九州大学数理生物学研究室 Mathematical Biology Lab., Kyushu University

-ME Seminar-

Understanding antiviral efficacy and resistance mutations in influenza virus infections in vitro

$\label{eq:speaker:Catherine Beauchemin} $7/23[{\tabularterine}] $15:00-$ at Room 3503 }$

Experimentation in vitro and in vivo has traditionally been the only way to study viral infections. This approach for deriving knowledge relies on commonsense assumptions (e.g., a higher viral count means a fitter virus). These assumptions often go untested due to difficulties in controlling individual components of infection without affecting others. Mathematical and computer models (MCMs), however, make it possible to deconstruct an experimental system into individual components and determine how the pieces combine to create the infection we observe.

In this talk, I will show how our MCMs can be used to determine the effect of a specific mutation (genotype)

on every aspect of the virus' replication fitness (phenotype). I will present the results of our analysis to determine whether resistance could establish itself in the 2009 influenza A/H1N1 pandemic strain. I will also demonstrate the MCMs' ability to identify flaws in experiments, and to determine antiviral efficacy and optimal antiviral combination therapy.



