Final Report: 2013 AARMS MATHEMATICAL BIOLOGY WORKSHOP

Wednesday, February 26, 2014
Amy Hurford

Summary

The 2013 AARMS Mathematical Biology Workshop was held on July 27-29, 2013 at Memorial University of Newfoundland (MUN) in St John's. Highlights of the workshop were plenary talks by Drs. Linda Allen, Edward Allen, Steve Cantrell, Odo Diekmann, Mark Lewis, and Philip Maini, a public lecture by Dr. Simon Levin, and a banquet held at the SUNCOR Energy Fluvarium. A summary of the workshop (and the concurrent AARMS Mathematical Biology Summer School) by Kelsey Gasior, a graduate student from North Carolina State University, was published in the Society for Mathematical Biology Digest (September 2013, vol 26, No 3) and the AARMS Newsletter (Autumn 2013). Ms. Gaisor described being part of the AARMS Mathematical Biology Summer School and Workshop as *'a once in a lifetime opportunity'*.

Financial

Total expenditure for the workshop was $13,141.55. This was lower than budgeted for because funding for US participants to attend the workshop was made available through a National Science Foundation grant held by Dr. Alan Hastings. This reduced the number of travel request made to the workshop itself. The workshop generated a surplus of $3,176.70. This surplus was used to evenly reduce the requested amounts from AARMS, the Math Department at MUN, the Faculty of Science at MUN and the Conference Fund administered by the Offices of the Vice President at MUN. A registration fee of $50 was charged (with postdocs and students exempt). Graduate students and postdocs were charged $10 for banquet tickets.

Income summary – AARMS ($5,132.51), Conference Fund ($5,514.68), Faculty of Science ($394.81), Mathematics Department ($789.62) and Registration and Banquet tickets ($1,309.93). In addition, $1,000 of support was provided by the Centre de Recherches Mathématiques (CRM). This support was deducted from the invoiced amount for the cost of Dr. Simon Levin's travel.

- Full details of conference income and expenditure are provided in the Appendix, p1-3.

Attendence

The workshop was attended by 84 participants: 2 undergraduates (2%); 51 graduate students (61%); 6 postdocs (7%) and 25 faculty members (30%). 25 participants were from Atlantic Canada (30%), 16 were from other parts of Canada (19%), 27 from the United States (32%), 10 from the European Union (12%) and 6 participants were from Asia (7%).

- A full list of conference attendees and their affiliations are provided in the Appendix, p4-5.

Scholarly Proceedings
The workshop consists of 30 contributed talks, 6 plenary lectures and a public lecture.

- The workshop schedule is provided in the Appendix, p6-7.
- The book of abstracts is provided in the Appendix, p8-17.
- The report on the AARMS Summer School and the AARMS workshop by Kelsey Gasior is provided in the Appendix, p18-19.

On behalf of the organizing committee, I would like to thank all of the funding bodies: AARMS, the Conference Fund, the Dean of Science at MUN, the MUN Math Department and CRM for their generous support, without which the workshop would not have been possible. Please contact myself or Ros English (renglish@mun.ca, 709-864-8917) should any questions pertaining to this final report arise.

Regards,

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APPENDIX

AARMS MATH / BIOLOGY WORKSHOP
DEPT. MATHEMATICS AND STATISTICS, MEMORIAL UNIVERSITY OF NEWFOUNDLAND
JuLY 27-29, 2013

FOAP: 280796 46310 2002 (A. Hurford)

	REVENUE	ACTUAL EXPENSES	BALANCE
	$ -		$ -
Printing Services - Simon Levin Public Lecture		$ 6.20	
Reim. - A. Hurford - Supplies		$ 9.91	
Aramark - Refreshments		$ 1,460.54	
Aramark - Refreshments		$ 1,120.62	
Aramark - Refreshments		$ 318.01	
Quidi Vidi Rennies River Develop. Foundation			
Banquet		$ 2,134.12	
Rental cost of Fluvarium for Banquet		$ 230.26	
Travel:			
Simon Levin (Invoiced)		$ 1,629.20	
Hongying Shu		$ 682.43	
Mohammad Smaily		$ 946.33	
Yuxiang Zhang		$ 514.21	
Ali Gharouni		$ 970.35	
Fang Yu		$ 1,092.33	
Mark Lewis		$ 2,027.04	
TOTAL EXPENSES		**$ 13,141.55**	
			-$ 13,141.55
			Deficit

INCOME - AARMS MATH BIO WORKSHOP

Total expenses 13141.55

Income	Awarded	Adjusted request
Registration	1309.93	1309.93
Conference Fund	6984.00	5514.68
Faculty of Science	500	394.81
AARMS	6500.00	5132.51
Math Dept	1000	789.62
	16293.93	13141.55

Surplus	3152.38	0

Total non-registration income	14984.00
Surplus/non-registration income	0.210383075
Multiplier	0.789616925

The adjusted request is calculated by multiplying the awarded amount by the multiplier

ITEMIZED INCOME AND EXPENDITURE

Expenses	Category	Amount	Registration	Conf Fund	Fac of Sci	AARMS	Math Dept
Mark Lewis	Travel/Accom	2027.04		858.72	394.81		773.51
Simon Levin *	Travel/Accom	1629.2		702.34		926.86	
El Smaily	Travel/Accom	946.33				946.33	
Yuxiang	Travel/Accom	514.21				514.21	
Yu	Travel/Accom	1092.33				1092.33	
Gharonui	Travel/Accom	970.35				970.35	
Shu	Travel/Accom	682.43				682.43	
Posters	Advertising	6.20					6.2
Fluvarium reception	Hosting - food	2364.38	1309.93	1054.45			
Conference food	Hosting - food	2899.17		2899.17			
Receipt book/Name tags	Administration	9.91					9.91
		13141.55	**1309.93**	**5514.68**	**394.81**	**5132.51**	**789.62**

*The travel of Dr Simon Levin was also supported by $1000 of funding from CRM. Dr Levin's receipts were submitted to CRM. $1629.20 is the total amount of Dr Levin's trip minus the $1000 of support from CRM.

