Recent Developments in Statistical Genomic Modelling and Analysis

Organizer and Chair: Jinko Graham (Simon Fraser University)

CELIA GREENWOOD, McGill University
Methods for Analysis of DNA Methylation

Methylation of DNA can alter DNA activity, by blocking access to the DNA at methylated sites. For example, DNA methylation determines cell-type-specificity. Recent interest in studying DNA methylation arises from the awareness that methylation patterns can change in response to age, disease or environmental exposures. Since DNA methylation can be measured by high-throughput experimental methods, analysts must cope with large data sets, undesired technical biases, and long-range correlations. The presentation will cover many of these issues, and focus on some proposed methods for studying local patterns in methylation, including dimension reduction methods and functional data analysis.

GABRIELA COHEN FREUE, University of British Columbia
Borrowing Information from Genomics Data to Boost Proteomics Discoveries

To date, there is an unmet clinical need to identify molecular indicators (e.g., proteins) of various diseases, including cancer, heart failure, and chronic obstructive pulmonary disease, among others. In this talk, I will focus on the problem of measurement errors in protein quantitations, which may affect the identification of protein biomarkers in a discovery study. As protein levels are regulated in part by gene expression, related genomic data can be integrated to address this problem through the implementation of instrumental variables estimators. The proposed methodology exploits the plausible mechanisms from existing biological knowledge that relate genes, proteins, and diseases and takes advantage of this knowledge to increase the signal strength of sometimes weak, but biologically relevant –omics signatures.

LAURENT BRIOLLAIS, University of Toronto
Bayesian Graphical Models for Gene Network Analysis in Large-Scale Problems

The detection of genetic interactions and inference about gene network topology can be a very valuable approach to understanding the joint basis of complex disease etiology. Network information is, unfortunately, extremely difficult to apprehend and only partially available. Bayesian Graphical models (BGMs) provide a probabilistic framework for making inference and representing our knowledge about these complex structured data. We discuss here the use of BGMs for gene network analysis in high-dimensional problems and how expert prior information and efficient algorithms can help inferring these complex networks. Applications to ongoing genetic and genomic problems in cancer research will be presented.