



THE UNIVERSITY OF
CHICAGO

Department of Statistics

STATISTICS COLLOQUIUM

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Inferring Gene Interactions and Functional Modules Beyond
Standard Models

MONDAY, December 4, 2017 at 4:30 PM

Eckhart 133, 5734 S. University Avenue
Refreshments before the seminar at 4:00PM in Jones 111

ABSTRACT

Identifying gene interactions has been one of the major tasks in understanding biological processes. However, due to the difficulty in characterizing/inferring different types of biological gene relationships, as well as several computational issues arising from dealing with high-dimensional biological data, finding groups of interacting genes remains challenging. In this talk, I will introduce our recent effort on identifying higher-level gene-gene interactions (i.e., gene group interactions) by evaluating conditional dependencies between genes, i.e., the relationships between genes after removing the influences of a set of other functionally related genes. The detailed technique involves performing sparse canonical correlation analysis with repeated subsampling and random partition. This technique is especially unique and powerful in evaluating conditional dependencies when the correct dependent gene sets are unknown or only partially known. When used effectively, this is a promising technique to recover gene relationships that would have otherwise been missed by standard methods. Comparisons with other methods using simulated and real data show this method achieves considerably lower false positive rates. In addition, an ongoing work on using a bagged semi-supervised clustering approach to study changes in the membership of functional gene pathways in response to genetic or phenotypic variation will be discussed.

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