Last name	First name	Affiliation
Xiaoyan	Chen	Hunan University
Xiaodong	Tai	University of Science and Technology Beijing
YUBIN	LIU	School of Mathematics,South China Normal University
Yijun	Lou	The Hong Kong Polytechnic University
Larisa	Tamjidi	UNB
Mahin Sadat	Chavoshi Jolfaei	Memorial University
Mohammad Jalal	Ahammad	Memorial University
Md Abdus Samad	Bhuiyan	Memorial University
Bassemah	Alhulaimi	Dalhousie university
Douglas	Staple	Dalhousie
Fang	Yu*	University of New Brunswick
Ali	Gharouni*	University of New Brunswick
Steven	Duffy	Memorial University
Xiao	Yu	Memorial University
Hongying	Shu*	University of New Brunswick
Xiang-Sheng	Wang	Memorial University of Newfoundland
Yanjing	He	MI/MUN
Amy	Hurford	Memorial University of Newfoundland
Israel	Ncube	Memorial University
David	Iron	Dalhousie
Chunhua	Ou	Memorial University
Xiaoqiang	Zhao	Memorial University of Newfoundland
Lin	Wang	UNB
Yuan	Yuan	Memorial University
James	Watmough	university of new brunswick
John	Craighead	MUN Math & Stats
Shawn	Leroux	MUN
Brian	Corbett	Memorial
Thomas	Meehan	Mun
Safia	Athar	University of Guelph
Xiaoying	Wang	University of Western Ontario
Xiulan	Lai	University of Western Ontario
Tingting	Zhao	The Department of Mathematics, The University of Ottawa
Artem	Kaznatcheev	McGill University
Amanda	Swan	University of Alberta
Michael Evrard	Makouangou Ngo	University of Ottawa
Frederic	Paquin-Lefebvre	University of Montreal
Alison	Wardlaw	University of Toronto
Surya	Lamichhane	Wilfrid Laurier
Mohammad	El_Smaily*	University of Toronto-NSERC
Yuxiang	Zhang*	University of Ottawa
Jian	Fang	York University
Mark	Lewis***	University of Alberta
Xiamei	Jiang	University of Toronto at Scar
Wenying	Feng	Trent University
Zhe	Huang	China Jiliang University
Fang	Li	university of science and technology of china
Helen	Henninger	INRIA Sophia Antipolis

Pawel	Zwolenski	Institute of Mathematics, Polish Academy of Sciences
Xiangyi	Li	Max-Planck Institute for Evolutionary Biology
Weiwei	DING	Aix-marseille university
sonia	pozzi	Insubria University
Marina	Ferreira	University of Coimbra
Odo	Diekmann	Utrecht University
Philip	Maini	Oxford
Frederic	Hamelin	Agrocampus Rennes
Maria	Florescu	University of Basel
Kaushik	Gorahava	The University of Texas at Arlington
Spencer	Carran	Pennsylvania State University
Oyita	Udiani	Arizona State University
Bismark	Singh	The University of Texas at Austin
John	McKay**	Arizona State University
Angela	Peace**	Arizona State University
Holly	Moeller**	Stanford University
Kelsey	Gasior	North Carolina State University
Easton	White	Arizona State University/University of California-Davis
Andrew	Foss-Grant	University of Maryland
Yi	Zhu	University of Central Florida
EMMANUEL	QUANSAH	CLARKSON UNIVERSITY
Xi	Huo	Vanderbilt University
Andrew	Blanchard	University of Illinois at Urbana-Champaign
Jessica	Hearns	University of Central Florida
Evan	Milliken	University of Florida
Philip	McDowall	Stony Brook University
Laurel	Ohm	University of Washington
Rebecca	Everett**	Arizona State University
Laine	Noble	The Ohio State University
Edward	Allen	Texas Tech University
Simon	Levin***	Princeton
Linda	Allen	Texas Tech University
Steve	Cantrell	University of Miami
Urszula	Ledzewicz	Southern Illinois University
Heinz	Schaettler	Washington University
Yun	Kang**	Arizona State University

* Travel award funded by AAMRS Math Bio Workshop
** Travel award through NSF funding
*** Travel support for plenary speaker

PARTICIPATION SUMMARY
84 participants (2 undergraduates; 51 graduate students; 6 postdocs; 25 faculty members)
6 Asia (5 grad; 1 professor)
25 Atlantic Canada (1 ugrad; 10 grad; 3 Postdocs; 11 faculty)
16 Canada (10 grad; 3 postdocs; 3 faculty)
10 EU (1 Ugrad; 6 grad; 3 faculty)
27 USA (20 grad; 7 faculty)
30 Contributed talks

2013 AARMS MATHEMATICAL BIOLOGY WORKSHOP

Day 1 – Saturday July 27
AA-1043
8:00 Registration
8:30 Welcome
ECOLOGY AND SPATIAL ECOLOGY - Amy Hurford (chair)
8:45 **Mohammad El Smaily** – *Influence of a turbulent advection on KPP evolutions*
9:15 **Xiang-Sheng Wang** – *Pulsating waves of a partially degenerate reaction-diffusion system in a periodic habitat*
9:45 Group photo
10:00 Coffee
ECOLOGY AND SPATIAL ECOLOGY - Yuan Yuan (chair)
10:30 **Holly Moeller** – *Optimal investment in a multi-mutualist system: trees and ectomycorrhizal fungi*
11:00 **Linda Allen** – *Relations between deterministic and stochastic thresholds for disease extinction*
12:00 Lunch
ECOLOGY AND SPATIAL ECOLOGY - James Watmough (chair)
1:30 **Xiaoqiang Zhao** – *A reaction-diffusion Lyme disease model with seasonality*
2:00 **Mark Lewis** – *Mathematics behind stream population dynamics*
3:00 Coffee
ECOLOGY AND SPATIAL ECOLOGY - Xiaoqiang Zhao (chair)
3:30 **Jian Fang** – *Mathematical modelling of invasive Asian clam in an unbounded one-dimensional habitat*
4:00 **Ali Gharouni** – *Integrodifference model of biological invasion of European green crab (Carcinus maenas): calculation and sensitivity analysis of invasion speed*
4:30 **Odo Diekmann** – *Infectious disease transmission on dynamic sexual networks*

AA-1046
EPIDEMIOLOGY - Hongying Shu (chair)
8:45 **Xuilan Lai** – *Modeling repulsion of superinfecting virions*
9:15 No talk
9:45 Group photo
10:00 Coffee
10:30 **Yijun Lou** – *Cost-effectiveness evaluation of gender-based vaccination programs against sexually transmitted infections*
11:00 No talk
12:00 Lunch
EPIDEMIOLOGY - Xiang-Sheng Wang (chair)
1:30 No talk
2:00 No talk
3:00 Coffee
3:30 **Xi Huo** – *Investigating contact tracing and quarantine in the control of epidemic diseases*
4:00 **Kaushik Gorahava** – *Controlling Leishmaniasis transmission in India by systematic insecticide allocation*
4:30 No talk

Day 2 - Sunday July 28
AA-1043
NEURAL SIGNALLING - Lin Wang (chair)
8:30 **Israel Ncube** – *Hopf bifurcation in a neuronal network with distributed delay*
9:00 **Yuan Yuan** – *Homogeneous auxin steady states and spontaneous oscillations in flux-based auxin transport models*
CELLULAR PROCESSES AND CANCER - Lin Wang (chair)
9:30 **Rebecca Everett** – *Predicting the time and mechanism for resistance in prostate cancer patients undergoing androgen suppression therapy*
10:00 Coffee
CELLULAR PROCESSES AND CANCER - Urszula Ledzewicz (chair)
10:30 **Heinz Schaettler** – *Tumor microenvironment and anti-cancer therapies: an optimal control approach*
11:00 **Edward Allen** – *Application, derivation, and computation of continuous- and discrete-delay SDE models in mathematical biology*
12:00 Lunch

