Department of Mathematics and Statistics Colloquium

Estimating Network Relationships for Non-Gaussian Data

Job Candidate

Abstract: Gene co-expression networks (GCNs) are widely used to understand gene regulations and infer gene functions. Both directed and undirected networks can be of biological interest. This talk will discuss two novel methods for constructing GCNs using RNA-Sequencing and single-cell RNA-Sequencing data. The first method, iCC, defines a new correlation measure that can be applied to data following any known distribution to construct undirected GCNs, and is robust to the effects of outliers. The second method, LEAP, incorporates the time information available through the use of pseudo-time algorithms and thereby captures directed relationships, and is available as an R package on CRAN. The effectiveness of both methods is examined using simulations and real datasets.

Monday, December 5 at 3:45 in Roop 103

refreshments at 3:30