

# Monday

Time	Plan	Theatre	Room 1	Room 2	Room 3	Room 4	Room 5	Room 6	Room 7	Room 8	Room 9	Room 10	
9:00 - 10:00	Plenary	Arthur Sherman (National Institutes of Health)					Type 2 diabetes: New equations, new thinking						
10:00 - 10:30	Break												
10:30 - 12:30	Minisymp.	<b>Recent advances on modelling and dynamics of vector-borne diseases (1)</b>	<b>Immunobiology and Infection Subgroup (1)</b>	Using ecological theory to understand cancer	Recent perspectives on mathematical epidemiology	Mathematical modeling of normal and abnormal tissue growth and development	<b>Spatial and evolutionary dynamics in mathematical ecology (1)</b>	Global Dynamics : Coexistence and Extinction in Mathematical Ecology and Epidemiology (1)	Applications of mathematical techniques to neuroscience: from molecules to networks	Wave propagation in biological media (1)	Mathematical modeling of cellular transitions en route metastasis: epithelial-mesenchymal plasticity and associated cellular traits (1)	Mentoring Room	
12:30 - 13:30	Lunch	Panel Discussion - Rules of life in the context of future math biology (Theatre)											
13:30 - 14:30	Plenary	Kim Cuddington (University of Waterloo)					Transients, autocorrelated variation, and invasive species impact						
14:30 - 15:30	Contributed Talks	CS1,0	CS 1,1	CS 1,2	CS 1,3	CS 1,4	CS 1,5	CS 1,6	CS 1,7	CS 1,8	CS 1,9	CS 1,10	
15:30 - 16:00	Break												
16:00 - 18:00	Minisymp.	Recent advances on modelling and dynamics of vector-borne diseases (2)	Algebraic tools for the analysis of biochemical reaction networks (1)	Modeling and analysis of the endocrine and neuroendocrine systems	Data-driven methods for biological modeling (1)	Resource explicit population models	Modeling to conquer: Understanding and controlling deleterious diseases using dynamical systems (1)	Population dynamics in heterogeneous landscapes: models, tool and data (1)	Modeling mosquito dynamics: the role of environmental variability	Multiscale modeling of biofilms as complex ecological systems	Mathematical modelling of hematopoiesis under stress and disease (1)		
18:00 - 21:00	Posters												

# Tuesday

Time	Plan	Theatre	Room 1	Room 2	Room 3	Room 4	Room 5	Room 6	Room 7	Room 8	Room 9	
9:00 - 10:00	Plenary	Lindi Wahl (Western University) Message in a bottleneck: How transmission bottlenecks shape the evolution of influenza and HIV										
10:00 - 10:30	Break											
10:30 - 12:30	Minisymp.	<b>Modeling time since infection: theory and implications (1)</b>	<b>Immunobiology and Infection Subgroup (2)</b>	Models of bacterial biofilms and biofilm control approaches	<b>Contemporary mathematical approaches in developmental biology</b>	<b>Spatial and evolutionary dynamics in mathematical ecology (2)</b>	Math psychology and psychiatry (1)	Mathematical modeling of cellular transitions en route metastasis: epithelial-mesenchymal plasticity and associated cellular traits (2)	Delay differential equation models in population biology (2)	Mathematical modelling of hematopoiesis under stress and disease (2)	Mathematical modeling in radiation oncology	Mentoring Room
12:30 - 13:30	Lunch											
13:30 - 14:30	Plenary	Mortiz Thon (Technical University of Munich) Toward a quantification of atherosclerosis Morgan Craig (McGill University) Novel physiological mechanisms revealed through mechanistic modelling of granulopoiesis guides the optimization of drug delivery										
14:30 - 15:30	Contributed Talks	CS 2,0	CS 2,1	CS 2,2	CS 2,3	CS 2,4	CS 2,5	CS 2,6	CS 2,7	CS 2,8	CS 2,9	CS 2,10
15:30 - 16:00	Break											
16:00 - 18:00	Minisymp.	<b>Modeling time since infection: theory and implications (2)</b>	Immune system modeling in the context of cancer growth and treatment	Hepatitis B viral dynamics: mathematical and numerical methods	Mathematical Modelling of Cancer Therapy (1)	Algebraic tools for the analysis of biochemical reaction networks (2)	Mathematical models for plants	The mechanics and biochemical signalling of cellular motility	Applications of mathematical drug development	Modelling intracellular transport (1)	Modeling and analysis of the endocrine and neuroendocrine systems (2)	Data-driven methods for biological modeling (2)
Business Meetings		<b>MathEpi</b>	<b>MathImmuno</b>		<b>DevBio</b>	<b>EcologyEvol</b>						
19:00 - 21:00	Posters											

# Wednesday

Time	Plan	Theatre	Room 1	Room 2	Room 3	Room 4	Room 5	Room 6	Room 7	Room 8	Room 9	Room 10
9:00 - 10:00	Plenary	Helen Byrne (Oxford University) Coming full circle in cancer modelling?										
10:00 - 10:30	Break	AARMS Reception										
10:30 - 12:30	Minisymp.	Setup for AGM	<b>Mathematical Modelling of Neuronal Networks (1)</b>	Mathematical models for infectious disease at population level	<b>Mathematical oncology from bench to bedside (1)</b>	Stochastic models in micro and macro biological systems (1)	Population dynamics in marine ecology	Individual- and agent-based models of within-host disease dynamics	Multiscale modeling of cytoskeleton-mediated cellular transport and aggregation (1)	Wave propagation in biological media (2)	Recent advances on modeling and dynamics of vector-borne diseases (3)	Mentoring Room
12:30 - 13:30	Lunch	AGM										
13:30 - 14:30	Plenary	Caroline Colijn (Simon Fraser University) Mathematical models, genomic data and prediction in infectious disease										
14:30 - 15:30	Contributed Talks	CS 3,0	CS 3,1	CS 3,2	CS 3,3	CS 3,4	CS 3,5	CS 3,6	CS 3,7	CS 3,8	CS 3,9	CS 3,10
15:30 - 16:00	Break											
16:00 - 18:00	Minisymp.	Math psychology and psychiatry (2)	Modeling approaches in the development of cancer immunotherapies and their combinations	Agent-based models in mathematical biology	Population dynamics in heterogeneous landscapes: models, tool and data (2)	Stochastic models in micro and macro biological systems (2)	Modeling the impact of vector behavior, pathogen ecology, and environmental factors on the transmission of vector borne diseases	Modelling gene transcription (1)	Analysis of doomed invasions in oncology, epidemiology and ecology (1)	Modeling in-host bacterial infections for prediction and prevention of disease	Recent advances on modeling and dynamics of vector-borne diseases (4)	Modeling to conquer: Understanding and controlling deleterious diseases using dynamical systems (2)
<b>Banquet</b>												

# Thursday

Time	Plan	Theatre	Room 1	Room 2	Room 3	Room 4	Room 5	Room 6	Room 7	Room 8	Room 9	Room 10
9:00 - 10:00	Plenary	Nick Monk										
10:00 - 10:30	Break											
10:30 - 12:30	Minisymp.	<b>Mathematical Modelling of Neuronal Networks (2)</b>	Stochastic models for biochemical reaction networks (1)	<b>Building bridges for mathematical biology education (1)</b>	<b>Mathematical oncology from bench to bedside (2)</b>	Global Dynamics : Coexistence and Extinction in Mathematical Models from Ecology and Epidemiology (2)	Vector-borne diseases: improving our understanding of underlying mechanisms and implications for disease control	Mathematical modelling of bees	Modelling intracellular transport (2)	Modeling, dynamics and control of African Swine Fever	Structured population models for disease transmission dynamics (1)	Mentoring Room
12:30 - 13:30	Lunch	Panel Discussion - Data Science Education for Biology (Theatre)										
13:30 - 14:30	Plenary	Naoki Masuda (University of Bristol) Network dynamics: Epidemic processes and energy landscape analysis										
14:30 - 15:30	Contributed Talks	CS 4,0	CS 4,1	CS 4,2	CS 4,3	CS 4,4	CS 4,5	CS 4,6	CS 4,7	CS 4,8	CS 4,9	CS 4,10
15:30 - 16:00	Break											
16:00 - 18:00	Minisymp.	<b>Mathematical Modelling of Neuronal Networks (3)</b>	Advances in cancer treatment scheduling and optimization	<b>Building bridges for mathematical biology education (2)</b>	Mathematical modelling of protein misfolding disease	Stochastic models for biochemical reaction networks (2)	Validation of mathematical models in immunology and cancer (1)	Modelling gene transcription (2)	Multiscale modeling of cytoskeleton-mediated cellular transport and aggregation (2)	Modeling Cancer within the patient: a host-level focus	Optimization and optimal control in mathematical biology	Analysis of doomed invasions in oncology, epidemiology and ecology (2)
Business Meetings		<b>MathNeuro</b>		<b>MathEd</b>	<b>MathOnco</b>							

# Friday

Time	Plan	Theatre	Room 1	Room 2	Room 3	Room 4	Room 5	Room 6	Room 7	Room 8	Room 9	Room 10	
9:00 - 10:00	Plenary	Jinzhi Lei (Tsinghua University) Evolutionary dynamics of cancer: From epigenetic regulation to cell population dynamics											
10:00 - 10:30	Break												
10:30 - 12:30	Minisymp.	<b>Mathematical Modelling of Neuronal Networks (4)</b>	Validation of mathematical models in immunology and cancer (2)	Structured population models for disease transmission dynamics (2)	Quantitative approaches to unravel immune function and immunity	Dynamics of immune system functions at the cellular and molecular level	Mathematical Modelling of Cancer Therapy (2)	Disease and control					Mentoring Room
12:30 - 13:30	Lunch												

Mini-Symposia

## **Advances in cancer treatment scheduling and optimization**

Chamseddine, Ibrahim, *H. Lee Moffitt Cancer Center & Research Institute*

Rejniak, Katarzyna A., *H. Lee Moffitt Cancer Center & Research Institute*

### **Abstract**

Applications of anti-cancer therapies are faced with fundamental challenges, such as cell resistance, treatment toxicity, and physiological barriers to treatment delivery. The effectiveness of these therapies depends on cancer properties (tumor structure, microenvironmental heterogeneity), treatment properties (drug diffusivity, immune cell potency), as well as treatment scheduling and dosage. The rational selection of these multiple parameters to improve therapeutic efficacy and to reduce toxicological effects requires novel computational methods. In this minisymposium, our speakers will present recent advances in treatment planning methodologies and in developing robust treatment protocols taking into account tumor heterogeneity. We will also highlight the applications of optimization methods, widely used in engineering design, to develop effective cancer therapies. Our minisymposium will include applications in nano-, immuno-, adaptive and targeted therapies.

**Thursday, 16:00-18:00; Room 1**

Jana Gevertz

Patrick Ellsworth

Ibrahim Chamseddine

Michael Kokkolaras

## **Agent-based models in mathematical biology**

Strickland, Christopher, *University of Tennessee*

### **Abstract**

Agent-based models are models in which individuals are described as autonomous entities which can then interact with each other and/or their environment. They are particularly well suited to exploring ways in which individual-level behavior can result in emergent population-level patterns – patterns which in turn often yield a nice mathematical description. Agent-based models are also useful for developing effective control strategies in stochastic systems with complex individual-level interactions. In this minisymposium, we will explore several ways in which agent-based models are being used in mathematical biology, by examining the behavioral response of swimmers in porous-layer fluid flow, the mechanics of pattern formation in locust swarms, control strategies for infection in healthcare facilities, and optimal spatiotemporal harvest strategies in agricultural settings.

