DEPARTMENT OF MATHEMATICAL SCIENCES

Colloquium

Reginald McGee
College of the Holy Cross

Uncovering linear and nonlinear relationships in leukemia

ABSTRACT: Complex protein interaction networks complicate the understanding of what most promotes the rate of cancer progression. High dimensional data provides new insights into possible mechanisms for the proliferative nature of aggressive cancers, but these datasets often require fresh techniques and ideas for exploration and analysis. In this talk, we consider expression levels of tens of proteins that were recorded in individual cells from acute myeloid leukemia (AML) patients via mass cytometry. After identifying immune cell subpopulations in this data using an established clustering method, we use topological data analysis to search for subpopulations that are most actively proliferating. To conduct the search within these subpopulations, we build on the differential geometric perspective that led to our recent statistic for testing aggregate differences in protein correlations between patients with different subtypes of AML.

Friday, March 15, 2019
11:00AM-12:00PM
Stratton Hall 203