Department of Applied and Computational Mathematics and Statistics Colloquium

Hulin Wu

Department of Biostatistics & Computational Biology
University of Rochester School of Medicine & Dentistry

Multiscale Systems Biology Modeling for Immune Response to Viral Infections: Statistical Inverse Problems

Many systems in engineering and physics such as a rocket system can be represented by differential equations, which can be derived from well-established physics laws and theories. However, currently no laws or theories exist to deduce exact quantitative relationships and interactions among the elements in a biological system. It is unclear whether the biological systems follow mathematical representations such as differential equations, similar to that for a man-made physics or engineering system. Fortunately, recent advances in cutting-edge biomedical technologies allow us to generate intensive high-throughput Big Data to gain new insights into biological systems and potentially discover quantitative laws for interactions among biological elements. However, it is very challenging to develop novel statistical methods to rigorously identify model structures and estimate parameters for a high-dimensional multiscale systems biology model based on experimental data. In this talk, I will present our recent work on how to construct high-dimensional differential equation (ODE) models to describe a multiscale immune response system to influenza infection. We propose to combine the high-dimensional variable selection approaches and ODE model estimation methods to construct the model based on the time course high-throughput data at transcriptomic, proteomic, molecular and cellular levels. The complex network relationships among these elements are established. We expect to quantitatively understand disease pathogenesis and discover new therapeutic targets using the systems biology modeling approach equipped with rigorous statistical reverse engineering methods.

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4:15 PM – 5:15 PM
127 Hayes-Healy Center

Colloquium Tea 3:45 PM to 4:15 PM 154 Hurley Hall