

ACMS Statistics Seminar

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101A Crowley Hall
3:30– 4:30 PM



From Form to Function: Predicting Altered Dynamics in Gene Regulatory Networks

Cellular processes are regulated by complex networks of molecular interactions involving thousands of elements. These systems are highly tuned to produce precise biological effects, robust enough to tolerate intrinsic and extrinsic variability, and flexible enough to adapt to environmental changes. The interplay of these microscopic interactions drives the emergence of complex macroscopic phenotypes, and aberrations in the structure and function of these networks can lead to disease. Advances in high-throughput assays now make it possible to probe samples in exquisite molecular detail, motivating the development of analytical techniques to detect functional differences in the behavior of regulatory networks. Despite many advances, several key analytical challenges remain, including integrating disparate data types, distinguishing combinations of alterations that are cumulatively deleterious from those that may compensate one-another, and making predictions about a network's dynamical behavior from static measurements. In this talk, I will present our recent work to address these challenges, focusing on a novel graph-theoretic strategy to analyze gene expression data at the systems level. Our approach incorporates putative network topologies with experimental data to summarize patterns of coordinated gene expression across the pathway, providing a rigorous means to characterize the connectivity – and hence the dynamical properties – of a regulatory network. I will detail the method and demonstrate its application to several cancer datasets.

The Department of Applied and Computational
Mathematics and Statistics

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