



The Chinese University of Hong Kong
Department of Statistics

Seminar

Statistical Methods for High-throughput Genomic Data

By

Dr. LIN, Zhixiang
Department of Statistics
Stanford University

Abstract

In the first part of the talk, a dimension reduction method will be introduced where we extend Principal Component Analysis to propose AC-PCA for simultaneous dimension reduction and Adjustment for Confounding variation. We show that AC-PCA can adjust for variations across individual donors present in a human brain dataset. For gene selection purposes, we extend AC-PCA with sparsity constraints, and propose and implement an efficient algorithm. The second part of the talk will be focused on clustering methods in single cell genomics. In single cell genomics, it is technically challenging to obtain chromatin accessibility and gene expression data for the same cell. We have developed a computational approach to this problem, where a model-based clustering method is proposed to match cell sub-populations in these two data types. We also demonstrate that using one data type can guide clustering of the other data type. Our proposed Bayesian model accounts for the stochasticity due to biological and technical effects. Last, methodologies motivated by spatial temporal modeling of gene expression dynamics during human brain development will be briefly discussed.

Date: February 22, 2018 (Thursday)
Time: 11:00 a.m. - 12:00 p.m.
Venue: Lee Shau Kee Building (LSK) - Room 515
The Chinese University of Hong Kong

ALL INTERESTED ARE WELCOME