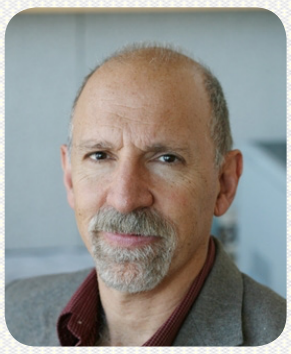
CIHR STAGE

Strategic Training for Advanced Genetic Epidemiology

The **Genetics and Genome Biology Program** is a proud partner of **CIHR STAGE** and jointly presents:



Dr. Neil Risch

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Genetic Epidemiology Research Based in Electronic Health Records

Part 1. Population Structure, Mating Patterns and Self-Identified Race/Ethnicity

Thursday **June 1, 2017** **9:00am to 10:00am**	Peter Gilgan Centre for Research and Learning Main Auditorium, Second Floor 686 Bay Street, Toronto, ON

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Part 2. Linking the genome to longitudinal disease and trait data

Friday **June 2, 2017** **12:00pm to 1:00pm**	The Hospital for Sick Children Daniels Hollywood Theatre Room 1246, 1st Floor, Black Wing, 555 University Avenue, Toronto, ON

Abstract:

These two talks will focus primarily on the Kaiser Permanente Northern California Research Program on Genes, Environment and Health (RPGEH), and the Genetic Epidemiology Research on Adult Health and Aging (GERA) cohort derived therefrom. This multi-ethnic cohort, established in 2005, is representative of Northern California and contains over 100,000 individuals with comprehensive electronic health record data that dates back over 20 years for most individuals. In 2009, genome-wide genotype and telomere length data were added through an NIH Grand Opportunity Award, facilitating genetic epidemiologic research on a large scale.

In the first of the two lectures, we will focus on the demographic structure of this cohort, which contains a large number of spouse, parent-child and sibling pairs. We show the relationship between how individuals self-identify in terms of race/ethnicity/nationality and their genetic ancestry, and also mating patterns that have and continue to determine the population genetic structure of the sample.

In the second of the two lectures, we will focus on the application of the genome-wide genotype and telomere data to a number of disease and clinical trait outcomes. The resource includes all aspects of care, including laboratory tests, pathology reports, physiologic tests and pharmacy prescription data, in addition to clinical diagnoses. Through examples, we demonstrate the power of this clinically homogeneous resource for gene discovery, as well as gene characterization through longitudinal analyses based in the EHR data. We also provide examples of cross-ethnic analyses, pleiotropy, pharmacogenetics and heritability.

CIHR **STAGE** is a training program in genetic epidemiology and statistical genetics, housed at the University of Toronto Dalla Lana School of Public Health, and 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 Lunenfeld-Tanenbaum Research Institute of Mount Sinai Hospital; the Ontario Institute for Cancer Research; the McLaughlin Centre of the University of Toronto; the Ontario Cancer Institute of the University Health Network; and the CIHR Institute of Genetics.

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