



Department of Mathematics and Statistics

Colloquium

Tuesday February 6

AMB 164 4:00 - 5:00 pm

From differential equations to computational biology: mathematical models and methods

Matthew Reyna

Princeton University

Abstract

Abstract: Mathematical models and computational methods are important tools for studying diverse systems. In this talk, I explore computational methods for solving both classical problems in physics and engineering as well as emerging problems in biology and medicine. First, I consider Runge-Kutta discontinuous Galerkin (RKDG) methods for solving partial differential equations. RKDG methods can provide high-resolution numerical solutions to a variety of problems, but they also suffer from restrictive stability conditions that can reduce their utility in practice. By providing analytical bounds for stability regions of these methods, I show that a modified discretization scheme substantially improves the stability of the method, especially for high-resolution schemes.

Second, I consider the problem of finding cancer genes. The somatic mutations that driver cancer development tend to be relatively rare and difficult to identify amid a much larger number of random passenger mutations. This difficulty complicates both our biological understanding of cancer as well as our capacity to treat it. However, computational methods founded on rigorous mathematical and statistical models extend our ability to identify cancer genes, including genes that are infrequently targeted by driver mutations. We present two novel computational methods, Hierarchical HotNet and WExT, for identifying biological pathways that are targeted by driver mutations in cancer. The results from these methods help provide additional insight into cancer as well as new diagnostic and clinical opportunities.

Refreshments at 3:45