CELLULAR PROCESSES AND CANCER - David Iron (chair)
1:30 **Urszula Ledzewicz** – *Optimal control of cell migration in Glioblastoma*
2:00 **Philip Maini** – *Modelling collective cell movement*
3:00 Coffee
CONSUMER-RESOURCE DYNAMICS - Yijun Lou (chair)
3:20 **Angela Peace** – *A stoichiometric producer-grazer model incorporating the effects of excess food-nutrient content on consumer dynamics*
3:50 **Shawn Leroux** – *A stoichiometrically-explicit model for predator control of ecosystem nutrient cycling*
4:30 No talk

AA-1046
PATTERN FORMATION - Chunhua Ou (chair)
8:30 **Wenying Feng** – *Turing instability for a two-innovation diffusion system*
9:00 **Marina Ferreira** – *Binding in pattern formation*
9:30 **David Iron** – *Dynamics of a model of signal transduction in a 3 dimensional domain*
10:00 Coffee
10:30 No talk
11:00 No talk
12:00 Lunch
POPULATION DYNAMICS - Jian Fang (chair)
1:30 **John McKay** – *Modeling minority group influence on larger community behavior: measles vaccine refusal and ant networks as examples*
2:00 No talk
3:00 Coffee
3:20 **Hongying Shu** – *Global dynamics of the Nicholson blowflies equation revisited: onset and termination of nonlinear oscillations*
3:50 **Fang Yu** – *Bifurcation analyses for a diffusive plant-herbivore model with a non-proportional numerical response*
4:30 No talk

Sunday IIC-2001
4:30 (public lecture) **Simon Levin** – *Challenges in mathematical ecology: scaling and collective phenomena*

Day 3 – Monday July 29
AA-1043
POPULATIONS, METAPOPULATIONS AND DISPERSAL - Wenying Feng (chair)
8:30 **Easton White** – *Metapopulation dynamics of the American pika*
9:00 **Yun Kang** – *Dynamics of intraguild predation models*
9:30 **Yuxiang Zhang** – *Stability and synchronization of a predator-prey metacommunity model with spatial dispersal and travel time delay*
10:00 Coffee
Amy Hurford/Xiaoqiang Zhao (chair)
10:30 **Xiaoying Wang** – *Two patch predator-prey model with adaptive movement of predators*
11:00 **Steve Cantrell** – *Nonlinear diffusion and resource matching in population dynamics*
12:00 Farewell

Monday AA-1046
EVOLUTION - Shawn Leroux (chair)
8:30 **Frederic Hamelin** – *Parasites also have sex: consequence on host-parasite population dynamics*
9:00 **Amy Hurford** – *Immune evasion and the evolution of molecular mimicry in parasites*
9:30 **Pawel Zwolenski** – *Phenotypic evolution in hermaphroditic populations*
10:00 *Coffee*
10:30 No talk
11:00 No talk

2013 AARMS MATHEMATICAL BIOLOGY WORKSHOP

Application, Derivation, and Computation of Continuous- and Discrete-Delay SDE Models in Mathematical Biology

Edward Allen, Texas Tech University
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Stochastic versions of discrete-delay and continuous-delay differential equations, useful in mathematical biology, are derived from basic principles carefully taking into account the randomness in the processes. In particular, stochastic delay differential equation models are derived and studied for glucose/insulin levels, bacteriophage/bacteria dynamics, and logistic population growth with delay. Numerical methods for approximating the delay SDE models are described. Comparisons between computational solutions of the delay SDEs and independently formulated Monte Carlo calculations support the accuracy of the derivations and of the numerical methods.

Relations Between Deterministic and Stochastic Thresholds for Disease Extinction

Linda Allen, Texas Tech University,
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Thresholds for population or disease extinction in terms of model parameters provide important information for control, eradication or management of populations or diseases. Through relations between branching process theory and the corresponding deterministic model, it is shown that the deterministic and stochastic thresholds are in agreement for discrete-time and continuous-time infectious disease models with multiple infectious groups. Branching process theory can be applied in conjunction with the deterministic model to give additional insight into the probability of disease clearance. These relations are illustrated, analytically and numerically, in two models, a discrete-time model with stage structure and a continuous-time model with spatially-dependent risk of infection. This is joint work with P. van den Driessche and G. E. Lahodny, Jr.

An SIR - migration model between cities with variational inequality formulations

Safia Athar, University of Guelph
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This talk presents a migration model used by Sattenspiel and Dietz (1994) reformulated and extended to a variational inequality (VI) problem. In the original paper the authors use an SIR model to further discuss the epidemics evolved through migration. Here we have modified the base model using the concept of utilities and costs associated with the migration of people between cities. Then using the concept of different classes within the population in these cities, will derive the VI problem whose solutions give the equilibrium population-flow values in the given geographic area. Further we will look into the evolution of the population-flow patterns under an epidemic.

Nonlinear diffusion and resource mathcing in population dynamics

Steve Cantrell, University of Miami
rsc@math.miami.edu

In this talk we will discuss how parabolic partial differential equations may be used to study the evolution of dispersal strategies. We will begin with a brief historical overview to set our context. We will then focus on our primary interest, namely exploring the relative advantages of fitness-dependent and random dispersal in a two species competition model in a bounded spatial habitat. Both species have the same population dynamics, but one species adopts a combination of random and fitness-dependent dispersal and the other adopts only random dispersal. In so doing we regard the species as ecologically identical, differing only in their dispersal strategies. The model is realized as a quasi-linear parabolic system. Global existence of smooth solutions to the system may be established in two dimensions for any smooth bounded habitat and in 3 or more dimensions when the habitat in question is convex. When the single species which combines random and fitness-dependent movement is considered in the absence of its competitor, we show that a strong tendency for the species to move up its fitness gradient leads to a stable equilibrium that approximates the ideal distribution. For the two species competition model, such approximately ideal free dispersal is evolutionarily advantageous relative to random dispersal. Further, bifurcation analysis shows that the two competing species can coexist when one species has only an intermediate tendency to move up its fitness gradient and the other species has a smaller diffusion rate. The work described in this talk is based on three papers due to: (1) R. S. Cantrell, C. Cosner and Y. Lou; (2) R. S. Cantrell, C. Cosner , Y. Lou and C. Xie; and (3) Y. Lou , Y. Tao and M. Winkler.

