Report on Mathematical Biology Workshop – August 18-19,2012

There are now well established mathematical biology groups at Dalhousie, Memorial and University of New Brunswick. As well the use of mathematical modelling and analysis has become increasing common among biologists and many members of biology departments have attended this meeting in the past. One of the key motivations for this meeting is provide an opportunity to for all of these groups to mix and interact. This is the fourth annual meeting of this group and the meetings have consistently grown each year.

This year we had 23 people attending the meeting with 14 presenting their research. Most of the participants come from Atlantic Canada. We had 3 international scholars and 1 postdoc from York. The workshop was well attended by graduate students and postdocs with 9 and 3 attending respectively.

Budget

Income	
AARMS	$2,000.00
Dynamical Systems CRG	$831.00
Total	$2640.00
Expenditures	
Student Travel	$1875.30
Student Accommodations	$755.70
Local Transport	$200.00
Total	$2831.00

The conference program is attached listing all the details of the meeting

4^{th} Annual Mathematical Biology Workshop 2012
Dalhousie University

Program

I would like to welcome everyone to 4th mathematical biology workshop. There are now well established mathematical biology groups at throughout Atlantic Canada. As well the use of mathematical modelling and analysis has become increasing common among biologists and many members of biology departments have attended this meeting in the past. One of the key motivations for this meeting is provide an opportunity to for all of these groups to mix and interact. We have several breaks during the meeting and I hope we can take advantage of the time to start some new collaborations.

A few pieces of information for everyone.

- To enter the building the key code is 071068*. If you have problems getting in, you can call me on my cell (902) 446-5512.
- There is a computer room in the basement (001). It is locked, but if anyone needs to use a computer/printer, there are several in that room.
- There are not a lot places open for lunch near the campus on weekends. There is the Cobourg Cafe on Cobourg St. They have sandwiches and soup. We can all meet to discuss the various options.

Acknowledgements

The organizers of this meeting would like to thank AARMS for providing funding for graduate students and postdocs to attend this meeting. We would also like to thank the Dalhousie mathematics department for providing the equipment and space.

Schedule

Saturday August 19		
Time	Speaker	Title
8:30-9:00	Registration-Coffee	
9:00-9:30	Yuxin Chen	Stability analysis of discrete and continuous predator-prey system
9:30-10:00	Yuxiang Zhang	Spatial Dynamics of A Reaction-Diffusion Model with Distributed Delay
10:00-10:30	Zhen Wang	A Within-host Virus Model with Periodic Multidrug Therapy
10:30-11:00	Coffee	
11:00-11:30	Hongying Shu	The immunosuppressive infection model with delayed immune response: oscillations and chaos
11:30-12:00	Chris Levy	Dynamics and Stability of a 3D Model of Cell Signal Transduction
12:00-1:30	Lunch	
1:30-2:00	Adriana Dawes	Modelling pronuclear rotation in the early C. elegans embryo
2:00-2:30	Christopher Whidden	Fixed-Parameter and Approximation Algorithms for Maximum Agreement Forests
2:30-3:00	Coffee	
3:00-3:30	Junping Shi	Spatiotemporal mutualistic model of mistletoes and birds
3:30-4:00	Junyuan Yang	A TB model with undetected compartment: an application to China
4:00-4:30	Amy Hurford	Using Mathematical Models to Inform Antimicrobial Stewardship in the Intensive Care Unit

Sunday August 19		
Time	Speaker	Title
9:30-10:00	Mike Dowd	An Overview of Statistical Estimation Methods for Dynamic Models of Ecological Systems
10:00-10:30	Jeffrey Picka	Quantifying Uncertainty in Ecological and Epidemic Modelling
10:30-11:00	Coffee	
10:30-11:00	Joe Mudge	What information can be gleaned from a Taylor's power law exponent?
11:00-11:30	Xiangsheng Wang	Avian influenza, migratory birds and dynamical threshold

List of Abstracts

Stability analysis of discrete and continuous predator-prey system
Yuxin Chen

Abstract:This talk is divided into two parts. In the first part, we will introduce an ODE system consisting of predator-prey particles with some numerical videos and analyze the stability problem of the system. In the second part, we will study the continuous form of the problem and show analytically that at the steady state, the prey particles will form an annulus with uniform density inside and zero density outside. This is an undergraduate summer research mentored by Prof. Theodore Kolokolnikov, and Drs Alethea Barbaro and Jesus Rosado.

Spatial Dynamics of A Reaction-Diffusion Model with Distributed Delay

Yuxiang Zhang

Abstract:In this talk, I will report our recent research on spreading speeds and traveling waves for a class of reaction-diffusion equations with distributed delay. Such an equation describes growth and diffusion in a population where the individuals enter a quiescent phase at random times. The existence of spreading speed and its coincidence with the minimum wave speed of monostable traveling waves are established via the finite-delay approximation approach. We also obtain the existence of bistable traveling waves in the case where the associated reaction system admits a bistable structure. This talk is based on a joint work with Dr. Xiaoqiang Zhao.

A Within-host Virus Model with Periodic Multidrug Therapy

Zhen Wang

Abstract:In this talk, we consider a standard within-host virus model with periodic drug treatment. We first introduce the basic reproduction ratio, and then show that the infection free equilibrium is globally asymptotically stable and the disease eventually disappears if the basic reproduction number is less than 1, there exists at least one positive periodic state and the disease persists when the basic reproduction number is greater than 1. We also consider an optimization problem by shifting the phase of these drug efficacy functions. It turns out that shifting the phase can certainly affect the stability of the infection free steady state. This talk is based on the joint work with Dr. Xiaoqiang Zhao.

