Numerical Analysis and Scientific Computing Seminar

Quantifying the geometry of immune response and infection

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Abstract: In improving outcomes for infection in humans and animals, it is important to understand how the body responds to an infection, whether infection has happened at all, and how this varies from individual to individual. Traditionally, this is a simple measurement – does someone have a fever or not? With more precise, high-frequency measurements of macro-scale data (e.g. body temperature time series) and micro-scale data (e.g. protein or RNA data from biological samples, i.e. "omics"), we can develop and study the efficacy of more sophisticated algorithms and diagnostics. I will present past and ongoing work in applying ideas from geometrical data analysis and machine learning which aid us in making predictions in classification questions such as early prediction of infection, model-free learning of time series patterns and anomaly detection, and "inverse" problems such as prediction of time since infection. We will introduce algorithmic ideas to newcomers as well as our quantitative results on data coming from clinical studies with humans challenged with influenza-like illnesses, and Collaborative Cross mice studies, in work with our collaborators at Colorado State University and Texas A&M University.

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