Infectious disease transmission on dynamic sexual networks

Odo Diekmann, Utrecht University
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First we introduce a population model that incorporates demographic turnover as well as, for each individual, a variable number of simultaneous partnerships. The resulting dynamic network next serves as a template for the transmission of an infectious disease. After introducing some general concepts underlying structured population models, in particular the notions of i-state (i for individual) and i-state-at-birth, I shall focus on the way to deduce generation dynamics from real time dynamics and show how to construct a next-generation matrix from a decomposition of the relevant Jacobi matrix into a transition part and a transmission part. The aim is to characterize R_0 and other severity indicators. The ultimate aim is to shed some light on the impact of concurrency on the spread of HIV. The talk is based on ongoing joint work with KaYin Leung and Mirjam Kretzschmar.

Influence of a turbulent advection on KPP evolutions

Mohammad El Smaily, University of Toronto-NSERC
elsmaily@gmail.com

Reaction diffusion equations in heterogeneous media turn out to be more realistic in describing biological, chemical and physical phenomena like population dynamics and biological invasions. Having a reaction-advection-diffusion equation, where the reaction term is a general KPP nonlinearity (which may depend on spatial variables) and the advection is an incompressible flow, leads to the question whether an invasion of a stationary state of the dynamical system (a nonlinear parabolic equation) by another stationary state could happen or not. The answer to this question is positive and this invasion was described by pulsating traveling fronts which exist in a range of speeds greater than a minimal threshold value c* (called the KPP minimal speed). Another main question in a heterogenous setting is whether an advective field with an amplitude M speeds up the propagation or not. The answer to this question turns out to be positive in some particular settings and negative in many others. The minimal KPP speed, treated as a function of the amplitude M of the advection field q and dented by c*(M), turns out to behave as O(M) when M is large in the 2D case under certain criteria: I plan to show in this talk a sharp criterion on the advective field under which the speed up of the propagation is linear with respect to the amplitude M. This talk is based on several joint works with S. Kirsch.

Predicting the time and mechanism for resistance in prostate cancer patients undergoing androgen suppression therapy

Rebecca Everett, Arizona State University
rarodger@asu.edu

Prostate cancer is the most common non-skin cancer in men and second most fatal in the United States. It is often treated by a hormone therapy called androgen suppression therapy since both normal and cancerous prostate cells depend on androgens for growth and survival. Due to the side effects of this treatment, the quality of life decreases for the patients while on the therapy. Thus patients often choose intermittent androgen suppression therapy (IAS), in which the patients alternate between durations of on and off treatment. However, the timing for the switching is dependent upon the doctor's experience and intuition. Using a mathematical model, we predict whether or not a patient can undergo another off treatment cycle and test this prediction with clinical data. We use our mathematical model to predict the time and the main mechanisms for the development of resistance to androgen suppression therapy for each patient. Clinically, this can become an important tool for determining the appropriate treatment option for individual patients.

Mathematical modelling of invasive Asian clam in an unbounded one-dimensional habitat

Jian Fang, York University
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Asian clam is a small bivalve that is recognized as one of the most important non-native aquatic invasive species in freshwater ecosystem due to their economic and ecological impact. In this talk, I present a simple mathematical model that phenomenally describes the basic life cycle of Asian clams and then study the invasion speed in an unbounded one-dimensional habitat using a nonlocal reaction-diffusion system with time delay. The invasion speed including its estimation and coincidence with the minimal wave speed of traveling waves is established by appealing to some recent developed dynamical system results. This talk is based on a joint work with Kunquan Lan, Gunog Seo and Jianhong Wu.

Turing Instability for a Two-innovation Diffusion System

Wenying Feng, Trent University
wfeng@trentu.ca

We study a dynamical system model that represents the process of two-innovation diffusion. Both the continuous and discrete forms of the model will be discussed. Stability and bifurcation regions are compared. We will also show that Turing instability conditions are satisfied by migration-diffusion of the discrete model and therefore Turing patterns can be produced from the numerical simulation.

Binding in Pattern Formation

Marina Ferreira, University of Coimbra
marfafe@gmail.com

Chemical reactions are local phenomena. To create spatial patterns they need to be coupled with other type of phenomena that transfer to the entire domain the information about local behavior. In his seed paper Turing proposed Brownian diffusion as a long range process that can originate pattern. However if there are processes that act faster than diffusion they influence the pattern formation. In this talk we will address the importance of binding. A linear approach will be used to analyze pattern formation when this mechanism coexists with diffusion and reaction. Numerical simulations which illustrate our analysis will be included.

Integrodifference Model for Biological Invasion of European Green Crab (Carcinus maenas): Calculation and Sensitivity Analysis of Invasion Speed

Ali Gharouni, University of New Brunswick
v3d66@unb.ca

A fundamental characteristic of any biological invasion is the invasion speed which is determined by population growth and dispersal pattern. In this talk we present a discrete-time model for biological invasion of European Green Crab (Carcinus maenas) in the Canadian Maritimes that couples matrix population models for population growth with integrodifference equations for dispersal. We calculate the population's asymptotic invasion speed and carry out the sensitivity analysis of the invasion speed with respect to changes in demographic and dispersal parameters.

Controlling Leishmaniasis Transmission in India by Systematic Insecticide Allocation

Kaushik Gorahava, The University of Texas at Arlington
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Leishmaniasis is a family of human infectious diseases spread by the bite of sand-flies. The Indian state of Bihar has the highest Leishmaniasis mortality rate in the world. Currently in Bihar, DDT (for controlling Leishmaniasis) is distributed (37.5 grams per individual, under WHO guidelines for achieving kala-azar elimination) only according to the size of the human population. Is the process of insecticide distribution optimal? In this research, we explore this question by using mathematical models. Since the species of the sand fly in India are zoophilic, we also considered the size of cattle population in the design of our models. We use cost and epidemiological data, obtained from Bihar State Health Society through our collaborators at Rajendra Memorial Research Institute of Medical Sciences, Patna, Bihar, in our optimization model to identify the optimal amount of insecticide allocation. Our model treats insecticide spraying at the human as well as cattle dwellings (or sites). The analysis of the model recommends optimal site-dependent allocation of insecticide based upon a lowest cost-benefit ratio (where cost was related to insecticide material and benefit was increase in the sand fly death rate). We derive decision criteria and analytical relationships between socio-economic and epidemiological parameters and the optimal insecticide distribution. This task of obtaining optimal allocation of resources is achieved systematically. Firstly, by minimizing only the cost of insecticide implementation and secondly, by minimizing both the cost and the number of Leishmaniasis cases. We hope the results from our analysis of various insecticide implementation scenarios might be helpful to the Bihar state public health department in designing effective Leishmaniasis control polices.