**Wednesday, 16:00-18:00; Room 2**

Christopher Strickland

Jasmine Kreig

Brittany Stephenson

Andrew Bernoff

## Algebraic tools for the analysis of biochemical reaction networks

Johnston, Matthew D, *San Jose State University*

Meshkat, Nicolette, *Santa Clara University*

### Abstract

It is common to model the dynamical behavior of biochemical reaction networks such as signal transduction pathways and gene regulatory networks with a system of ordinary differential equations. The analysis of such systems has been crucial in understanding the biological mechanisms underlying such processes as apoptosis, circadian rhythms, and the cell cycle, and diseases like diabetes and cancer. Nevertheless, mathematical analysis of such models is challenging as a result of the high dimensionality of the systems, parameter uncertainty, significant nonlinearities, and time-scale separations between reactions. To address these challenges, tools from computational algebra and numerical algebraic geometry have been particularly fruitful and significant progress towards answering some of the more challenging questions in this area has resulted. In this session, we will give a forum to the latest advances on the analysis of such systems, with an emphasis on contributions from dynamical systems theory, algebraic geometry, and symbolic/numeric computation.

### Monday, 16:00-18:00; Room 1

Elizabeth Gross

Nicolette Meshkat

Matthew Johnston

Adrian Tudorascu

### Tuesday, 16:00-18:00; Room 4

Alan Rendall

Gabor Szederkenyi

Abhishek Deshpande

Polly Yu

## Analysis of doomed invasions in oncology, epidemiology and ecology

Mililken, Evan, *Arizona State University*

### Abstract

Stochastic models of population dynamics are used to study biological invasions in a wide variety of applications. Whether studying ecological invasion, success of a mutant species, metastasis or eradication of a tumor or outbreak or extinction of an infectious disease, important statistics of these models are the probability of and mean time until extinction. This mini-symposium proposes to bring together researchers studying the probability of and mean time to extinction using a wide variety of techniques including Little's Law, Galton Watson and multitype branching processes, local approximation in time and space, diffusion approximation, and Wentzel-Kramers-Brillouin approximation. Biological subject matter of the presentations will be varied.

### Wednesday, 16:00-18:00; Room 7

Ohad Vilk

Malwina Luczak

Kaniz F Nipa

Julien Arino

### Thursday, 16:00-18:00; Room 10

Fred Adler

Evan Milliken

Tom Chou

Peter Pang

## Applications of mathematical drug development

Ahamadi, Malidi, *Merck Research Laboratory*

Mehta, Khamir, *Amgen*

Vargo, Ryan, *Merck*

### Abstract

Mechanistic mathematical models based on fundamental biochemical and physiological principles have been increasingly used to enable improved decision making at various stages in drug development process across pharmaceutical industry. This mini-symposium aims to present examples applications of such models, e.g. in making assessment of drug safety and efficacy, quantify first-in-human dosing strategy, dose optimization, optimal study design etc. The presenters will showcase and highlight the usage of quantitative mechanistic models that capture the essential elements of pharmacology to aid the optimization of treatment regimens. The diverse group of speakers bring together members of industry with that bring very different perspectives on how to implement and leverage mathematical models to answer specific questions in drug development. This mini-symposium will encourage the exchange of ideas and opportunities in using mathematical approaches in drug development and benefit both industry as well as academic participation.

**Tuesday, 16:00-18:00; Room 7**

Ryan Vargor

Chi-Chung Li

Khamir Mehta

Mindy Magee

## Applications of mathematical techniques to neuroscience: from molecules to networks

Brake, Niklas, *McGill University*

Farjani, Saeed, *McGill University*

### Abstract

The brain is a highly complex system. To understand its behavior under (ab)normal conditions, researchers explore brain activity at many different levels: genetic, molecular, cellular, circuit, and network. Traditional biological approaches are not well adapted to complex, nonlinear interactions or large data sets, both of which are inherent to many areas of brain research. In this minisymposium, we intend to bring together scientists who take interdisciplinary approaches to answer questions related to brain dynamics. Topics covered in the minisymposium include all those that apply mathematical techniques to solve problems at various spatial and temporal scales of the brain in health and disease.

**Monday, 10:30-12:30; Room 7**

Niklas Brake

Saeed Farjani

Ryan Phillips

Sue Ann Campbell

## Building bridges for mathematical biology education

Diaz Eaton, Carrie, *Bates College*

Gaff, Holly, *Bates College*

Jungck, John, *University of Delaware*

### Abstract

This minisymposium will focus on bridge building for the future of mathematical biology education. We will explore approaches to teaching mathematical biology education using a variety of modalities to engage students, enhance learning, and enhance relevance to 21st century needs. We will also explore the interdisciplinary nature of our community, how new technology is changing that landscape, and what we can do as educators to meet these needs.

**Thursday, 10:30-12:30; Room 2**

John Jungck

Holly Gaff

Meredith Greer

Carrie Diaz Eaton

**Thursday, 16:00-18:00; Room 2**

Paul Macklin

Reggie McGee

Hwayeon Ryu

Eberhard Voit

## Contemporary mathematical approaches in developmental biology

Fletcher, Alex, *University of British Columbia*  
Buttenschoen, Andreas, *University of Sheffield*

### Abstract

Recent technological advances have revolutionised the field of developmental biology: phenotypic analyses have been transformed from simple qualitative observations to quantitative characterisations, enabling the extraction of parameters with which to model complex processes and facilitating an unprecedented understanding of diverse aspects of development. As a result, this fast-moving field now impacts on key biomedical disciplines, from oncology to regenerative medicine. Alongside continual advancement of genetic and imaging techniques, developmental biology is increasingly benefiting from the use of mathematical modelling to help interpret and predict behaviour. Novel mathematical and computational tools are often required for model analysis. Key ongoing challenges in this area include understanding how single-cell behaviours determine tissue-level function, the roles of noise, the interplay between mechanical and chemical signalling, and the evolution of such mechanisms across species. The aim of this Developmental Biology Subgroup activity is to showcase the cutting edge of research in this area, with a focus on emerging talent. This will raise the profile of contemporary mathematical approaches to development within the SMB, encourage new members to join the Subgroup and work in the area, and provide a platform for new interactions between SMB members working in the area.

**Tuesday, 10:30-12:30; Room 3**

Adam MacLean  
Lisanne Rens  
Ruben Perez Carrasco  
Renske Vroomans

## Data-driven methods for biological modeling

Rutter, Erica, *North Carolina State University*  
Nardini, John, *North Carolina State University*  
Flores, Kevin, *North Carolina State University*

### Abstract

In the advent of big data and increased data availability in biology, mathematical modelers are faced with many opportunities and challenges, such as capturing heterogeneity, model selection and refinement, and utilizing multiscale models with data. This minisymposium will present advances in the development or novel application of statistical and machine learning methods towards modeling. These methods enable the use mathematical models to assess hypotheses and propose biological mechanisms leading to the observed data. The first session applies data-driven methods to cancer, while the second session considers applications to a variety of biological phenomena such as wound healing, disease spread, and epidemiology.

**Monday, 16:00-18:00; Room 3**

Lee Curtin  
Yang Kuang  
Erica Rutter  
Christina Vaghi

**Tuesday, 16:00-18:00; Room 10**

Harry Dudley  
John Nardini  
Suzanne Sindi  
Marisa Eisenberg

## Delay differential equation models in population biology

Hurford, Amy, *Memorial University*  
Wang, Lin, *University of New Brunswick*

### Abstract

Delay differential equation (DDE) models consider dependencies on the past states of a population and many biological processes involve such dependencies. DDEs offer a realistic framework for modeling populations and novel dynamics may arise due to the delay-related assumptions. This minisymposium considers distributed, periodic, and dispersal delays and the population dynamics that arise from these model assumptions.

**Tuesday, 10:30-12:30; Room 7**

Gail Wolkowicz  
Lin Wang  
Kyeongah Nah  
Fuxiang Li

## **Disease and control**

Khan, Adnan, *Lahore University of Management Sciences*

Imran, Mudassar, *Gulf University of Science & Technology*

### **Abstract**

Compartment models have found wide applications in in-vivo and in-vitro modeling of dynamics of diseases and in their transmission. Therefore, modeling of disease control is typically based on these compartmental models using ordinary and partial differential equations and Markov process models. Optimal control techniques are an important mathematical tool to model transmission control and therapeutic control in non-infectious and in infectious diseases. This focus of this session is modeling the transmission dynamics and control strategies for infectious diseases. We aim to bring in people from a variety of geographical locations with modeling experience relevant to local problems.

**Friday, 10:30-12:30; Room 6**

Abba Gumel

Mudassar Imran

Folashade Augusto

Adnan Khan

## **Dynamics of immune system functions at the cellular and molecular level**

Jameleddine, Hassan, *McGill University*

### **Abstract**

The immune system plays a fundamental role in defending complex organism against pathogens, and in some cases can also trigger autoimmune diseases. The general theme of this mini-symposium involves the use of theoretical and computational approaches to understand the dynamics of various features of the immune response. Topics include viral infections, cytokine and metabolite profiles throughout the immune response, and population dynamics of immune cells. Speakers will present techniques used in their research to analyze these systems at the sub- and supra-cellular levels.

**Friday, 10:30-12:30; Room 4**

Alan Perelson

Hassan Jamaledine

Catherine Byrne

David Schneider

## **Global Dynamics : Coexistence and Extinction in Mathematical Models from Ecology and Epidemiology**

Salceanu, Paul L, *University of Louisiana at Lafayette*

### **Abstract**

This minisymposium is intended to bring into discussion two fundamental outcomes of mathematical models from ecology and epidemiology : coexistence and extinction. A variety of aspects of analysis, including modeling techniques, numerical methods and the use of mathematical tools (such as stability analysis, bifurcation theory, persistence theory) are expected to be represented.

**Monday, 10:30-12:30; Room 6**

Linda Allen

Ruiwen Wu

Zahid Mondal

Xiunan Wang

**Thursday, 10:30-12:30; Room 4**

Jim Cushing

Amy Veprauskas

Alex Farrell

Shigui Ruan

## Hepatitis B viral dynamics: mathematical and numerical methods

Reinharz, Vladimir, *Institute for Basic Science*

Dahari, Harel, *Loyola University*

### Abstract

An estimated 300 million people are chronically infected with hepatitis B virus (HBV), the leading cause for hepatocellular carcinoma. This mini-symposium brings together modelers and mathematicians who are experts in the study of HBV dynamics and numerical methods to discuss current challenges in the field of viral dynamics with the emphasis on understanding viral-host interactions. This mini-symposium is targeted to both young and established mathematical modelers and clinical researchers interested in modeling HBV dynamics and immune responses.

**Tuesday, 16:00-18:00; Room 2**

Stanca Ciupe

Jonathan Forde

Harel Dahari

Vladimir Reinharz

## Immune system modeling in the context of cancer growth and treatment

Altrock, Philipp, *Moffitt Cancer Center*

Robertson-Tessi, Mark, *Moffitt Cancer Center*

### Abstract

The immune system is increasingly being recognized as a fundamental component of the tumor microenvironment that affects cancer progression at all stages from initiation to treatment. Given the immense complexity of the immune system, many details of tumor-immune interactions remain elusive. The non-linear, multi-dimensional nature of this interacting system provides ample opportunity for investigation with theoretical modeling. This minisymposium will offer four talks on important aspects of immune mechanisms that are relevant to oncology. In keeping with the theme of the conference, the speakers will present models that examine the immune system and tumor-immune interactions at different scales.