The immunosuppressive infection model with delayed immune response: oscillations and chaos

Hongying Shu

Abstract:Sustained and transient oscillations are frequently observed in clinical data for immune responses in viral infections such as HIV and HBV. To account for these oscillations, we incorporate the time lag needed for the expansion of immune cells into an immunosuppressive infection model. It is shown that the delayed antiviral immune response does induce sustained periodic oscillations, transient oscillations and even sustained aperiodic oscillations (chaos). Both local and global Hopf bifurcation theorems are applied to show the existence of periodic solutions, which are illustrated by bifurcation diagram and numerical simulations. The model can admit two stable equilibria and can also allow a stable equilibrium to coexist with a stable periodic solution. These findings may provide some insights on designing effective treatment regimes to boost sustained immune-mediated control on the viral infection.

Dynamics and Stability of a 3D Model of Cell Signal Transduction
Chris Levy

Abstract:In this talk, we consider a three-dimensional model of cell signal transduction modelled by a system of reaction diffusion equations in a spherical domain with small holes. We use matched asymptotic expansions to construct the dynamic solutions of signalling protein concentrations. The result of the asymptotic analysis is a system of ordinary differential equations. This reduced system is compared to numerical simulations of the full three-dimensional system. As well, we consider the stability of equilibrium solutions. We then add a constant time delay to the system and redo some of the analysis. We also talk about solving the full 3D system with delay numerically.

Modelling pronuclear rotation in the early C. elegans embryo
Adriana Dawes

Abstract:After fertilization, the male and female pronuclei of the nematode worm Caenorhabditis elegans meet via a microtubule mediated process. Microtubules are nucleated by centrosomes located on the male pronucleus. Once the pronuclei meet, the pronuclei and centrosome complex undergoes a 90 degree rotation so that the centrosomes are aligned along the long axis of the ellipsoidal embryo. In this talk I will discuss modelling efforts to understand the spatial distribution of forces needed to effect the rotation and the relationship to asymmetrically distributed proteins.

Fixed-Parameter and Approximation Algorithms for Maximum Agreement Forests
Christopher Whidden

Abstract:I present new efficient algorithms for computing maximum agreement forests (MAFs) of binary and multifurcating evolutionary trees. Their sizes correspond to the subtree-prune-and-regraft (SPR) distance of the trees and are intimately connected to the hybridization number of the trees. These distance metrics are essential tools for understanding reticulate evolution-lateral gene transfer (LGT/HGT), recombination, and hybridization-and multifurcating trees are necessary given incomplete data or closely related organisms. As such, I have applied these algorithms to building large bacterial supertrees and propose methods of building evolutionary networks.

Using Mathematical Models to Inform Antimicrobial Stewardship in the Intensive Care Unit
Amy Hurford

Abstract:In recent decades, physicians have prescribed antimicrobials to patients more often, while over the same period, a greater number of infections are resistant to certain types of treatments. Patients in the intensive care unit are particularly susceptible to hospital-acquired infections, and among these patients, infections with antimicrobial-resistant microorganisms are particularly common. Recognizing this problem, various healthcare advisory committees suggest antimicrobial stewardship programs, however, the best design, and the anticipated effects of such programs, are poorly understood. In this talk, I will discuss how mathematical modelling can contribute to our understanding of the spread of antimicrobial-resistant organisms and describe key considerations for the derivation of such models.

Spatiotemporal mutualistic model of mistletoes and birds

Junping Shi

Abstract:A mathematical model which incorporates the spatial dispersal and interaction dynamics of mistletoes and birds is derived and studied to gain insights of the spatial heterogeneity in abundance of mistletoes. Fickian diffusion and chemotaxis are used to model the random movement of birds and the aggregation of birds due to the attraction of mistletoes respectively. The spread of mistletoes by birds is expressed by a convolution integral with a dispersal kernel. Two different types of kernel functions are used to study the model, one is Dirac delta function which reflects one extreme case that the spread behavior is local, and the other one is a general non-negative symmetric function which describes the nonlocal spread of mistletoes. When the kernel function is taken as the Dirac delta function, the threshold condition for the existence of mistletoes is given and explored in term of parameters. For the general non-negative symmetric kernel case, we prove the existence and stability of non-constant equilibrium solutions. Numerical simulations are conducted by taking specific forms of kernel functions. Our study shows that the spatial heterogeneous patterns of the mistletoes are related to the specific dispersal pattern of the birds which carry mistletoe seeds. This is a joint work with Chuncheng Wang, Rongsong Liu, Carlos Martinez del Rio (University of Wyoming).

A TB model with undetected compartment: an application to China

Junyuan Yang

Abstract:This article introduces a novel model that studies the major factors jeopardizing tuberculosis (TB) control programme in China. A previously developed two-strain TB model is augmented with a class of individuals not registered under the TB control program. The paper investigates the basic reproduction number and proves the global stability of the disease-free equilibrium. The presence of three endemic equilibria is established in the model. With the help of numerical simulations, a comparative study has been performed to test the validity of the model presented here to the real data available from the Ministry of Health of the Peoples Republic of China. Sensitivity and elasticity analysis give the key parameters that would govern successful TB control in China.