Parasites also have sex: consequences on host-parasite population dynamics

Frederic Hamelin, Agrocampus Rennes
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To date, relatively few studies have focused on the effects of sex on population dynamics. Previous models found that sexual reproduction may either dampen or accentuate population fluctuations, depending notably on the mating system. Here, we were interested in the effect of mate limitation in pathogens in which both sexual and asexual reproduction occur simultaneously within direct life cycles, a life history typical of fungal plant pathogens for instance. We modeled the epidemiological dynamics of such species by considering a SIR model with two modes of transmission, one linear and the other bilinear in infected density. R0, as derived from the disease-free equilibrium stability condition, does not depend on sexual reproduction, so it provides limited insight. We observe that sexual spore production promotes more complex dynamics than strictly asexual reproduction. In addition, for parameter ranges where population dynamics fluctuate, long-term coexistence of parasites is possible, whereas it is not in the asexual case. We discuss the implications of these results for understanding complex epidemiological dynamics and point to some consequences for epidemics management. This is a joint work with Virginie Ravigné, Valérie Lemesle and Ludovic Mailleret.

Investigating Contact Tracing and Quarantine in the Control of Epidemic Diseases

Xi Huo, Vanderbilt University
xi.huo@vanderbilt.edu

The theoretical impact of isolation before symptom onset on disease transmission has been demonstrated in early works. Thus the potential benefit of interventions such as contact tracing and quarantine are worth investigating. Our age-structured SIR model deals with the case when we have isolation as the main case management, and contact tracing and quarantine as the main contact management in the control of an epidemic disease. In the talk, I would like to introduce the background of contact tracing and quarantine, present our age-structured model, and provide some of our simulation results using data of 2003 SARS, Taiwan.

Immune evasion and the evolution of molecular mimicry in parasites

Amy Hurford, Memorial University of Newfoundland
ahurford@mun.ca

Parasites that are molecular mimics express proteins that resemble host proteins. This resemblance facilitates immune evasion because the immune molecules with the specificity to react with the parasite also cross-react with the host's own proteins, and these lymphocytes are rare. Given this advantage, why aren't most parasites molecular mimics? Here we explore potential factors that can select against molecular mimicry in parasites and thereby limit its occurrence. We consider two hypotheses: 1) molecular mimics are more likely to induce autoimmunity in their hosts, and hosts with autoimmunity generate fewer new infections (the 'costly autoimmunity hypothesis'); and 2) molecular mimicry compromises protein functioning, lowering the within-host replication rate and leading to fewer new infections (the 'mimicry trade-off hypothesis'). Our analysis shows that while both hypotheses may select against molecular mimicry in parasites, unique hallmarks of protein expression identify whether selection is due to the costly autoimmunity hypothesis or the mimicry trade-off hypothesis. We show that understanding the relevant selective forces is necessary to predict how different medical interventions will affect the proportion of hosts that experience the different infection types, and that if parasite evolution is ignored, interventions aimed at reducing infection-induced autoimmunity may ultimately fail.

Dynamics of a model of signal transduction in a 3 dimensional domain

David Iron, Dalhousie University
iron@mathstat.dal.ca

In this talk I will present some on going work with my student Chris Levy. I will present the model of cell signal transduction. We reduce the complex system of partial differential equations to a simple system of ordinary differential equations. Analyze a Hopf bifurcation using the method of strained co-ordinates. Finally I will discuss the effects of Delay.

Dynamics of intraguild predation models

Yun Kang, Arizona State University
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Intraguild predation (IGP) is a combination of competition and predation which is the most basic system in food webs that contains three species (e.g., resource, IG prey and IG predator) where two species that are involved in a predator/prey relationship are also competing for a shared resource or prey. We formulate and study the dynamics of three different types of IGP models to investigate the following ecological questions: i) How do Allee effects in resource affect the dynamics of IGP models? ii) How does generalist vs. specialist IG predator affect species persistence and extinction of IGP models? iii) How do different functional responses between IG prey and IG predator affect the dynamic patterns of IGP models?

Modeling repulsion of superinfecting virions

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In this talk, I discuss the repulsion of superinfecting visions by infected cells via mathematical modeling. A reaction diffusion model for virus infection dynamics is considered, where the diffusion of virus depends not only on its concentration gradient but also on the concentration of infected cells. The basic reproductive ratio, linear stability of steady states, existence of traveling wave solutions for the model are discussed. We see that virus spread more rapidly with the repulsion effect of infected cells on superinfecting virions, than random diffusion. For our model, the spreading speed of free virus is not consistent with the minimal traveling wave speed.

Optimal Control of Cell Migration in Glioblastoma

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Glioblastoma multiforme (GBM) is an aggressive form of brain cancer with a median survival time of just about one year from the time of diagnosis. GBM is characterized by alternating phases of rapid proliferation and aggressive invasion as a response to metabolic stress in the microenvironment. In this talk, based on a recently formulated mathematical model for the relative balance of growth and invasion, we consider the control problem of maintaining certain levels of a particular microRNA, miR-451 and its counterpart AMPK (adenosine monophosphate-activated protein kinase). These are conditions which are expected to prevent the migration of the cancer cells before surgery and lead to the localization of these cells at the surgical site. These levels represent states of the system and the control is given by dose rates of outside glucose administration. In the talk, some dynamical properties of the model will be discussed including the difference in the speed of the dynamics of the two states, which leads to a modified differential algebraic model. The model will be formulated as an optimal control problems with the objective to minimize the total amount of the glucose administration, through both bolus injections and continuous infusions subject to the state constraints, which guarantee that the miR451 is kept in the upregulated state. Mathematically this leads to state space constraints that are of order 2, which makes the concatenations between the boundary and the interior controls challenging. This difficulty is overcome by solving a modifying problem with the state constraints of order 1. Medical interpretation, including the structure of suboptimal protocols for glucose intake will be discussed. Co-authors: H. Schaettler, Washington University, Department of Electrical and Systems Engineering, St. Louis, MO, USA Y. Kim, University of Michigan, Department of Mathematics and Statistics, Dearborn, MI, USA

A stoichiometrically-explicit model for predator control of ecosystem nutrient cycling

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Predators influence ecosystem nutrient cycling through a number of consumptive (i.e. density) and non-consumptive (i.e. trait) mechanisms. We derive a stoichiometrically-explicit ecosystem model to investigate the relative importance of consumptive vs non-consumptive mechanisms for predator control of ecosystem nutrient cycling. The model tracks N and C through ecosystem compartments. We allow for herbivore stoichiometric plasticity in the presence of predation risk and we investigate the role of producer quality (i.e. soluble C:N ratio) on ecosystem dynamics. Under predation risk, herbivores have a heightened basal metabolic rate, are limited by soluble-C and consequently recycle excess N in their diet. The physiological adaptation of herbivores to predation risk leads to large soil and producer nutrient stocks, low predator stocks and production and high N flux from consumers to the soil nutrient pool. Under predation only, herbivores are N-limited and respire excess C in their diet. Predation leads to high predator stocks and production and low N flux from consumers to the soil nutrient pool. Overall, higher quality plants improve the ecological efficiency of nutrient transfer throughout the ecosystem. Since environmental warming also induces elevated metabolism in consumers, the mechanistic framework we present may be useful for predicting the consequences of warming on ecosystem nutrient cycling.