**Tuesday, 16:00-18:00; Room 1**

Ami Radunskaya

Luis Zapata Ortiz

Ardith El-Kareh

Morgan Craig

## Immunobiology and Infection Subgroup

Conway, Jessica M, *Pennsylvania State University*

Day, Judy, *University of Tennessee*

Reynolds, Angela, *Virginia Commonwealth University*

Smith, Amber M, *University of Tennessee Health Science Center*

### Abstract

The Immunobiology and Infection Subgroup was created to bring together researchers in the SMB community who are interested in the modeling and analysis of immune processes in human disease and of host-pathogen interactions. Our broad objective is to discuss various topics including - within-host infectious diseases - host immune responses - causes and effects of inflammation - disease progression and outcome - integration of experimental and clinical data into models - model-driven experimental design. In our 2019 minisymposium, we will focus on infection and host immune responses to both infectious and non-infectious insults. We will have 7 speakers with expertise in these areas. The talks will also showcase diverse modeling styles and integration with data.

**Monday, 10:30-12:30; Room 1**

Rustom Antia

Esteban Hernandez-Vargas

Rosemary Aogo

Carmen Lia Murall

**Tuesday, 10:30-12:30; Room 1**

Katharine Best

Chase Cockrell

Richard Allen

Jared Barber

## Individual- and agent-based models of within-host disease dynamics

Evans, Stephanie, *University of Michigan*  
Renardy, Marissa, *University of Michigan*  
Kirschner, Denise, *University of Michigan*

### Abstract

Individual/agent-based models have been used to study a wide range of diseases in a multi-scale manor. These models are important for determining mechanisms of disease initiation and progression, evaluating treatment protocols, and exploring the effects of heterogeneity within populations, tissues, and cell types. This minisymposium focusses on agent-based modeling of within-host disease development, and brings together different applications, modeling approaches, and methods for model analysis.

**Wednesday, 10:30-12:30; Room 6**

Gary An  
Stephanie Evans  
Jill Gallaher  
Jesse Kreger

## Mathematical modeling in radiation oncology

Enderling, Heiko, *H. Lee Moffitt Cancer Center & Research Institute*

### Abstract

Since the early days of radiotherapy, mathematical modeling has played a pivotal role in analyzing radiosensitivity and calculating radiation treatment protocols. With increasing radiobiological knowledge and numerous biological agents that synergize with radiation, mathematical modeling is poised to continue to make significant contributions to the field of radiation oncology. In this minisymposium web ring together a group of leading international researchers from different research groups and hospitals that demonstrate the integration of experimental and clinical data to build mathematical models that help optimize cancer radiotherapy.

**Tuesday, 10:30-12:30; Room 9**

Sarah Bruning  
Jamie Dean  
Juan Carlos Lopez Alfonso  
Clemens Grassberger

## Mathematical modeling of cellular transitions en route metastasis: epithelial-mesenchymal plasticity and associated cellular traits

Jolly, Mohit K, *Indian Institute of Science*  
Levine, Herbert, *Rice University*

### Abstract

Metastasis – the cause of almost all cancer-related deaths – is a highly dynamic process where cells need to adapt to changing biochemical and biomechanical surroundings. No unique mutational signature has yet been associated with metastasis, emphasizing the importance of phenotypic plasticity – the ability of genetically identical cells to alter their phenotypes in response to many signals – in driving metastasis. Recent studies have identified the role of epithelial-mesenchymal plasticity in driving multiple facets of metastasis : collective cell migration, tumor-initiation, resistance against therapies including immunotherapy etc. A mapping of signaling networks driving this plasticity has motivated many mathematical models to elucidate the dynamics of such plasticity, to suggest experiments to quantify such plasticity, and to design treatment strategies to restrict this plasticity. This minisymposium focuses on inviting leaders in modeling cellular transitions during metastasis, and is proposed to last for two periods. The first period will involve speakers who have offered valuable insights into the intracellular and tissue-level dynamics of epithelial-mesenchymal plasticity, while the second period will gather experts who have investigated the emergence of EMT-associated cellular traits such as therapy/drug resistance and tumor-initiation potential, through mathematical modeling approaches.

**Monday, 10:30-12:30; Room 9**

Loukia Karacosta  
Shubham Tripathi  
Melissa Davis  
Mingyang Lu

**Tuesday, 10:30-12:30; Room 6**

Kaitlyn Johnson  
Mohammed Kohandel  
David Wooten  
Jason Somarelli

## Mathematical modeling of normal and abnormal tissue growth and development

Wu, Min, *Worcester Polytechnic Institute*

### Abstract

The minisymposium is intended to describe the contributions of mathematical modeling and computation to topics at the interface between developmental biology and oncology. Topics of 1) brain tumor development, 2) growth regulation in intestinal crypts, 3) pancreatic cancer invasion in extracellular matrix and 4) cell intercalations during *Drosophila* germband extension will be presented to gain a broader understanding of the similarity and difference between normal growth and abnormal growth.

**Monday, 10:30-12:30; Room 4**

Vivek Shenoy  
Clinton Durney  
Axel Almet  
Meghan Hall

## Mathematical modelling of bees

Ratti, Vardayani, *Dartmouth College*

### Abstract

Pollinators, mostly bees, provide pollination for approximately 75% of the world's food crops. These pollinators however, are in significant decline globally, raising serious concerns about our food security and ecosystem stability. Mathematical modeling has greatly aided in understanding of these stressors and in suggesting remedial strategies using approaches from infectious disease modeling and theoretical ecology. The proposed minisymposium will bring together well-recognized speakers who are actively developing mathematical models on bees using differential equations techniques. The minisymposium will promote the communication and cross-fertilization of ideas amongst participants. This minisymposium follows similar and highly successful symposiums held at the SMB annual meetings in 2013, 2016, and 2017.

**Thursday, 10:30-12:30; Room 6**

Hermann Eberl  
Yun Kang  
Nourridine Siewe  
Ezio Venturino

## Mathematical Modelling of Cancer Therapy

Liao, Kang-Ling, *University of Manitoba*

### Abstract

The last few years, have seen many promising developments in cancer therapy including immunotherapy, radiotherapy, and chemotherapy. But there is still much work needs to be done to bring drugs from the bench through clinical trials. We need to find better ways to judge the success of the new therapies and to work out the optimal dose and treatment schedule. Right now, it is difficult to predict tumor response to a particular treatment by experiments or clinical trials. The long term benefits and remission of these new therapies are also not yet determined. Thus, the focus of this session will be on the combination of mathematical modeling and experiments to help overcome these problems.

**Tuesday, 16:00-18:00; Room 3**

SeokJoo Chae  
Yangjin Kim  
Kang-Ling Liao  
Xiulan Lai

**Friday, 10:30-12:30; Room 5**

Wing Cheong Lo  
Leli Shahriyari  
Daewook Kim  
Jaehyung Hong

## Mathematical modelling of hematopoiesis under stress and disease

Humphries, Tony, *McGill University*

Stiehl, Thomas, *Heidelberg University*

### Abstract

Hematopoietic stem cells (HSC) are responsible for life-long blood cell formation, and play a pivotal role in many diseases of the blood forming (hematopoietic) system. HSCs carrying mutations give rise to a wide range of diseases including pre- malignant and malignant diseases such as leukemias (blood cancers). Our intuitive understanding of the underlying dynamics is limited due to their complex and nonlinear nature. Mathematical models are an excellent tool to study complex phenomena and to provide insights into processes that cannot be measured directly. This minisymposium aims to bring together mathematical modellers and medical doctors contributing to a rigorous understanding of the hematopoietic system. The topics covered range from applied questions such as bone marrow transplantation, blood cancer evolution and cell-cell interactions in the stem cell niche to mathematical problems such as model reduction and multi-scale dynamics.

### Monday, 16:00-18:00; Room 9

Michael Mackey

Peter Ashcroft

Joseph Mahaffy

Anna Miller

### Tuesday, 10:30-12:30; Room 8

Thomas Stiehl

Kolja Eppert

Morten Andersen

Dominik Wodarz

## Mathematical Modelling of Neuronal Networks

Best, Janet, *The Ohio State University, Mathematical Biosciences Institute*

Campbell, Sue Ann, *University of Waterloo*

Crodelle, Jennifer, *Courant Institute, New York University*

Ryu, Hwayeon, *University of Hartford*

Pyzza Pamela, *Ohio Wesleyan University*

### Abstract

Mathematical modeling is an important tool used to study neuronal dynamics and neural systems, leading both to better biological understanding of neuronal phenomena and to new mathematical questions. This session will feature recent contributions of mathematics to neuroscience, with an emphasis on the computation of neuronal networks in revealing underlying biological function.

### Wednesday, 10:30-12:30; Room 1

Horacio Rotstein

Kanika Bansal

Daniel Park

Stefanos Folias

### Thursday, 10:30-12:30; Theatre

Frances Skinner

Nicola Wilton

Shusen Pu

Youngmin Park

### Thursday, 16:00-18:00; Theatre

Jennifer Crodelle

Yangyang Wang

Anca Radulescu

Janet Best

### Friday, 10:30-12:30; Theatre

Cheng Ly

Christina Hamlet

Rodica Curtu

Pamela Pyzza

## Mathematical modelling of protein misfolding disease

Sindi, Suzanne S, *University of California, Merced*

Pujo-Menjouet, Laurent, *University Claude Bernard Lyon 1*

### Abstract

Protein misfolding diseases, such as Alzheimer's and Parkinson's disease, result from the accumulation and aggregation of incorrectly folded proteins. These diseases can be genetic or spontaneous and in the special case of prion disease infectious. Because these diseases occur in different biological settings (e.g. humans, yeast) and time-scales (e.g. years, hours) a variety of mathematical models and experimental techniques have been employed. This minisymposium brings together biologists and mathematicians from a variety of fields with the goal of exploring the latest approaches towards studying protein misfolding diseases.

**Thursday, 16:00-18:00; Room 3**

Justin Torok

Paul Lemarre

Human Rezaei

Mikahl Banwarth-Kuhn

## Mathematical models for infectious disease at population level

Ponce, Joan, *Purdue University*

### Abstract

Infectious diseases are caused by a wide variety of organisms such as bacteria, viruses, fungi and parasites. The dynamics of infectious diseases have been studied from several perspectives and levels (population and individual levels), which help determine transmission mechanisms of the diseases and effective forms of control. The main purposes of this session are i) bring together researchers working on modeling infectious diseases and share recent developments and modeling strategies ii) Foster connections between modelers of different scales of infectious disease processes: from individuals to the population level iii) Inspire questions and collaborations between early career and experienced researchers. Topics: Dr Christopher Kribs: "Invasion reproductive numbers for discrete and periodic systems" Yuanchi Ha: "Persistence and Reversal of Plasmid Mediated Antibiotic Resistance" Joan Ponce: "Dynamics of a childhood disease model with isolation" Kyle Dahlin: "Mathematical Modeling of Avian Malaria in Hawaiian Honeycreepers"

**Wednesday, 10:30-12:30; Room 2**

Christopher Kribs

Joan Ponce

Kyle Dahlin

Pradyuta Padmanabhan

## Mathematical models for plants

Ledder, Glenn, *University of Nebraska-Lincoln*

Russo, Sabrina, *University of Nebraska-Lincoln*

### Abstract

Plants play a critical role in Earth's environment, and it is important to understand their impact on climate change and the impact climate change has on them. This minisymposium looks at issues that arise in modeling of plant functioning, such as water flow in plants, stomatal control, and allocation of resources.

