

Department of Mathematics and Statistics

Tuesday, April 18th, 2017

4:00 – 5:00 pm, Adel Mathematics Bldg., Room 164 (refreshments at 3:45)

Dr. Ye Chen

West Virginia University

Tenure-Track Mathematics Position

Candidate Interview Talk

Modeling Gene Expression Data with Graph Theory Methods

Abstract: Many of the RNA sequencing experiments are designed to quantify the gene expression level for each individual sample or cell. Such an experiment can generate a real-valued matrix with rows labeled by genes and columns labeled by samples/cells. Based on this matrix, we are able to narrow down the list of disease associated genes.

I will first summarize the pseudo-temporal ordering methods that are used in the cell differentiation study, and then introduce two network modeling methods for identifying disease associated genes. The first method is to identify disease perturbed pathways using the distribution of graph spectra, and I will address the related graph theory problems. The second method is to use multi-level networks to split the sample/cells in different stages, and then for each stage, we narrow down the list of disease associated genes by comparing some network characteristics.