May 15th, 4:30 PM

Understanding toxin production during Clostridioides difficile infection using high dimensional data

Samantha Erwin
North Carolina State University, sherwin@ncsu.edu

Joshua R. Fletcher
North Carolina State University

Casey M. Theriot
North Carolina State University

See next page for additional authors

Presenter Information
Samantha Erwin, Joshua R. Fletcher, Casey M. Theriot, and Cristina Lanzas

The main virulence factors in C. difficile infection are toxins, yet little is known about the specific mechanism leading to it. In recent years, new technology has allowed us to achieve measurements of hundreds of metabolites and the expression of thousands of genes which maybe crucial to understand the driving factors in C. difficile colonization and toxin production. It is believed that toxin production is mediated by competition for nutrients in the gut metabolome which makes the large-scale metabolomics data useful. However, with this all-encompassing ‘omics’ data comes a critical need to reduce these datasets to the most functional elements so that we can discover key components driving toxin production. We use a recent animal model for C. difficile infection in which mice were antibiotic treated with cefoperazone and challenged with C. difficile 2 days following treatment. We develop sparse graphical networks to identify correlations between metabolites and toxins within high dimensional data sets and develop a mechanistic model of processes related to our network. We find the Stickland reaction to by critical in toxin production and suggest potential mitigation strategies for reducing toxin production.