**Tuesday, 16:00-18:00; Room 5**

Danielle Way

Sabrina Russo

Nicholas Smith

Glenn Ledder

## Mathematical oncology from bench to bedside

Anderson, Alexander, *H. Lee Moffitt Cancer Center & Research Institute*

### Abstract

Mathematical modeling in oncology has a long history. Recent advances in mathematical oncology have focussed on a fully integrated, iterative workflow of experimental or clinical data motivating mathematical models, and model-generated hypothesis to inform subsequent validation experiments or clinical trials. This 2-part minisymposium showcases research from the SMB Mathematical Oncology Subgroup by members that are experts in either basic mathematical oncology (focus on experimental data and cancer biology questions) or translational mathematical oncology (focus on clinical data with oncology questions). Subjects vary from cancer development, progression and evolution to cancer treatment by radiotherapy, hormone therapy or chemotherapy.

### Wednesday, 10:30-12:30; Room 3

Jacob Scott  
Mohit Kumar Jolly  
Russ Rockne  
Philipp Altmann

### Thursday, 10:30-12:30; Room 3

Gibin Powathil  
Renee Brady  
Thomas Yankeelov  
Kristin Swanson

## Mathematical psychology and psychiatry

Hurdal, Monica, *Florida State University*

Cochran, Amy, *University of Wisconsin-Madison*

Forger, Daniel, *University of Michigan*

### Abstract

Mathematics is important for addressing emerging challenges in psychiatry and abnormal psychology. One objective is to reorganize diagnostic criteria consisting of subjective symptoms, thoughts, and behavior into testable mathematical frameworks. For example, reinforcement learning provides a framework to understand human learning and decision-making and their neural correlates. Another mathematical direction lies in using dynamical systems to describe severe fluctuations in symptoms that mark chronic disorders such as depression, bipolar disorder, or schizophrenia. This minisymposium brings together a diverse group of researchers to highlight different mathematical approaches in psychology and psychiatry.

### Tuesday, 10:30-12:30; Room 5

Daniel Forger  
Shelby Weaver  
Joel Nishimura  
Zoran Tiganj

### Wednesday, 16:00-18:00; Theatre

Monica Hurdal  
John Murray  
Amy Cochran  
Jeff Dunworth

## Modeling and analysis of the endocrine and neuroendocrine systems

Bertram, Richard, *Florida State University*

Ha, Joon, *National Institutes of Health*

### Abstract

The endocrine system is composed of glands that contain hormone-secreting cells. The secretion of some hormones is under the direct control of the hypothalamus in the brain, forming the neuroendocrine system. Examples of endocrine glands are the pituitary, the adrenal, the pancreas, and the gonads. The hormones travel through the blood stream to target tissues throughout the body, including the brain, and regulate their function. They are responsible for mood, reproduction, sexual behavior, temperature and water regulation, growth, and glucose homeostasis, among many other things. The speakers in this minisymposium will discuss recent research utilizing mathematical models to understand the activity of cells in the endocrine or neuroendocrine system, and the effects of the released hormones on target tissue. The minisymposium is held in honor of Arthur Sherman, this year's Winfree Award recipient and a pioneer in the modeling and analysis of these systems.

### Monday, 16:00-18:00; Room 2

Anmar Khadra

Eder Zavala

Joon Ha

Cecilia Diniz Behn

### Tuesday, 16:00-18:00; Room 9

Benoit Huard

Brad Peercy

Patrick Fletcher

Richard Bertram

## Modeling approaches in the development of cancer immuno-therapies and their combinations

Lemaire, Vincent, *Genentech*

### Abstract

Cancer immuno-therapy is a cancer treatment that aims to improve or restore the patient's own immune functions in order to fight cancer development. The immune system and cancer are two of the most complex biological systems; understanding their interaction and controlling it is an even more challenging problem. The use of mechanistic modeling may help in the development of cancer immuno-therapies, in particular for questions involving the complex nature of these systems. These include intricate dose-response relationships, identifying signals of response, assessing synergy or sequencing effects in combination treatments, and assessing best target population. For this minisymposium, we gathered experts from academia and the pharmaceutical industry to discuss how modeling approaches may be used to aid in the development of cancer immuno-therapies, such as checkpoint inhibitors, T cell engaging molecules, oncolytic viral therapies, personalized cancer vaccines, cytokine-based therapies, and their combinations.

### Wednesday, 16:00-18:00; Room 1

Colling Zhen

Mary Spilker

Roy Song

Andrzej Kierzek

## Modeling Cancer within the patient: a host-level focus

Wilkie, Kathleen, *Ryerson University*

### Abstract

Cancer does not grow in isolation. It grows within a body, constantly receiving and sending signals that alter the future state. This mini symposium will look at ways in which the body alters tumour fate (such as immune responses), or at ways in which tumours alter the body, (such as cancer cachexia).

### Thursday, 16:00-18:00; Room 8

Suzan F Sardroodi

Chiara Nicolo

Adrienne Jenner

Kathleen Wilkie

## **Modeling in-host bacterial infections for prediction and prevention of disease**

Erwin, Samantha, *North Carolina State University*

### **Abstract**

Bacteria are mostly harmless single-celled organisms thriving in the human body. However, in some cases, these microbes can lead to disease states. This minisymposium features researchers from both mathematical and biological backgrounds who present recent modeling efforts to study infectious bacteria in-host including: *Clostridiois difficile*, *Mycobacterium tuberculosis*, and *Francisella tularensis*. Speakers will discuss a variety of mathematical

techniques and tools used to study the different organisms such as agent- based models, graphical models, stochastic models, and ordinary differential equations. This session aims to bring together researchers of different backgrounds and expertise to encourage innovative approaches for modeling bacterial colonization and infection.

**Wednesday, 16:00-18:00; Room 8**

Denise Kirschner

Martin Lopez

Matthew Jenior

Samantha Erwin

## **Modeling mosquito dynamics: the role of environmental variability**

Blackwood, Julie C, *Williams College*

Childs, Lauren M, *Virginia Tech*

### **Abstract**

Vector-borne diseases such as dengue, malaria, and Zika impact billions of people around the world. An essential component of their transmission cycle involves a life- cycle stage within the mosquito. In this mini-symposium, models of mosquitoes incorporating variability in stages will inform mosquito population dynamics. Such heterogeneity, altering population dynamics, can have important impact on transmission of vector-borne diseases.

**Monday, 16:00-18:00; Room 7**

Megan Greischar

Brandon Hollingsworth

Michael Robert

Kaitlyn Martinez

## **Modeling the impact of vector behavior, pathogen ecology, and environmental factors on the transmission of vector borne diseases**

Johnson, Leah R, *Virginia Tech*

Gaff, Holly D, *OldDominion University*

El Moustaid, Fadoua, *Virginia Tech*

### **Abstract**

Vector-borne diseases are indirectly transmitted infectious diseases that require the presence of a vector such as mosquitoes for Dengue, ticks for Lyme, and midges for Bluetongue disease. These vectors are highly sensitive to environmental conditions and very hard to control in order to monitor these diseases. This session will show a variety of mathematical and statistical models that have been used to understand the transmission process of vector-borne diseases as well as the role of environmental factors.

**Wednesday, 16:00-18:00; Room 5**

Fadoua El Moustaid

Cynthia Lord

Miranda Teboh Ewungkem

Marta Shocket

## Modeling time since infection: theory and implications

Earn, David, *McMaster University*

Dushoff, David, *McMaster University*

Feng, Zhilan, *Purdue University*

Glasser, John, *Centers for Disease Control and Prevention*

### Abstract

The classic SIR model that is attributed to Kermack and McKendrick was initially derived from their more general time-since-infection model by assuming that the infectious period is exponentially distributed. That mathematically convenient, but biologically unrealistic, assumption characterizes much of the subsequent infectious disease modeling literature. We have invited a few of the researchers who in recent years have examined models with non-exponentially distributed stage durations. The goal of the symposium is to present the state-of-the-art in modelling this aspect of infectious disease transmission, and to consider its implications for data analysis and epidemic forecasting.

### Tuesday, 10:30-12:30; Theatre

Maia Martcheva

Lorenzo Pellis

Zhilan Feng

John Glasser

### Tuesday, 16:00-18:00; Theatre

Glenn Webb

Helen Wearing

David Champredon

David Earn; Jonathan Dushoff

## Modeling to conquer: Understanding and controlling deleterious diseases using dynamical systems

Clifton, Sara M, *University of Illinois at Urbana-Champaign*

Rapti, Zoi, *University of Illinois at Urbana-Champaign*

### Abstract

The world's most harmful human diseases are complex dynamical systems. Mathematical modeling of disease dynamics, both within and between hosts, offers new insights into disease emergence, progression, transmission, and evolution. In this minisymposium, dynamical systems models will inform control strategies for a wide range of deadly human diseases, from malaria and Zika to cancer and polio.

### Monday, 16:00-18:00; Room 5

Deborah Shutt

Kamaldeen Olatunde

Sara Clifton

Hayriye Gulbudak

### Wednesday, 16:00-18:00; Room 10

Adam Rhodes

Gregory Kimmel

Zoi Rapti

Celeste Vallejo

## Modeling, dynamics and control of African Swine Fever

Zhang, Xianghong, *York University*

Li, Juan, *China Animal Health and Epidemiology Center*

### Abstract

Brief abstract: African swine fever (ASF), caused by African swine fever virus (ASFV), is a highly contagious virus causes high fever, hemorrhages, ataxia, and severe depression in domestic pigs and wild boar, a notifiable threat to the World Organization for Animal Health. ASFV has swept over many countries including Caucasus, European countries and the Baltic countries. In August 2018, the first outbreak of ASF was reported in Liaoning province, China, since then it has rapidly spread to over 25 provinces in China, causing 102 outbreaks till the end of January 2019. The spread of ASF in China has posed serious threat on both local and the world pig industry. Both Canada and USA have serious concerns of the spreading of the virus due to vast and rapid human travel and globalized trade. This mini-symposium, the few interdisciplinary speakers will focus on recently modeling, dynamical and computational study of the transmission and control of ASFV.

**Thursday, 10:30-12:30; Room 8**

Xinmiao Rong

Liping Wang

Pei Yuan

Juan Li

### Modelling gene transcription

Kursawe, Jochen, *University of Manchester*

### Abstract

Abstract : Transcriptional gene regulation plays a key role in many biological contexts, including patterning during embryonic development and cellular timing. Existing models investigate the effect of spatial, stochastic and dynamic aspects of gene promoter regulation. The aim of this mini-symposium is to gather researchers from different fields of mathematics and biology who are interested in gene transcription in order to facilitate communication and work towards a greater understanding of transcriptional mechanisms. We focus on mathematical models that illuminate transcriptional regulation and on statistical approaches for interpreting experimental data on promoter interactions. Additional information : This mini-symposium proposal is relevant to multiple of the SMB subgroups, including Developmental Biology, Immunobiology and Infection, and Mathematical Oncology. The list of invited speakers achieves gender balance and geographical balance, with contributions from three different continents. If accepted, this mini- symposium will provide a platform specifically for outstanding early-career researchers. All listed speakers have agreed to present at this symposium.

