# CIHR STAGE

Strategic Training for Advanced Genetic Epidemiology

International Speaker SEMINAR Series

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**Harvard School of Public Health**

# Statistical Genetics and Genomics in the Big Data Era: Opportunities and Challenges in Research and Training

**Friday**
**June 6, 2014**
**12:00 – 1:00 pm**

The Hospital for Sick Children
CDIU Multimedia Theatre
Room 4132, 4th Floor, Elm Elevators
555 University Avenue, Toronto, ON

**Abstract:** The human genome project in conjunction with the rapid advance of high throughput technology has transformed the landscape of health science research. The genetic and genomic era provides an unprecedented promise of understanding genetic underpinnings of complex diseases or traits, studying gene-environment interactions, predicting disease risk, and improving prevention and intervention, and advancing personalized medicine. A large number of genome-wide association studies conducted in the last ten years have identified over 1,000 common genetic variants that are associated with many complex diseases and traits. Massive next generation sequencing data as well as different types of 'omics data have become rapidly available in the last few years. These big genetic and genomic data present statisticians with many exciting opportunities as well as challenges in data analysis and interpretation of results. They also call for more interdisciplinary knowledge and research, e.g., in statistics, machine learning, data curation, molecular biology, genetic epidemiology and clinical science. In this talk, I will discuss some of these challenges, such as analysis of next generation sequencing association studies; integrative genomics, which integrates different types of 'oimcs data; and reproducible research. I will also discuss strategies of training next generation quantitative genomic scientists at the interface of statistical genetics and genomics, computational biology and genetic epidemiology, to meet these challenges.

**Profile:** Dr. Lin is Professor of Biostatistics and Coordinating Director of the Program of Quantitative Genomics at the School of Public Health of Harvard University. Dr. Lin's research interests lie in statistical genetics and 'omics, especially development and application of statistical and computational methods for analysis of high-throughput genetic, and 'omics data in epidemiological and clinical studies; and in statistical methods for analysis of correlated data such as longitudinal, clustered and family data. Dr Lin's specific areas of expertise include statistical methods for genome-wide association studies and next generation sequencing association studies, genes and environment, mixed models, and nonparametric and seimparametric regression. She received the 2006 Presidents' Award for the outstanding statistician from the Committee of the Presidents of Statistical Societies (COPSS), and the 2002 Mortimer Spiegelman Award for the outstanding biostatistician from the American Public Health Association. She is an elected fellow of the American Statistical Association, Institute of Mathematical Statistics, and International Statistical Institute. Dr. Lin was the Chair of the Committee of the Presidents of the Statistical Societies (COPSS) between 2010 and 2012. She is currently a member of the Committee of Applied and Theoretical Statistics of the US National Academy of Science. Dr. Lin is a recipient of the MERIT (Method to Extend Research in Time) from the National Institute of Health, which provides a long-term research grant support. She is the PI of the T32 training grant on interdisciplinary training in statistical genetics and computational biology. She has served on numerous editorial boards of statistical journals. She was the former Coordinating Editor of Biometrics, and currently the co-editor of Statistics in Biosciences, and the Associate Editor of Journal of the American Statistical Association and American Journal of Human Genetics. She was the permanent member of the NIH study section of Biostatistical Methods and Study Designs (BMRD), and has served on a large number of other study sections at NIH and NSF.

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