Challenges in mathematical ecology: scaling and collective phenomena

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The subject of mathematical ecology is one of the oldest in mathematical biology, having its formal roots a century ago in the work of the great mathematician Vito Volterra, with links, some long before, to demography, epidemiology and genetics. Classical challenges remain in understanding the dynamics of populations and connections to the structure of ecological communities. However, the scales of integration and scope for interdisciplinary work have increased dramatically in recent years. Metagenomic studies have provided vast stores of information on the microscopic level, which cry out for methods to allow scaling to the macroscopic level of ecosystems, and for understanding biogeochemical cycles and broad ecosystem patterns as emergent phenomena; indeed, global change has pushed that mandate well beyond the ecosystem to the level of the biosphere. Secondly, the recognition of the importance of collective phenomena, from the formation of biofilms to the dynamics of vertebrate flocks and schools to collective decision-making in human populations poses important and exciting opportunities for mathematicians and physicists to shed light. Finally, from behavioral and evolutionary perspectives, these collectives display conflict of purpose or fitness across levels, leading to game-theoretic problems in understanding how cooperation emerges in Nature, and how it might be realized in dealing with problems of the Global Commons. This lecture will attempt to weave these topics together and both survey recent work, and offer challenges for how mathematics can contribute to open problems.

Mathematics behind stream population dynamics

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Human activities change the natural flow regimes in streams and rivers and this impacts ecosystems. In this talk I will mathematically investigate the impact of changes in water flow on biological populations. The approach I will take is to develop process-oriented advection-diffusion-reaction equations that couple hydraulic flow to population growth, and then to analyze the equations so as to assess the effect of impacts of water flow on population dynamics. The mathematical framework is based on critical domain size, spreading speeds and new theory for the net reproductive rate Ro as applied to advection-diffusion-reaction equations. I will then connect the theory to populations in rivers under various flow regimes. This work lays the groundwork for connecting Ro to more complex models of spatially structured and interacting populations, as well as more detailed habitat and hydrological data. This is achieved through explicit numerical simulation of two dimensional depth-averaged models for river population dynamics.

Cost-effectiveness Evaluation of Gender-based Vaccination Programs Against Sexually Transmitted Infections

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For sexually transmitted diseases the determination of an optimal vaccination program is not straightforward due to sexual heterogeneity since (1) the transmission probabilities between two different sexes are normally unequal (weighted to a greater probability from males to females than vice versa), (2) demographic parameters between the two sexes are unequal, (3) the prevalence of disease in one sex may have a greater impact on the morbidity and mortality of the next generation (transmission to the neonate). In this talk, we will present two models of sexually transmitted infections (with and without age structure) to evaluate the cost-efficacy of vaccination programs for different sexes in the context of sexually transmitted disease control, with special application to potential genital herpes vaccination programs. For both models, we find that the stability of the system and ultimate eradication of the disease depend explicitly on the corresponding reproduction number. We also find that vaccinating females is more cost-effective, providing a greater reduction in disease prevalence in the population and the number of infected females of childbearing age. This result is counter-intuitive since vaccinating super-transmitters (males) over sub-transmitters (females) usually has the greatest impact on disease prevalence. Sensitivity analysis is implemented to investigate how the parameters affect the control reproduction numbers and infectious population sizes. This is joint work with Drs. Jane Heffernan, Marc Steben and Jianhong Wu.

Modelling collective cell movement

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The collective movement of cells in tissue is vital for normal development but also occurs in abnormal development, such as in cancer. We will review three different models: (i) A vertex-based model to describe cell motion in the early mouse embryo; (ii) An individual-based model for neural crest cell invasion; (iii) A model for acid-mediated tumour invasion. In each case we shall use the model to answer important issues concerning biology. For example, in (i) we shall propose a role for rosette formation, in (ii) we propose that two cell types are necessary for successful invasion, and in (iii) we shall show how the model suggests possible therapeutic strategies for tumour control.

Modeling Minority Group Influence On Larger Community Behavior: Measles Vaccine Refusal and Ant Networks as Examples

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Throughout biological systems, we see small communities of individuals influencing their encompassing larger body. Two specific examples of this which I have worked on are measles vaccination refusal and task member interactions within ant colonies. By using an agent based model, a team including Dr. Eunha Shim and I were able to investigate how pockets of vaccination skeptics can promote disease spread within an entire urban setting. With Dr. Jennifer Fewell and Dr. Yun Kang, I and others were able to find disparities in antennation patterns between ants participating in different tasks necessary for proper colony functions. While seemingly very different, these two project demonstrate the abilities of small group dynamics to impact systems.

Optimal investment in a multi-mutualist system: Trees and ectomycorrhizal fungi

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Many tree species form mutualistic partnerships with a group of belowground fungi known as ectomycorrhizae. The maintenance of these partnerships depends upon tree payments of photosynthetically fixed carbon to the fungi. In return, the fungi provide nutrients, water, and pathogen defense services to the host tree. Interestingly, an individual tree may host dozens of species of ectomycorrhizae simultaneously, including fungi which appear to be less beneficial than other community members at that time. Empirical evidence suggests that some of this diversity may be explained by niche differences among fungi, with some species better able than others to access particular nutrient pools, provide pathogen defense, and so on. Here, we examine the importance of temporal variation to the maintenance of fungal diversity. In particular, we ask whether a tree that experiences environmental variation might bet hedge, by investing in a suite of fungi more diverse than its present environmental settings dictate because future conditions might require ready access to other partners.

Hopf bifurcation in a neuronal network with distributed delay

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We consider a network of three identical neurons incorporating distributed and discrete signal propagation time delays. The model for such a network is a coupled system of nonlinear delay differential equations. This presentation looks at the simple root single Hopf bifurcation of the trivial equilibrium of the network, and establishes some stability criteria. The results are based on the exact analysis of the characteristic equation of the system of delay differential equations.

A stoichiometric producer-grazer model incorporating the effects of excess food-nutrient content on consumer dynamics

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There has been important progress in understanding ecological dynamics through the development of the theory of ecological stoichiometry. For example, modeling under this framework allows food quality to affect consumer dynamics. While the effects of nutrient deficiency on consumer growth are well understood, recent discoveries in ecological stoichiometry suggest that consumer dynamics are not only affected by insufficient food nutrient content (low phosphorus (P): carbon (C) ratio) but also by excess food nutrient content (high P:C). This phenomenon is known as the stoichiometric knife edge, in which animal growth is reduced not only by food with low P content but also by food with high P content, and needs to be incorporated into mathematical models. Here we present a Lotka-Volterra type model to investigate the growth response of Daphnia to algae of varying P:C ratios capturing the mechanism of the stoichiometric knife edge.