**Wednesday, 16:00-18:00; Room 6**

Huy Vo

Barbel Finkenstadt

Giorgos Minas

Rachel Waymack

**Thursday, 16:00-18:00; Room 6**

Jacqueline Dresch

Jae Kyoung Kim

Cicely Macnamara

David Rand

## Modelling intracellular transport

Zhelezov, Gleb, *University of Edinburgh*

Chumakova, Lyubov, *University of Edinburgh*

### Abstract

Cellular components are delivered to their biologically relevant locations by molecular motors moving along the cytoskeleton. Correct outcomes of this intracellular transport is crucial to the proper cellular, and therefore, organismal, function. Among the processes strongly reliant on intracellular transport are cell-cell adhesion, cell division, and cell motility. Our proposed minisymposium is aimed at modelers of intracellular transport, who are in active conversation with biologists. Although intracellular transport is an active research area in experimental biology [1], and has also been the focus of some modelling work in the mathematical biology community [2], several recent advances in the field are the result of collaborative investigations between mathematicians and cell biologists. Today, mathematical modelling is not only used to explain experimental results, but also to guide experiments. The goal of this minisymposium is to highlight such projects. This session will not only serve as a platform for disseminating novel research results, but will also present an opportunity for the mathematical community to discuss how to effectively communicate research with cell biologists, and work around experimental constraints. The invited speakers are a diverse, gender-balanced group, at different career stages. [1] J. L. Ross, M. Y. Ali, D. M. Warshaw, Cargo transport: molecular motors navigate a complex cytoskeleton. *Current Opinion in Cell Biology*. 20 (2008), pp. 41–47. [2] C. Appert-Rolland, M. Ebbinghaus, L. Santen, Intracellular transport driven by cytoskeletal motors: General mechanisms and defects. *Physics Reports*. 593 (2015), pp. 1–59.

### Tuesday, 16:00-18:00; Room 8

Gleb Zhelezov  
Stephanie Portet  
John Fricks  
Calina Copos

### Thursday, 10:30-12:30; Room 7

Lyubov Chumakova  
Aleksandra Plochocka  
Eric Cytrynbaum  
Thomas Fai

## Models of bacterial biofilms and biofilm control approaches

Eberl, Hermann J., *University of Guelph*

### Abstract

Many bacterial infections are caused by bacterial biofilms, i.e. microbial depositions on biotic or abiotic surfaces. In engineered systems, such biofilms can enhance system failure, e.g. via microbially induced corrosion or biofouling. On the other hand many environmental engineering technologies are based on such biofilms. By 'biofilm control' we refer to measures that eliminate biofilms, prevent them or suppress their negative facets, or, in the case of beneficial biofilms, that enhance their performance. Biofilms are spatially and temporally heterogeneous systems, in which bacterial population and resource dynamics, cellular biochemistry, and physical processes are intertwined and interact. This minisymposium will focus on models of such multi-facted interactions.

### Tuesday, 10:30-12:30; Room 2

John Ward  
Maria Rosaria Mattei  
Harry Gaebler  
Maryam Ghasemi

## Multiscale modeling of biofilms as complex ecological systems

Ghasemi, Maryam, *University of Waterloo*

Mattei, Maria Rosaria, *University of Naples 'Federico II'*

Polizzi, Bastien, *Institute Camille Jordan of the University of Lyon 1*

### Abstract

Biofilms are microbial communities on immersed surfaces, embedded in layers of a self-produced extracellular matrix, which mainly provide increased resistance against traditional methods of disinfection and eradication. Biofilms are ubiquitous and play beneficial or detrimental roles in many industrial and medical applications. For instance, they can lead to corrosion problems in freshwater pipes, and oil pipelines; they are recognized as the main cause of infections in host tissues or medical implants; they are involved in crop disease in plants and biofouling of industrial equipments. However, the adsorption and absorption properties and enhanced mechanical stability of biofilms make them advantageous to environmental engineering technologies, such as wastewater treatment, elimination of petroleum oil from contaminated systems or biofuel production.

Understanding and mastering these systems is therefore a major industrial, economic and health issue. The processes and factors affecting biofilm growth are diverse and can be highly complex. They often involve direct and indirect interaction of several (up to hundreds) species including bacteria, micro-algae, archaea and fungi, complex biochemical reactions, and often depend on the physical conditions of the surrounding environment such as fluid dynamics and shear fields. Biofilm models are critical to improve our understanding of biofilm formation, structure and function. Mathematical models in this field range from stochastic individual based models to cellular automata models to deterministic continuum models. In many cases hybrid models are proposed to bridge various length and/or time scales, including PDE-ODE coupled systems of various types, mixed hyperbolic-elliptic free boundary value problems with non-local effects, etc. This raises the questions regarding well-posedness, stability, long term behavior and numerical treatment.

The aim of this minisymposium is to bring together researchers from the fields of Applied Mathematics more specifically Mathematical Biology with interest in diffusion-reaction equations, free boundary problems, mixture theory, multi-scale/multi-physics

phenomena, complex systems modeling and microbial population dynamics, providing a platform to discuss techniques and innovations related to modeling biofilm formation, growth, and morphology. Major emphasis will be placed on multi-scale models which describe biofilm development and its architecture under various environmental conditions. The minisymposium is intended for those studying biofilms in the context of complex ecological systems. The talks will be useful for researchers in the aforementioned fields as well as biofluids and biomechanics.

### Monday, 16:00-18:00; Room 8

David Chopp

Ana Carpio

Isaac Klapper

Sara Jabbari

### Multiscale modeling of cytoskeleton-mediated cellular transport and aggregation

Ciocanel, Veronica, *Mathematical Biosciences Institute, OhioState University*

Dawes, Adriana, *Department of Mathematics/Department of Molecular Genetics, Ohio State University*

### Abstract

Many cellular functions rely on active transport of components or nonrandom aggregation in order to promote gene expression, correctly position organelles, or activate signaling pathways. Cytoskeletal filaments such as actin and microtubules often play critical roles in these movement processes. In this minisymposium, speakers will present a number of different quantitative approaches to studying cytoskeleton-mediated transport and aggregation applied to biological systems ranging from mRNA localization in *Xenopus* embryos to receptor clustering in immune cells.

### Wednesday, 10:30-12:30; Room 7

Adriana Dawes

Daniel Cortes

Garegin Papoian

Ying Zhang

### Thursday, 16:00-18:00; Room 7

Jay Newby

Abhishek Choudhary

Diana White

Veronica Ciocanel

## Optimization and optimal control in mathematical biology

Kearsley, Anthony J., *National Institute of Standards and Technology (NIST)*

Melara, Luis, *Shippensburg University*

### Abstract

The minisymposium seeks to sponsor talks from graduate students, mid-level professionals and more senior researchers. The composition of the speakers is quite varied and with two graduate students and two professionals, one of whom is an academic and one who is working at a US national laboratory. Proposed Abstract: Solutions to most optimal control problems that arise in mathematical biology applications must be approximated by numerical methods. This minisymposium brings together several presentations that will introduce examples of these problems and will include newly developed mathematical models, novel mathematical analysis and specialized numerical approximation methods. Optimal control problems of ordinary and partial differential equations as well as of coupled systems will be considered.

**Thursday, 16:00-18:00; Room 9**

Margaret Grogan

Anthony J Kearsley

Adarsh Kumbhari

Luis Melara

## Population dynamics in heterogeneous landscapes: models, tool and data

Lutscher, Frithjof, *University of Ottawa, University of Glasgow*

Cobbold, Christina, ???

### Abstract

Many populations live in heterogeneous environments, and individuals encounter habitats of significantly different quality. Fragmentation levels increase through human activities and other factors. Early models for population dynamics in such landscapes consisted of coupled systems of equations (one for each patch) and simple linear exchange terms between them. Recent modelling approaches include spatially explicit models with detailed individual-level movement descriptions. In all these models, the scale difference between regions of similar quality and the overall biological system play an important rôle. They allow us to study appropriate scaling limits (homogenization). This minisymposium will bring together modellers, analysts and empirical researchers to discuss the latest developments of such models, ranging from model formulation to analytical tools to data availability.

**Monday, 16:00-18:00; Room 6**

Christina Cobbold

Chris Cosner

Elizabeth Crone

Thomas Hillen

**Wednesday, 16:00-18:00; Room 3**

Nazanin Zaker

James Powell

Martha Garlick

Jane MacDonald

## Population dynamics in marine ecology

Hurford, Amy, *Memorial University*

### Abstract

The dynamics of marine populations in distinct regions are linked by dispersal and movement, and the analysis of these spatially- explicit population models provides insight into the design of marine protected areas. This minisymposium will discuss next generation approaches, population models inspired by dynamic energy budget models, species interactions, behavior, and harvesting.

**Wednesday, 10:30-12:30; Room 5**

Frithjof Lutscher

Frederic Guichard

Peter Harrington

Joany Marino

## Quantitative approaches to unravel immune function and immunity

Cassidy, Tyler, *McGill University*

Craig, Morgan, *Université de Montréal*

### Abstract

Complex networks of cells and proteins regulate both immune cell production and function to protect the host against pathogenic intrusion. This minisymposium brings together researchers across disciplines to tackle quantitative aspects of immune function and immunity including host-pathogen and T lymphocyte trafficking kinetics, the role of iron during infection, and the instigation of immune response against cancer.

**Friday, 10:30-12:30; Room 3**

Reinhard Laubenbacher

Tyler Cassidy

Amber Smith

Judith Mandl

## Recent advances on modeling and dynamics of vector-borne diseases

Fan, Guihong, *Columbus State University*

Liu, Rongsong, *University of Wyoming*

Shan, Chunhua, *The University of Toledo*

Zhu, Huaiping, *York University*

### Abstract

Vector-borne diseases are a big threat to public health since some of them can kill an unprotected individual very quickly like malaria. The study of vector-borne diseases has become one of the most promising interdisciplinary areas in mathematical biology. This mini symposium will focus on recent advances on a variety of modeling and computational developments for studying vector-borne diseases. Topics cover malaria, West Nile virus, Lyme disease and etc. We highlight the importance of potential collaboration between mathematicians, entomologists, epidemiologist, and modelers in the prediction, prevention, and control of vector-borne diseases.

**Monday, 10:30-12:30; Theatre**

Jacques Belair

Jie Gao

Xi Huo

Ling Xue

**Monday, 16:00-18:00; Theatre**

Binxiang Dai

Shujing Gao

Rongsong Liu

Dane Patey

**Wednesday, 10:30-12:30; Room 9**

Zhigui Lin

Luana Bassani

Ahmed Abelrazec

Bruna Santos

**Wednesday, 16:00-18:00; Room 9**

Daozhou Gao

Haotao Song

Chengjun Sun

Xianghong Zhang

## Recent perspectives on mathematical epidemiology

Smith?, Robert, *Université d'Ottawa*

### Abstract

This minisymposium will bring together researchers to examine up-to-the-minute disease problems that showcase the usefulness and applicability of mathematical modelling to a world far beyond the mathematical community. The audience is the mathematical biologist with an interest in infectious disease. This includes students and researchers, mathematicians interested in seeing applications and biologists who wish to see how mathematics can be used to solve real problems. The minisymposium is interdisciplinary in nature and includes those trained as mathematicians, epidemiologists and immunologists.

### Monday, 10:30-12:30; Room 3

Robert Smith?

Aili Wang

Cameron Browne

Katia Vogt Geisse

## Resource explicit population models

Peace, Angela, *Texas Tech University*

Heggerud, Christopher M., *University of Alberta*

### Abstract

We present a collection of biological and mathematical findings in novel mathematical models where resource quantities are explicitly incorporated. The research presented will include an assortment of mathematical models based on biological stoichiometry where limiting resource quantity and quality are both present. Biological stoichiometry is the study of the balance of energy and multiple chemical elements in living organisms. Stoichiometric modeling, a relatively young branch of mathematical biology, has been greatly expanded in the past two decades, and population models inspired by biological stoichiometry have produced complex but strikingly realistic dynamical behaviors. Applications of resource explicit population models range from aquatic and terrestrial food webs, as well as within host systems such as cancer dynamics.

