



Dr. Sharon Browning

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Department of Biostatistics
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Identity by descent in “unrelated” individuals

Friday
October 5, 2012
12:00 – 1:00 p.m.

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

Sharon Browning is a Research Associate Professor in the Department of Biostatistics at the University of Washington in Seattle. She earned her PhD in Statistics from the University of Washington under the supervision of Elizabeth Thompson. She has previously held positions at North Carolina State University, GlaxoSmithKline and the University of Auckland in New Zealand.

Dr. Browning’s research involves development of statistical methods for analyzing large-scale genetic data, with a particular focus on models for haplotype frequencies. With Dr. Brian Browning she developed the methodology implemented in the BEAGLE software package. This methodology includes haplotype phase inference, genotype imputation, inference of identity by descent segments, and haplotypic association testing. Dr. Browning was also co-developer (with Dr. Bo Madsen) of the weighted-sum method for rare variant association testing.

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.

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