Tumor Microenvironment and Anti-cancer Therapies: An Optimal Control Approach

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A systematic study of cancer treatment requires that we take into account not only the cancerous cells and their growth, but also various aspects of the tumor microenvironment. Its elements include various types of cancer cells, sensitive and resistant to the treatment, healthy cells, tumor vasculature, immune system and more. We shall discuss mathematical models that describe the dynamics of tumor growth in relation to its supporting vasculature under reciprocal angiogenic signaling. For such models, in addition to standard direct treatments that kill cancer cells, one can introduce a second indirect treatment by means of angiogenic inhibitors that target the tumor vasculature. A second indirect approach is to consider the interactions between the tumor and the immune system, including tumor surveillance. Here a simple classical model by Stepanova will be discussed in connection with optimizing the treatment that combines the traditional chemotherapy with a stimulatory effect on the immune system. We will also outline some future work on a more complex model which encompasses more elements of the microenvironment and multi-target therapies. Some connection with the medical research concerning metronomic therapies and other alternative to the MTD (Maximum Tolerated Dose) will be discussed. Co-authors: Urszula Ledzewicz, Dept. of Mathematics and Statistics, Southern Illinois University Edwardsville, USA.

Global dynamics of the Nicholson blowflies equation revisited: onset and termination of nonlinear oscillations

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We revisit the Nicholson blowflies model with natural death rate incorporated into the delay feedback. We consider the delay as a bifurcation parameter and examine the onset and termination of Hopf bifurcations of periodic solutions from a positive equilibrium. We show that the model has only a finite number of Hopf bifurcation values and we describe how branches of Hopf bifurcations are paired so the existence of periodic solutions with specific oscillation frequencies occurs only in bounded delay intervals. This is joint work with Profs. Lin Wang and Jianhong Wu.

Pulsating waves of a partially degenerate reaction-diffusion system in a periodic habitat

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For a partially degenerate reaction-diffusion system in a periodic habitat, we study the existence, stability and uniqueness of pulsating waves. This is an ongoing joint work with Dr. Xiao-Qiang Zhao (MUN).

Two patch predator-prey model with adaptive movement of predators

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A two patch predator-prey model with the Holling type II functional response is studied, where predators adopt adaptive dispersal to move towards the better patch to gain more fitness. Analytical conditions for the persistence and extinction of predators are obtained under either case where prey and predators tend to steady state, or prey and predators tend to limit cycles in two patches. Numerical simulations are conducted to identify rich patterns of dynamic behaviors and bifurcations under influences of dispersal adaptation. It is found that adaptive dispersal can stabilize the system under either weak or strong adaptation.

Metapopulation dynamics of the American pika

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Conventionally, population biologists have tended to focus on deterministic properties of population dynamics, like equilibrium population sizes, minimum viable populations and cyclic population dynamics. Recently, however, there has been a shift toward incorporating stochastic processes into population models. Stochastic phenomena are likely to drive metapopulations, populations of disjoint habitat ”patches” connected by dispersal, with small patches. Here we report on a newly developed computational model designed to evaluate the significance of random fluctuations in general metapopulations. The model is formulated as a birth-death stochastic process on a finite, spatially explicit array of patches. Probability of successful dispersal is modeled as a function of distance between patches. As a test of the model, we apply it to the best-known mammalian metapopulation in North America: the American pika (emphOchotona princeps) population living on the ore dumps in the ghost mining town of Bodie, California. The model was parameterized with demographic and spatial data from the Bodie population, which has been studied nearly continuously for 6 decades. The model is able to predict extinction events that have occurred at the site over the study period. In addition, the model is able to shed light on how the Bodie population may have actually been colonized by pikas over 110 years ago. This type of model is flexible enough to be applied to many types of metapopulation structures.

Bifurcation analyses for a diffusive plant-herbivore model with a non-proportional numerical response

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In this talk, I will present a diffusive plant-herbivore model with a Holling type II functional response and a non-proportional numerical response subject to Neumann boundary conditions. Detailed Hopf bifurcation and steady-state bifurcation analyses are carried out.

Homogeneous auxin steady states and spontaneous oscillations in flux-based auxin transport models

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We consider patterns formed by active transport of auxin in a tissue, where the accumulation of transporters is activated by local fluxes of auxin. We characterize the steady states for which auxin is homogeneous in the tissue. Under a condition of regularity of the dependence of transporters to the flux, we can prove that one of these steady states, with zero flux everywhere, is always locally asymptotically stable. When the condition of regularity is not satisfied, by a combination of analytic and numeric results, we show that the same steady state may undergo bifurcations and become unstable. In particular, we can observe stable oscillations via Hopf bifurcation in the system having the form in a of row of cells. This presents that flux-based active transport alone is enough to induce spontaneous oscillations of auxin in a tissue.

Stability and synchronization of a predator-prey metacommunity model with spatial dispersal and travel time delay

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In this work, we investigate the effect of the spatial dispersal and travel time delay on the regional dynamics of a two-patch predator-prey metacommunity model. Our analytic results show that the density-independent dispersal does stabilize the system at the coexistence equilibrium, while the density-dependent dispersal destabilizes the system. Simulations show that the spatial dispersal may synchronize or desynchronize the system when the isolated single-patch model admits a stable limit cycle. Moreover, when the dispersal is weak, using the weakly connected network theory, we reduce the model to a phase model and the effect of the dispersal delay on the phase synchronization is further analyzed theoretically and numerically. This is an ongoing project with Frithjof Lutscher and Frederic Guichard.

A reaction-diffusion Lyme disease model with seasonality

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In this talk, I will report our recent research on a reaction-diffusion Lyme disease model with seasonality. In the case of a bounded habitat, we obtain a threshold result on the global stability of either disease-free or endemic periodic solution. In the case of an unbounded habitat, we establish the existence of the disease spreading speed and its coincidence with the minimal wave speed for time-periodic traveling wave solutions. We also estimate parameter values via some published data, and use them to study the Lyme disease transmission in Port Dove, Ontario. Our numerical simulations are well consistent with the obtained analytic results. This talk is based on my joint work with Dr. Yuxiang Zhang.

Phenotypic evolution in hermaphroditic populations

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We consider an individual based model of phenotypic evolution in hermaphroditic populations, which includes semi-random and assortative mating of individuals. By increasing the number of individuals to infinity and proper rescaling of coefficients we obtain Boltzmann-type partial integro-differential equation, which describes the evolution of probability density function of phenotypic traits. Moreover, we present some results concerning asymptotic behavior of solutions, and the formula for the density of phenotypic traits in the limiting population.