### Monday, 16:00-18:00; Room 4

Christopher M Heggerud

Md Nazmul Hassan

Lale Asik

Angela Peace

## Spatial and evolutionary dynamics in mathematical ecology

Cantrell, Robert S, *University of Miami*

Lam, King-Yeung, *The Ohio State University*

### Abstract

This workshop will focus on the spatial and evolutionary dynamics of organisms submitted to a changing environment. An interdisciplinary approach to the modeling and analysis of the problem will shed new light to this area. It is the goal of this mini-symposium to bring together biologists and mathematicians working on those problems, and to foster the development of new ideas and tools to understand the ecology of organisms in a changing world.

### Monday, 10:30-12:30; Room 5

Xiaoyang Wang

Yuan Lou

Zhisheng Shuai

Guo Hongjun

### Tuesday, 10:30-12:30; Room 4

Joy Zhou

Robert S Cantrell

Chunhua Ou

King-Yeung Lam

## Spatial interactions in cell biology

Isaacson, Samuel A, *Boston University*

Zhang, Ying, *Boston University*

### Abstract

The dynamics of cellular processes can depend critically on interactions between particles undergoing spatial transport. Participants in this mini-symposium will investigate the effect of spatial transport and interactions on the dynamics of cellular processes. In particular, these include 1. The interplay between diffusion and clustering of transmembrane receptors on the surface of immune cells. 2. Interactions that facilitate the transport of proteins through nuclear pore complexes spanning the nuclear membrane. 3. Mechanisms by which mRNAs are trafficked both within and between cells within *Drosophila* oocytes. The mathematical models used to investigate these processes involve both deterministic PDEs and stochastic particle-based approaches, which will be studied by asymptotic analysis and novel numerical methods. In several cases, these modeling studies will be closely coupled to single-molecule imaging assays, which are common in calibrating model parameters and improving model accuracy.

**Monday, 16:00-18:00; Room 10**

Daniel Coombs

Alan Lindsay

Ruth Baker

Samuel Isaacson

## Stochastic models for biochemical reaction networks

Anderson, David F, *UW-Madison*

Popovic, Lea, *Concordia*

### Abstract

Stochastically modeled biochemical reaction networks are used to model the time-evolution of biochemical processes when the counts of the constituent molecules are low. The standard model is a continuous-time Markov chain whose states represent the number of molecules present and whose transitions mark the occurrence of chemical transformations. In recent years stochastic models have been playing an increasing role in the mathematical biology literature. However, our understanding of their possible behaviors is still limited. For example, we still do not have robust/general results characterizing when a particular model is positive recurrent (stable), when it is explosive, when it will undergo an extinction event, etc. In this minisymposium, we attempt to bridge this gap by considering mathematical results that characterize the emergent behavior of these models. We will also consider computational methods for these stochastic models.

**Thursday, 10:30-12:30; Room 1**

David Anderson

Tung Nguyen

Andrea Agazzi

Jinsu Kim

**Thursday, 16:00-18:00; Room 4**

Badal Joshi

Chaojie Ortiz-Munoz

German Enciso

## Stochastic models in micro and macro biological systems

Rempala, Grzegorz, *The Ohio State University*

Kang, Hye-Won, *University of Maryland, Baltimore County*

### Abstract

Stochastic approaches to modeling phenomena in life sciences at various scales are becoming increasingly important as they allow to account for aggregate and disaggregate data, intrinsic and extrinsic biological noise, missing data and lack of experimental reproducibility. This minisymposium will cover several topics within broad area of stochastic modeling where recently some interesting advances have been made. The topics will include methods for aggregation/disaggregation of stochastic systems, parameter estimation, incorporation of network/contact structure, modeling of survival dynamics and stochastic compartmental models. They will be illustrated with examples from immunology and infectious diseases such as moderating immunoresponse or disease spread across scales, optimal contact tracing, mitigating transmission rates and network topology estimation.

### Wednesday, 10:30-12:30; Room 4

Jon Fintzi

Lea Popovic

Forrest Crawford

Wasiur Khudabukhsh

### Wednesday, 16:00-18:00; Room 4

Grzegorz Rempala

Daniel Linder

Hye-Won Kang

Boseung Choi

## Structured population models for disease transmission dynamics

Gao, Daozhou, *Shanghai Normal University*

van den Driessche, Pauline, *University of Victoria*

Wu, Jianhong, *York University*

### Abstract

Structured population models provide an important framework to examine disease transmission through host-pathogen interaction when key structures such as demographic ages and physiological sizes, time since infection, and /or time since a particular intervention are important for the disease spread, prevention and control. Despite substantial advance in model formulation, analysis and applications, challenges remain. These challenges include: identification of structures; estimation of structure variables; data integration and data fitting to surveillance, field study and lab experiment data. This mini- symposium aims to present some samples of recent progress to address these challenges. The focus of eight invited speakers is expected to be (i). structured models for vector-borne disease transmission dynamics; (ii) system and structure identifiability; (ii). data fitting to estimate key epidemiological parameters and vector-host behaviors; (iii). estimation of development delay from laboratory data and environmental conditions; (iv). impact of physiological structures on co-feeding transmission. This session is organized as part of the Canada-China bilateral collaboration, however, we have also secured substantial international participation with excellent diversity.

### Thursday, 10:30-12:30; Room 9

Yijun Lou

Justin Munganga

Francesca Scarabela

Jorge Velasco Hernandez

### Friday, 10:30-12:30; Room 2

Felicia Magpantay

Chadi Saad-Roy

Biao Tang

Jane Heffernan

## The mechanics and biochemical signalling of cellular motility

MacKay, Laurent, *McGill University*

Khadra, Anmar, *McGill University*

### Abstract

Cellular motility is critical for physiological processes such as embryonic development, localized immune responses, and wound healing. Furthermore, disruption of the machinery involved in motility is associated with pathological conditions such as metastatic cancer and autoimmune diseases. This minisymposium will focus on the dynamics which govern various aspects of cellular motility. The mechanical processes required to physically displace cells across space are regulated by biochemical pathways. Together, these lead to nonlinear dynamics resulting in complex spatiotemporal patterns of activity. These dynamics are analyzed using dynamic systems theory, producing theoretical predictions that allows us to further understand the motility machinery and how it may be harnessed for therapeutic purposes.

**Tuesday, 16:00-18:00; Room 6**

Laurent MacKay

Lennart Hilbert

Adam Hendricks

Leah Edelstein-Keshet

## Using ecological theory to understand cancer

Adler, Frederick A, *University of Utah*

Griffiths, Jason I, *University of Utah*

### Abstract

The complexity of cancer has inspired the use of ecological thinking to understand the network of cell-cell and cell-environment interactions that make up the cancer ecosystem. Ecologists have long embraced the challenge of making sense of complex systems despite incomplete information about underlying mechanisms, and shown that carefully crafted theories provide precisely the tools needed to integrate the multiple streams of partial information into a useful whole. Speakers in the minisymposium will examine cancer from multiple theoretical perspectives, ranging from community ecology, behavioral ecology, restoration ecology, and evolutionary ecology.

**Monday, 10:30-12:30; Room 2**

Jason Griffiths

Irina Kareva

Robert Beckman

John Pepper

## Validation of mathematical models in immunology and cancer

Dobreva, Atanaska, *North Carolina State University*

Brady, Renee, *H. Lee Moffitt Cancer Center & Research Institute*

### Abstract

Mathematical models serve as invaluable tools in biomedical research, helping to uncover underlying disease mechanisms, analyze clinical data, and improve treatments. Achieving explanatory and predictive power requires that models are validated against data, observed biological behaviors, and known patient responses. This minisymposium will showcase validation techniques used in immunology and cancer, particularly to identify actionable biomarkers, make meaningful clinical predictions and evaluate therapeutic protocols. The session will cover methods including, but not limited to, simulation analysis, parameter estimation, sensitivity analysis, and uncertainty quantification.

**Thursday, 16:00-18:00; Room 5**

Maria D'Orsogna

Angela Reynolds

David Swigon

Atanaska Dobreva

**Friday, 10:30-12:30; Room 1**

Heiko Enderling

Susan Massey

Meghan Ferrall-Fairbanks

Angela M Jarrett

## **Vector-borne diseases: improving our understanding of underlying mechanisms and implications for disease control**

Agusto, Folashade, *University of Kansas*

Teboh Ewungkem, Miranda, *Lehigh University*

### **Abstract**

Infectious diseases are caused by different agents such as bacteria, viruses, fungi, protozoa, and helminths. Some of these disease agents are transmitted through the bites of infected arthropods such as mosquitoes, ticks, and sandflies. According to the World Health Organization, vector-borne diseases constitute more than 17 infectious diseases. In recent times, the number of vector-borne diseases emerging and re-emerging have been on the increase; for instance, 2013 saw the emergence of Chikungunya in the Americas. Similarly, the Americas witnessed the emergence of Zika in 2014. Aside from emerging vector-borne diseases, other diseases such as Leishmaniasis have been on the increase, with an estimated 200,000 to 400,000 new cases of Visceral Leishmaniasis occurring annually worldwide. On the other hand, malaria experienced a downtrend in the number of cases from 2010 to 2015 as a result of active intervention. Hence it is imperative to review and improve our understanding of the underlying modeling mechanisms of these vector-borne diseases and their subsequent implications for disease control. Modeling, in particular mathematical, is, therefore, a powerful tool to devise a possible means of achieving permanent elimination of these diseases.

**Thursday, 10:30-12:30; Room 5**

Lauren Childs

Guido Camargo Espana

Jeffery Demers

Omar Saucedo

## **Wave propagation in biological media**

Mei, Ming, *McGillUniversity*

Ou, Chunhua, *Memorial University of Newfoundland*

Wu, Yaping, *Capital Normal University*

### **Abstract**

Since the pioneer work of Fisher and KPP, Wave Propagation in Biological Media has been widely studied in various mathematical models establishing the movement or invasion of species in heterogenous media or the spread of infectious disease among species. Recently, there have been tremendous advancements in the theory of traveling wavefronts itself, with considerable applications to competition or predation models in the biological field. The purpose of this session is to invite mathematical researchers with biological backgrounds to work together and contribute to the study of biological waves. It will serve as a platform to report new breakthroughs, exchange research ideas and extend academic networks. New collaborations are also expected during and after the meeting. Speakers and talks are carefully selected to make the session attractive to a diverse audience. Especially, PhD students or post-doctoral fellows are encouraged to attend this session for getting research insight in their recent study.

