The College of Arts & Sciences

Department of Mathematical Sciences

Colloquium

Dr. HoGeun Sun

Pusan National University

Thursday November 7th
Room 608, 2925 Campus Green Drive
4:00 – 5:00 pm

Incorporating genetic networks into case-control association studies with high-dimensional DNA methylation data

In human genetic association studies with high-dimensional gene expression data, it has been well known that statistical selection methods utilizing prior biological network knowledge such as genetic pathways and signaling pathways can outperform other methods that ignore genetic network structures in terms of true positive selection. In recent epigenetic research on case-control association studies, relatively many statistical methods have been proposed to identify cancer-related CpG sites and their corresponding genes from high-dimensional DNA methylation array data. However, most of existing methods are not designed to utilize genetic network information although methylation levels between linked genes in the genetic networks tend to be highly correlated with each other. In this article, we propose new approach that combines data dimension reduction techniques with network-based regularization to identify outcome-related genes for analysis of high-dimensional DNA methylation data. The proposed approach first captures gene level signals from multiple CpG sites using data a dimension reduction technique and then performs network-based regularization based on biological network graph information. In simulation studies, we demonstrated that the proposed approach overwhelms other statistical methods that do not utilize genetic network information in terms of true positive selection. We also applied it to the 450K DNA methylation array data of the four breast invasive carcinoma cancer subtypes from The Cancer Genome Atlas (TCGA) project.

Refreshments will be served 3:00 – 3:30 pm in the Faculty & Graduate Student Lounge Room 4118 French Hall West

UNIVERSITY OF Cincinnati