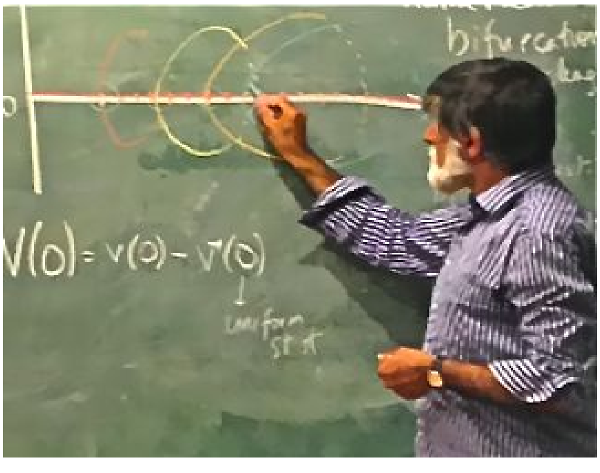
AARMS-Summer School on Dynamical Systems and Mathematical Biology

Memorial University of Newfoundland , July 15 - August 9, 2013

by Kelsey Gasior

The Atlantic Association for Research in the Mathematical Sciences (AARMS) Summer School took place at Memorial University of Newfoundland (MUN) in historic and scenic St. John's, Newfoundland, Canada between July 15 and August 9, 2013. Dr. Xiaoqiang Zhao from the Department of Mathematics and Statistics at MUN organized the program, which gave participants from around the world the opportunity to study under several respected mathematical biologists.

During these four weeks, 44 students and two postdoctoral fellows were able to participate in four different classes, each of which exposed them to a variety of advanced mathematical techniques. Two of the more technical subjects were Stochastic Modeling with Applications in Biology, co-taught by Drs. Linda and Edward Allen, and Reaction-Diffusion Equations and Applications, taught by Dr. Steve Cantrell. In one of the most popular courses, Mathematical Modeling in Developmental Biology and Medicine, Dr. Philip Maini integrated the introduction of bifurcation analysis and Michaelis-Menten kinetics with a discussion on substrate activity and cellular dynamics. Similarly, in Mathematical Methods to Gain Biological Insights, Dr. Odo Diekmann used discussions on enzyme kinetics, population modeling, and diffusion models as catalysts for his mathematically based lectures.



Prof. Maini lecturing on Mathematical Modeling in Developmental Biology and Medicine

In addition to the courses, what made the summer school unique was the atmosphere. The courses pushed students to extend the concepts via-out-of class projects, which encouraged a collaborative environment. Students were able to seek each other out in order to discuss possible ideas and perspectives and, due to the vast array of backgrounds present, they were able to see that working with biologists, ecologists, and other biomathematicians can lead to a better understanding of the topics at hand. Ultimately, this experience gave the students a taste of what it is truly like to work in the collaborative field that is mathematical biology.

The summer school also fostered an informal environment that allowed attendees to take advantage of all the knowledge the professors had to offer. The professors were always very welcoming to those who stopped by their offices, whether it was to discuss the class material or shared research interests. As a young scientist who is just entering the field of mathematical biology, the opportunity to extend my learning outside of the classroom was actually an excellent way to deepen my understanding of my current research. I found it quite interesting to learn more about the derivation of Michaelis-Menten and mass action kinetics, which I have been recently studying. Also, as someone who is interested in cancer and cell biology, I thoroughly enjoyed the opportunity to speak with Dr. Maini about the recent advances and changes occurring in the field.

Even though the coursework was their first priority, students made sure to take advantage of their free time and all that St John's had to offer. Summertime was in full swing in July, which allowed for a lot of outdoor activities. During the first weekend, some students went on a whale watching boat tour. The following day, a few brave souls hiked 15 miles along the East Coast Trail in order to visit Cape Spear, the most easterly point in North America. The hike was by far a highlight of the trip, allowing classmates to bond and enjoy breath-taking views of the Atlantic Ocean and Newfoundland coastline. Students also took part in a lot of activities that were located in downtown St John's. One spot that was very popular with students was Signal Hill, which was only a few miles from campus. Many students woke up early in the morning on several different occasions to see the sun rise over the Atlantic Ocean. Additionally, a small group embraced the tourism industry and went on a "haunted ghost tour" with Drs. Maini and Cantrell. The tour was very charming and an excellent way to learn more about the history and folklore surrounding the town.

While participating in the summer school, students also had the opportunity to attend the 2013 AARMS Mathematical Biology Workshop that took place at MUN from July 27- 29, 2013. The workshop was organized by Drs. Amy Hurford and Xiaoqiang Zhao and featured several parallel sessions and seven plenary lectures. Including the summer school students, there were 84 attendees from Europe, Canada, the United States, and Asia.

The first day of the conference focused on the discussion of ecology and epidemiology. After several parallel sessions in the morning, Dr. Linda Allen gave a plenary lecture on "*Relations Between Deterministic and Stochastic Thresholds for Disease Extinction*". Dr. Allen's talk was further complemented by the plenary lecture given in the afternoon by Dr. Odo Diekmann entitled "*Infectious Disease Transmission on Dynamic Sexual Networks*". Additionally, following the parallel sessions, Dr. Mark Lewis spoke about "*Mathematics Behind Stream Population Dynamics*". In between the lectures and parallel sessions, junior and senior scientists had the chance to interact with one another and extensively discuss the research topics presented at the conference.

The second day of the conference was geared towards cellular processes, pattern formation, and population dynamics and the discussion of these topics was enhanced by the plenary lectures given. Dr. Edward Allen spoke on "*Application, Derivation, and Computation of Continuous and Discrete Delay SDE Models in Mathematical Biology,*" while Dr. Philip Maini later spoke on "*Modeling Collective Cell Movement*". Following the lectures of the second day, attendees were treated to a public lecture by Dr. Simon Levin, as well as a banquet at the Suncor Energy Fluvarium. Dr. Levin's lecture on "*Challenges in Mathematical Ecology: Scaling and Collective Phenomena*" was an excellent discussion on how the concepts observed in ecology help humans question their own financial and global resource sustainability.

The third and final day of the conference focused on population dispersal and evolution. A series of parallel presentations were followed by the final plenary lecture: Dr. Steve Cantrell concluded the conference with his discussion of "*Nonlinear Diffusion and Resource Matching in Population Dynamics*".

Being a part of the AARMS Summer School and Workshop was a once in a lifetime experience and we would like to thank all of those that made it possible. Substantial financial support for both events was provided by AARMS. In addition, the National Science Foundation provided funding for the US participants to travel to the AARMS Summer School, as well as for US scientists to attend the AARMS Workshop. Additional support for the AARMS Mathematical Biology Workshop was provided by The Conference Fund, the Dean of Science, and the Mathematics and Statistics Department at Memorial University, and by the Centre of Recherches Mathématiques that provided travel support for Dr. Simon Levin. Thank you to Easton White of the University of California Davis and Amanda Swan of the University of Alberta for sharing their notes, as well as Dr. Urszula Ledzewicz of Southern Illinois University Edwardsville, Sonia Pozzi of the University of Insubria and Xiaodong Tai of the University of Science and Technology Beijing for sharing their photos. Finally, thank you to Drs. Zhao and Hurford for organizing such amazing events. Further information about the meetings can be found here: http://www.aarms.math.ca/summer/2013/index.html and `http://www.math.mun.ca//~ahurford/aarms/`

Group Photo of AARMS Mathematical Biology Workshop attendees