

Department Colloquium

Mathematics and Statistics
York University



Date, Time, and Room

Friday January 17, 2025
1:30PM-2:30PM
Stong College 224

Speaker

Dr. Kaiqiong Zhao
York University

Title

A novel high-dimensional model for identifying regional DNA methylation quantitative trait loci (QTLs)

Abstract

Varying coefficient models offer the flexibility to learn the dynamic changes of regression coefficients. Despite their good interpretability and diverse applications, in high-dimensional settings, existing estimation methods for such models have important limitations. For example, we routinely encounter the need for variable selection when faced with a large collection of covariates with nonlinear/varying effects on outcomes, and no ideal solutions exist. One illustration of this situation could be identifying a subset of genetic variants with local influence on methylation levels in a regulatory region. To address this problem, we propose a composite sparse penalty that encourages both sparsity and smoothness for the varying coefficients. We present an efficient proximal gradient descent algorithm to obtain the penalized estimation of the varying regression coefficients in the model. A comprehensive simulation study has been conducted to evaluate the performance of our approach in terms of estimation, prediction and selection accuracy. We show that the inclusion of smoothness control yields much better results than having the sparsity-regularization only. Using an adaptive version of our penalty function, we can achieve notable additional performance gains. Furthermore, we applied our method to identify genetic variations that affect methylation variability in gene-based regulatory regions using asymptomatic samples drawn from the CARTaGENE cohort. The methodology development has been implemented in R package sparseSOMNiBUS available on GitHub.

Refreshments in Ross N620 at 2:30PM

science

