

CIHR STAGE

*Strategic Training
for Advanced Genetic
Epidemiology*



**Lunenfeld-Tanenbaum
Research Institute**
Sinai Health System

The **Lunenfeld-Tanenbaum
Research Institute** is a proud
partner of **CIHR STAGE** and jointly
presents:



Dr. Daniel J. Schaid

Curtis L. Carlson Professor of Genomics Research
Division of Biomedical Statistics and Informatics
Mayo Clinic

Statistical Fine-Mapping: Methods to Move Beyond Genome- Wide Association Studies

**Friday
March 2, 2018
12:00 – 1:00 pm**

The Hospital for Sick Children
Daniels Hollywood Theatre
Room 1246, 1st Floor, Black Wing
555 University Avenue, Toronto, ON

Abstract:

Advancing from statistical associations of complex traits with genetic markers to understanding the functional genetic variants that influence traits is often a complex process. Fine-mapping genetic variants can prioritize and select variants for further study, yet the multitude of analytic strategies and study designs makes it challenging to choose an optimal approach. I will review the strengths and weaknesses of different fine-mapping approaches, emphasizing the main factors that lead to success. Topics include interpreting results from genome-wide association studies, the role of linkage disequilibrium, statistical fine-mapping approaches, trans-ethnic studies, genomic annotation and data integration, and other analysis and design issues.

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