

APPLIED MATHEMATICS COLLOQUIUM

Date: Wednesday, November 16, 2016

Time: 2:30 – 3:30 p.m.

Location: Middlesex College Room 204

Viruses, computers, and the shapes of trees

Dr. Art Poon

Department of Pathology and Laboratory Medicine
University of Western Ontario

Abstract: A phylogeny is a tree that represents how different populations are related through a series of common ancestors. Although we cannot directly observe these ancestors in the past, we can infer these relationships from the genetic similarity of their descendants in the present. Many viruses evolve so quickly that each infection becomes genetically unique before it is transmitted to the next host. Consequently, a virus phylogeny bears an imprint of how the infections spread through the host population. The emerging field of phylodynamics attempts to reverse this flow of information to reconstruct epidemic processes from the shapes of trees. Phylodynamic methods have already had a tremendous impact on our understanding of recent epidemics including Ebolavirus, influenza A virus and HIV. I present recent work from my lab adapting computational techniques from machine learning and Bayesian inference to understand how the genetic diversity of HIV is shaped by the social structure of human populations.