



The Hong Kong University of Science and Technology

Department of Mathematics

Seminar on Statistics

**Simultaneous dimension reduction and adjustment
for confounding variation**

By

Dr. Zhixiang LIN
Stanford University

Abstract

Dimension reduction methods are commonly applied to high-throughput biological datasets. However, the results can be hindered by confounding factors, either biological or technical in origin. In this study, 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 a) variations across individual donors present in a human brain exon array dataset, and b) variations of different species in a model organism ENCODE RNA-Seq dataset. Our approach is able to recover the anatomical structure of neocortical regions, and to capture the shared variation among species during embryonic development. For gene selection purposes, we extend AC-PCA with sparsity constraints, and propose and implement an efficient algorithm. The methods developed in this paper can also be applied to more general settings.

Date: Thursday, 9 November, 2017

Time: 11:00a.m.-12:00noon

***Venue: Room 4472, Academic Building,
(near Lifts 25&26), HKUST***

All are welcome!