sobel Seminar)

SOBEL LECTURE

Sobel Lecture Series

The Sobel Lecture is an annual lecture series in memory of Professor Milton Sobel funded by an endowment from Mrs. Florence Sobel, his wife.

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Statistics and Applied Probability*

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Fuzzy p-values in the detection of genetic linkage

Genetic linkage between two genome locations is dependence in the inheritance of genome at those locations. This dependence leads to individuals who share a trait of interest having increased probability of sharing genome at locations that are linked to genes that affect the trait. Tests for genetic linkage capitalize on detection of regions of the genome that exhibit this increased sharing among individuals of like trait phenotype. However, genome sharing is unobservable, and in standard testing approaches the uncertainty in latent genome sharing is confounded with strength of the evidence for linkage. Fuzzy p-values have recently been introduced by Geyer and Meeden (2005: in press) in a different context. In the current context, they provide a way to express both the strength of the evidence for linkage and the uncertainty in that evidence. The approach is applicable to any situation where the ideal measure of evidence is a function of unobservable latent variables, provided only realization of these variables conditional on observed data is possible.

Dr. Thompson is a Professor of Statistics and an Adjunct Professor of Genome Sciences at University of Washington. Her research interest is in the development of methods for inference from genetic data, and particularly from data observed on large and complex pedigree structures. Questions of interest range from analyses of long-term gene frequency differentiation in widely dispersed populations, to short-term extinction of genes in the small population of a highly endangered species; from inference of genealogical relationships among individuals to inference of the genetic basis of traits from data observed on members of a known pedigree; and from analyses of patterns of genome sharing in plants to modern methods for human linkage analysis. In recent years, several of these questions have been addressed using Monte Carlo likelihood.

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