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:

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Addressing the Correlated Feature in Sequencing-Based DNA Methylation Data for Detection of Differentially Methylated Regions

Friday
June 3, 2016
12:00 – 1:00 pm

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

Abstract:
DNA methylation is an epigenetic change occurring in genomic CpG sequences that contribute to the regulation of gene transcription both in normal and malignant cells. In recent years, aided by fast parallel sequencing technology, a number of genome-wide platforms have been developed to provide high throughput DNA methylation data. They can be classified as bisulfite-based (BS-seq) or capture-based (Cap-seq), both producing a massive amount of data. Numerous sophisticated statistical methods have been developed to analyze both types of data, but methods for BS-seq data are mainly for detecting differentially methylated loci (DMLs), although differentially methylated regions (DMRs) are often of more relevance biologically. The most prominent feature that is often overlooked in DML detection methods is the correlation in methylation signals in neighboring CpG sites. In this talk, I will discuss several statistical methods for analyzing both BS-seq and Cap-seq data for detecting DMRs between two groups. In particular, I will highlight methods that take correlations into consideration and provide confidence bounds of DMRs.

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