**Monday, 10:30-12:30; Room 8**

Xiaoqiang Zhao

Wan-Tong Li

Zhongwei Shen

Tianyuan Xu

**Wednesday, 10:30-12:30; Room 8**

Yuanwei Qi

Chunhua Jin

Kun Zhao

Rui Huang

## Contributed Talks

Monday, CS 1

Buttenschoen, Andreas

Spatio-temporal heterogeneities in a mechano-chemical model of collective cell migration

Zmurchok, Cole

Modeling cell shape diversity arising from complex Rho GTPase dynamics

Owen, Jennifer

Understanding zebrafish pigment pattern formation using mathematical modelling

Monday, CS 2

Van Steijn, Leonie

Modeling zebrafish metabolism

Faria, Matthew

Determination of a kinetic model of nanoparticle-cell interaction

Ruegg-Ereymond, Pauline

Pre-menstrual inflammatory processes in the uterine endometrium

Monday, CS 3

Hult, Caitlin

Understanding the role of neutrophils in *M. tuberculosis* infection: Modeling approaches and visualization techniques

Dobrovolny, Hana

An agent-based model of viral transmission

Islam, MD Rafiul

Identifying the dominant transmission pathway in a multi-stage infection model of the emerging fungal pathogen *Batrachochytrium salamandrivorans* on the Eastern Newt

Monday, CS 4

Jung, Eunok

Dynamical Models of the 2009 A/H1N1 Influenza and Effective Intervention Strategies in the Republic of Korea

Omori, Ryosuke

Difference in seasonal variations between transmission rate and re-activation rate explains the epidemic curves of Varicella and Zoster

Hurford, Amy

Eliminating stage-structured pests with temperature-dependent life histories

Monday, CS 5

Ballesta, Annabelle

P-glycoprotein (Abcb1) expression and activity are sex-, feeding-, and circadian time-dependent, implications for mechanistic pharmacokinetics modeling

Fry, Brendan

Modeling bloodflow and oxygenation in a retinal microvascular network

Voorsluijs, Valerie

Impact of mitochondrial exchanges on calcium wave propagation in astrocytes

Monday, CS 6

MacKay, Vincent

Double-wave Reentry in Excitable Media

George, Uduak

Stretching the Embryonic Lung Tissue May Affect the Length of its Epithelial Tubes

CortesPoza, Yurinia

Spatial dynamics in flower organ formation

Monday, CS 7

Karev, Georgiy

Struggle for Existence: models for Darwinian and non-Darwinian selection

Li, Guanlin

Why be Temperate: On the Fitness Benefits of Lysis vs. Lysogeny

Rouzine, Igor

Evolutionary footprint of epistasis

Monday, CS 8

Kelly, Michael

Marine Reserves and Optimal Dynamic Harvesting When Fishing Damages Habitat

Hurtado, Paul

A General 'Linear Chain Trick' for building ODE models with flexible dwell times

Campos, Paulo

Functional specialization under multiple tradeoffs mediated by resources

Monday, CS 9

Jerry, Chakib

Controlled Switched System for Cancer Model

Abler, Daniel

Capturing variability of tumor-induced mass-effect in glioma growth models

Basanta, David

Evolutionary tempo and the tumor microenvironment

Tuesday, CS 1

Kursawe, Jochen

Stochastic amplification of gene oscillations during embryonic neurogenesis

Dallon, John

A Stochastic Model of Filament Transport by Motor Proteins

Roussel, Marc

Developing a left and a right side: bistability in the Lefty-Nodal network

Tuesday, CS 2

Anelone, Anet

Elite control of HIV exhibits some robustness properties

Cao, Youfang

Mechanistic Immuno-Viral Dynamics Modeling Platform for HIV Cure Drug Development

Stroberg, Wylie

Information Processing by Endoplasmic Reticulum Stress Sensors

Tuesday, CS 3

Adekunle, Adeshina

A pandemic tool for emerging disease monitoring: Ebola as a case study

Schmidt, Deena

Contagion dynamics on adaptive networks: Norovirus as a case study

Pedro, Cardenas

Qualitative behavior of AIDS in a homosexual population

Tuesday, CS 4

Jiao, Jing

The influences of host evolution on host-pathogen interactions across space

Arceo, Carlene

Stochastic SEIR Dynamics on an Edge-based Network Model

Milwid, Rachael

Assessing the impact of empirical contact patterns on disease dynamics within an equine population

Tuesday, CS 5

Ly, Cheng

Spike statistics during olfactory stimulation via orthonasal and retronasal inhalation

Fokoue, Diane

Numerical Methods for the Microscopic Cardiac Electrophysiology Model

Bulai, Iulia Martina

Geometrical analysis of mixed-mode bursting oscillations in a multiple-timescale model of bursting electrical activity

Tuesday, CS 6

Deka, Aniruddha

Individual vaccination choice and optimal budget allocation for vaccination campaign

Sun, Anthony

On the mathematical form of an incentive in a socio-ecological model

Mohapatra, Anushaya

The Evolutionary Stability of Partial Migration Under Different Forms of Competition

Tuesday, CS 7

Brunner, James

Modeling microbial community dynamics using genome scale metabolic models.

MacDonald, Jane Shaw

The impact of edge behaviour on population persistence in a moving habitat model

Collera, Juancho

HOPF BIFURCATION IN A THREE-SPECIES INTRAGUILD PREDATION MODEL WITH STAGE STRUCTURE

Tuesday, CS 8

Liu, Pengyu

A polynomial metric on rooted binary tree shapes

Arumugan, Ramesh

Tracking unstable states: A complicated dance in a changing world

Laverty, Sean

Modeling woundwood rib formation and fire scar closure in fire-scarred oaks

Tuesday, CS 9

Maestrini, Davide

On the concept of temperature in the process of aging and AML development

Kose, Emek

Modeling the Stem Cell Hypothesis for Cancer

West, Jeffrey

Tissue structure accelerates evolution: premalignant sweeps precede neutral expansion

Wednesday, CS 1

Sadria, Mehrshad

Network Analysis of Eye-Gaze Pattern in Autism

Buenzli, Pascal

Patterns in Turing patterns: Segmental growth and the inhibitory cascade

Perez-Buendia, Rogelio

Forest Structure in Epigenetic Landscapes

Wednesday, CS 2

Strube, Laura

Activation of the integrated stress response: Does it tune or tame?

Bridge, Lloyd

LINEAR TRANSIT COMPARTMENT PHARMACOKINETIC MODELS AND EQUI-DOSING REGIMEN REGIONS

Jegatheesan, Thulasi

Model-Based Analysis of Recovery of Gut Microbiota after Antibiotic Disturbance

Wednesday, CS 3

Fu, Feng

Evolutionary Game Theory with Applications to Behavioral Epidemiology

Philips, Tricia

Modeling the Heroin Epidemic

Renardy, Marissa

Evaluating vaccination strategies for tuberculosis in endemic and non-endemic settings

Wednesday, CS 4

Volkening, Alexandria

Forecasting elections using compartmental models of infection

Mema, Ensela

Modeling the Influence of Social Interactions on Physical Fitness

Ye, Ping

Prenatal alcohol exposure in American Indian and Caucasian mothers in the US Northern Plains

Wednesday, CS 5

MacLaurin, James

Phase Reduction and Synchronization Through Environmental Noise in Stochastic Biochemical Oscillations

Latulippe, Joe

A mathematical model of the effects of Amyloid beta on IP3 signaling mechanisms.

Stolerman, Lucas

Stability analysis of a bulk-surface model for membrane-protein clustering

Wednesday, CS 6

Vaughan, Benjamin

Mathematical Model of Biofilm-Mediated Pathogen Persistence in a Water Distribution Network with Time-Periodic Flows

Hutchinson, Chantal

Mechanisms of stability for migratory food webs using a hybrid systems framework

Stefaniak, Elisa

On the probability distribution of resource allocation strategies in plants

Wednesday, CS 7

- Marleau, Justin      When activators become inhibitors: emergent spatial patterns in meta-ecosystems
- Sheppard, Lawrence      Examining the plankton paradox with timescale-specific predictors of abundance changes
- Basiri, Maryam      Pushing Boundaries: The existence of solutions for a free boundary problem modelling the spread of ecosystem engineers

Wednesday, CS 8

- Ryan, Shawn      Mathematics Provides Insight into Self-Organization in Biology
- Morris, Tricia      Modelling the evolution of flowering onset in perennial plants
- Calcagno, Vincent      Life is not a long quiet river: modelling population genetic divergence when migration is fluctuating

Wednesday, CS 9

- Sordo Vieira, Luis      An intracellular model linking iron metabolism to the cell cycle
- Robertson-Tessi, Mark      Evolution of T-cell receptors in the context of cancer and self-antigens
- Przedborski, Michelle      A systems biology approach to study adaptive drug resistance in acute myeloid leukemia

Thursday, CS 1

- Zobitz, John      Development of computational tools in R for an undergraduate mathematical biology and modeling course
- Fuhrman, Kseniya      Progression of Numerical Techniques for Model Construction and Analysis

Thursday, CS 2

- Pinky, Lubna      Quantifying Kinetic Differences in Two Recombinant Parainfluenza Viruses
- Myerscough, Mary      A Structured Population Model for Lipid Accumulation in Macrophages
- PuelmaTouzel, Maximilian      Inferring population dynamics from high-throughput sequencing

Thursday, CS 3

- Bannish, Brittany      Effects of clot contraction and fiber distribution on blood clot degradation
- Rozins, Carly      Can phage therapy replace antibiotics?
- Moran , E Joe      Understanding rabies persistence in low density fox populations

Thursday, CS 4

Tunde, Yusuf

APPLICATION OF OPTIMAL CONTROL THEORY IN MODELLING MENINGOCOCCAL MENINGITIS TRANSMISSION DYNAMICS.

Pham, Thi Mui

Tracking *P. aeruginosa* transmission routes in intensive-care units using mathematical models

Stockdale, Jessica

Modelling and genomics to identify dangerous *Streptococcus pneumoniae* strains

Thursday, CS 5

Roberts, Paul

Investigating the functional connectivity of the zebrafish retina

Pearsons, Sean

Coupled oscillators in the gut

Means, Shawn

Weaving a Tangled Web: Neurons and Networks

Thursday, CS 6

Gjini, Erida

How mathematical modeling of *Trypanosoma brucei* population dynamics in mice can test hypotheses for parasites growing in adipose tissue versus blood

Berezovsky, Faina

Modeling of "replicator - genetic parasites" dynamics and coexistence

Abbas, Fazal

A New Approach to Substrate Flux Approximation for Monod Boundary Value Problem Arises in the Study of Biofilms

Thursday, CS 7

Legros, Mathieu

Gene drive strategies of pest control and resistance management in agriculture

Adamson, Matthew

Predicting resilience proles of the run-up to regime shifts in nearly-1D systems

Souza, Max

From fixation probabilities to d-player games: an inverse problem in evolutionary dynamics

