

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. Goncalo Abecasis

Felix E. Moore Collegiate Professor and Department Chair
Department of Biostatistics
University of Michigan School of Public Health

Sequencing and Analysis of 10,000s of Human Genomes: Challenges and Opportunities

**Friday
February 3, 2017
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:

Rapid advances in genome sequencing and genotyping technology are enabling increasingly detailed analysis of human genetic variation. In the next year, we expect to analyze >50,000 deeply sequenced human genomes, corresponding to ~5 million billion bases of raw sequence data. The generation, transfer and analysis of the data present many opportunities for scientific discovery - enabling better understanding of human history, biology and disease. It also presents varied computational and analytical challenges as well as opportunities to develop and implement new analytical strategies and modes of data sharing. I will illustrate these challenges and opportunities with examples from ongoing studies.

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