



Dr. Clarice Weinberg

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Using nuclear families to find genes related to conditions with onset early in life

**Note Time Change from
Regular Schedule!**

**Friday, Jan 27th, 2012
1:00–2:00 p.m.**

The Hospital for Sick Children

CDIU Multimedia Theatre

Room 4132, 4th Floor, Elm Elevators

555 University Avenue, Toronto, ON

Abstract: For complex but rare conditions, such as birth defects, where genetic variants confer a fairly small relative increase in risk, pedigree-based linkage studies have limited ability to localize risk-relevant genes. For such conditions, geneticists can use other approaches, such as family-based or population-based association studies. This talk will introduce some approaches to association mapping.

Likelihood-based methods of analysis based on genotyping affected individuals and their parents, as a “triad,” allow for use of standard software, permit estimation of relative risks, provide robustness against bias due to self-selective recruitment and population stratification, and allow for extensions that can account for missing parental genotypes, for maternally-mediated genetic effects, and for parent-of-origin effects. If time permits, extensions to quantitative traits and gene-by-environment effects will be explored, together with an extension of the design to include an unaffected sibling, which produces a tetrad and enables estimation of main effects of exposures.

Profile: Dr. Weinberg earned her Ph.D. in Biomathematics from the University of Washington in Seattle in 1980. After serving on the faculty of the Department of Biostatistics in Seattle for two years, she came to the biostatistics group at NIEHS in 1983, where she has headed up the Biostatistics Branch since 1997. She was elected Fellow of the American Statistical Association in 1995, and is on the editorial board of Environmental Health Perspectives and serves as statistical editor for the American Journal of Epidemiology. She holds adjunct professorships in both the Department of Epidemiology and the Department of Biostatistics at the School of Public Health at UNC, and has coauthored more than 200 peer-reviewed publications. She delivered the distinguished Greenberg lectureship in Biostatistics at the UNC School of Public Health in 1998, and was awarded both the Nathan Mantel award and the Janet Norwood award in 2005 for her contributions to statistical epidemiology and genetics. Her current research interests are in statistical methods related to the design and analysis of studies in epidemiology, statistical genetics as applied to family-based studies of qualitative and quantitative traits, and data mining for analysis of high-dimensional data.

Housed at the University of Toronto Dalla Lana School of Public Health, **CIHR STAGE** is a training program in genetic epidemiology and statistical genetics funded by the Canadian Institutes of Health Research through the Strategic Training Initiative in Health Research program. Seminars are sponsored by The Hospital for Sick Children, the Samuel Lunenfeld Research Institute of Mount Sinai Hospital, the Ontario Institute for Cancer Research, the Department of Statistics of the University of Toronto, the Ontario Cancer Institute of the University Health Network, and the CIHR Institute of Genetics.