Thursday, CS 8

Osojnik, Ana

Systematic analysis of a bifurcating model of tumour-immune interactions

Miller, Anna

Towards a Multiscale Model of the Bone Microenvironment in Multiple Myeloma

delosReyes, Aurelio

STRATEGIES IN CONTROLLING GLIOBLASTOMA INVASION

Thursday, CS 9

Wu, Min

Stress generation, relaxation and size control in restricted tumor growth

Johnston, Stuart

Modelling nanoparticle transcytosis in microfluidic intestine experiments

Bitsouni, Vasiliki

Modelling calcium signalling in cancer growth

Poster Sessions

## Monday

Abboud, Candy	Model & data-based prediction of invasive species dynamics
Alkarkhi, Tahani	Stability analysis in prey predator model using Beddington-DeAngelis functional response.
Althubyani, Mohammed	A two species model to study the transmission and persistence of MERS-COV
Ardaseva, Aleksandra	Analysis of cancer dynamics in fluctuating environments
Bajiya, VijayPal	A Mathematical Model for Cholera Transmission: Most Effective Control Strategy
Baratchart, Etienne	Computational modeling of macrophage polarization dynamics during bone healing
Barendregt, Nicholas	Analyzing Dynamic Decision Models Using Differential Chapman-Kolmogorov Equations
Bayani, Anahita	Modelling the inflammatory response - spatial considerations in the resolution of inflammation
Bolonan, Noah	Seasonal Variation in a Predator-Predator-Prey Model
Brechman, Pia	Dynamics of the Selkov oscillator
Campbell, Kelly	A mathematical model of osteochondral defect regeneration
Ceres, Kristina	A hidden Markov model to describe Johnes's disease progression in dairy cows
Chae, Seokjoo	Network inference of the circadian clock
Chavez, Luciana	How to incorporate genetic information into models for pesticide degradation in soils
Dengos, Isabel	Modeling the growth and sustainable control of invasive eurasian watermilfoil
Farahbakhsh, Isaiah	The evolution of strategies within a network harvesting common-pool resources
Fonseka, Dilini	The dynamics of stoichiometric plant-pollinator-herbivore models and parameter sensitivity analysis
Go, Clark Kendrick	Modelling the Herding of Garrano Horses in the Wild
Grosklos, Guen	The effects of metapopulation dispersal theory on Columbia spotted frog population dynamics
Halloway, Abdel	Non-Equilibrium Dynamics in Under-Saturated Communities
Hill, Edward	Seasonal influenza in England: Modelling approaches to capture immunity propagation
Hong, Jaehyoung	Analyzing the Sleep Patterns of Shift Workers using the neuronal population model of sleep-wake cycle
Hormuth, David A	Patient specific, predictive modeling of the response to chemoradiation via MRI
Inafuku, Daniel	Toward a new theory of biological information
Jansen, Joanneke E	Inference of an inflammatory cytokine interaction network
Jentsch, Peter	Fire Mediates Bark Beetle Outbreaks in Serotinous Forests
Johnson, Kaitlyn	An integrated approach to calibrate and validate mathematical models of therapy-induced resistance from in vitro drug response data in cancer
Kawaksatsu, Mari	Self-organized division of labour leads to behavioural contagion in mixed social groups
Kelley, Michael	A mathematical model of thrombin-fibrin binding
Kim, Daewook	Systems model reveals the sources of the inter- and intraspecies variability in drug efficacy
Kim, Soyoung	Mathematical model and intervention strategies for mitigating tuberculosis in the Philippines
Kravtsova, Natalia	Modified Metropolis-Hastings Algorithm for Efficiently Searching Parameter Space

Lanz, Aprillya	An epidemic model of the spread of mobile phone malware with quarantine and removal classes
Lavigne, Michael	Upscaling Individual Based Models to PDEs with Equation Learning
Liu, Junyan	Development of an experiment-driven time-resolved model of response to radiation therapy
Loo, Sara	An evolutionary model of within-host mutation and between-host pathogen transmission
Makarayan, Sahak	MODELING THE STIMULATORY NETWORK IN NATURAL KILLER CELLS
Martinson, Duncan	Applications of Multiscale Simulation Algorithms to Angiogenesis Models
McGahan, Ian	A parameterization method for multi-scale wildlife disease models
Meyer, Alexander D	Sensitivity to larval settlement cues affects marine population viability
Minucci, Sarah B	Mathematical modeling of the role of macrophages in lung inflammation
Motassem, Alarydah	TITLE
Mulberry, Nicola	Long-term coexistence in dual-strain models
Negelja, Rigobert C	Seasonal weather variation and the dynamics of infectious diseases
Oke, Segun	Mathematical Modeling of Breast Cancer and Optimal Control Analysis of Treatment Strategies
Olivenca, Daniel	Phosphoinositides and DGK control of the epithelial sodium channel in cystic fibrosis
Pak, Thomas	Pakman: a modular and efficient software tool for approximate Bayesian inference
Papaxenopoulou, Lito	Model-driven experiments induce elimination of Staphylococcus aureus chronic infection
Park, Daniel	Impact of adaptive myelination on synchrony in coupled oscillator networks
Pattenden, Tyler	Why fast-growing bacteria carry more DNA of viral origin
Patwadhan, Janita	$\beta$ cell network dysfunction in pancreatic islets by silencing hub cells
Pedersen, Rasmus	Modelling the Dynamics of Hematopoietic Stem Cells.
Pellowe, Moriah	A system biology approach to study anti-PD-1 cancer immunotherapy
Phillips, Brendon	Early-warning signals of epidemics in a multiplex disease-behaviour model
Rather, Mubasher	Feedforward regulation of nitrate transporter NRT1.1 bi-functional activity depending on soil nitrate availabilities
Renton, Jessica	Evolution of cooperation on an epithelium
Rezzy, Eko Caraka	Zero-Inflated and Over-Dispersed Species Arthropods Count Data With Fast Estimation of GLLVM
Ridouan, Bani	Marine Metapopulation: Pelagic larval duration and ocean currents mediated effects of climate change
Roberts, Paul A	Using mathematics to investigate the mechanisms behind vision loss
Saha, Raj	Oscillation and Data in a Simple Epidemic Model
Schenck, Ryan O	The tick-tock of the molecular clock: A story from the crypt
Scott, Shelby	Handguns and Hotspots: Spatio-Temporal Models of Gun Crime in Chicago, Illinois
Smith-Roberge, Julien	Effects of alignment on contact dependent cell-cell interactions

Strobl, Maximilian	Man vs Machine: in silico and in vitro comparison of a mechanistic and a machine learning model for guiding cancer treatment
Susswein, Zachary	Borrowing ecological theory to infer interactions between sensitive and resistant cancer cell populations
Walton, Jack	Inferring collective behaviour rules from field data
Wang, Wendy	Dynamics of a state dependent delay model of the tryptophan operon
Yang, Jianchen	Modeling the effect of glucose availability on tumor cell growth guided by in vitro microscopy
Zahid, Mondal H	Ebola: Impact of hospital's admission policy in an overwhelmed scenario
Zou, YiMing	Integrated Analysis of Gene Regulatory Networks

## Tuesday

Adabor, Emmanuel	New inference of transcriptional regulatory relationships among genes in cancer
Amoah-Darko, Frederick L.	Continuous model of dynamics instability of microtubules with pausing
Aruffo, Elena	Measles: Insights into waning immunity
Ballif, Guillaume	An application of spatial stochastic interacting systems on multiple time scales to biological systems
Bashir, Umar	USING MATHEMATICAL MODEL TO ASSESS THE IMPACT OF VACCINATION OF MEASLES
Betti, Matthew	The transfer of honey bee disease in heterogeneous landscapes
Beykzadeh, Ali	A matrix form of the general Laplace kernel
Braniff, Nathan	Optimal experimental design for bistable networks at steady-state
Brindle, Benjamin	The Mathematical Role of Immunity on the Within-Host Malaria Parasite Dynamics
Bury, Thomas	Spectral early warning signals improve tipping point detection and description
Choi, Wonhyung	Evolution of dispersal toward fitness for predators with predation-induced dispersal
Chu, Olivia	Evolutionary Dynamics in a Group Population Structure with Barriers to Entry
Cooney, Daniel	THE REPLICATOR DYNAMICS FOR MULTILEVEL SELECTION IN EVOLUTIONARY GAMES
Cresswell, Evan	Compartmental modeling of calcium dynamics in astrocytes
Dam, Marc JB	Comparing efficacy of hydroxyurea and IFN- treatment in MPN patients
Dang, Yiteng	Cellular dialogues that enable self-organization of dynamic spatial patterns
Das, Parthasakha	Noise Assisted Extinction of Chaotic Cancer Model
Davis, Jacob	Metrics for regulated biological systems
Dobrovolny, Hana M	Oncolytic virus treatment of cancer
Fair, Kathryn	Spatially explicit models simulate rich forest-grassland mosaics
Flores, Pavel	Networks provided from neuronal activity
Franssen, Linnea	A mathematical framework for modelling the metastatic spread of cancer
Geng, Yunfeng	The coexistence of competing consumers on a single resource in a hybrid model

Giniunaite, Rasa	Investigating the effect of domain growth on the collective migration of neural crest cells
Gunaratne, Ravinda	MUTLI-RESOLUTION MODELLING IN MOLECULAR DYNAMICS
Herrera-Reyes, Alejandra Donaji	Identifying unique observations dSTORM with a spatiotemporal model
Holmes, William	Microtubules Negatively Regulate Insulin Secretion in Pancreatic Beta Cells
Hong, Hyukpyo	Product-Form Stationary Distributions for Non-Complex Balanced Networks
Jeong, Eui Min	Mathematical Modeling to Reveal Molecular Differences Causing Pacemaker-neuron-dependent Rhythm Alteration by Mutant
Katebi, Ataur	Dynamics of gene regulatory circuits drive irreversible transition of cell cycle
Khan, Amjad	The evolutionary forces acting on prophages: A mathematical study
Kramer, Sean	An observer for an occluded reaction-diffusion system with spatially varying parameters
Kumbale, Carla M	Dynamic modeling sheds light on links between metal uptake and antibiotic resistance in plants
Larsson, Jenny	A growth based method for investigating the high shell shape variability in of the marine snail Littorina saxatilis
Lester, Christopher	Multi-level Approximate Bayesian Computation
Lindwall, Gustav	An interacting position jump model of glioblastoma growth
Macfarlane, Fiona	Modelling approaches to describe tumour-immune competition and tumour development
Malik, Bhawna	Emergence of Antibiotic Drug Resistance and Socio-economic Factors: A scope of mathematical modelling research
Marinelli, Isabella	Can One Enzyme Isoform Compensate for Knockout of Another in Cellular Rhythmogenesis?
Masud, M A	A theoretical model of optimal fluid maintenance for clinical dengue patients
Meadows, Tyler	Growth on multiple essential resources in a self-cycling fermentor
Mgbara, Whitney	Modeling the multiple-wave pattern of the 2009 A/H1N1 pandemic
Moore, Hayley EL	Extracting positions of sheep from drone footage for model comparisons
Obeid, Hussein	The minimal model of Hahn for the Calvin cycle
Olaniyi, Adeniyi	Impact of Information on the Usage of Pesticide-Treated Bed-nets in the Control of Malaria Disease Prevalence
Pal, Sapatarshi	Impact of Agricultural Tariffs and Trade Wars on Global Land Use: A Dynamic Network Model
Parades Bonilla, Rosalba V	Maximizing tumour killing and minimizing neutropenia to optimize chemotherapy regimens
Park, Derek	The Goldilocks Window of Personalized Chemotherapy: An Immune Perspective
Pressley, Mariyah	Comparing strategies for HIF-1 activation in fluctuating hypoxic environment
Roth, Samantha	Predicting Zika Outbreaks Using Statistical Models
Royce , Katherine	Modelling spillover mutations in zoonoses with intermediate hosts
Sajid, Zamra	MODELLING MYELOPROLIFERATIVE NEOPLASMS - Dynamics of myeloid cell line for Ph-negative MPNs
Si, Ychen	Coalescent model of imputation accuracy

Smith, Cameron	Unbiased on-lattice domain growth
Spencer , Julie A	Fitness differences between drug resistant and sensitive strains of <i>Mycobacterium tuberculosis</i>
Stephens, Roisin	Optimising biopsy scheduling, integrating digital pathology and agent-based modelling.
Stevens, Michael	Geographic Profiling: Accounting for Absences and Inferring Population Density
Sulyok, Cara	Contribution of Environmental Pathways to the Transmission of <i>Clostridioides difficile</i>
Sundus, Aneequa	Modeling pattern formation in multicellular systems using an optical genetic switch
Syga, Simon	A new lattice-gas cellular automaton model explains plasticity of breast cancer invasion
Talkington, Anne M	Dermal lymphatic capillaries do not obey murray's law
Treloar, Neythen	Reinforcement learning for the control of bacterial populations in bioreactors
Tunde, Yusuf	Optimal Control Strategy for Hepatitis B Virus Epidemic in Areas of High Endemicity
Vander Velde, Robert	Distinguishing between evolutionary processes in cancer drug resistance
Wadkin, Laura	Modelling and optimising the growth and clonality of human embryonic stem cell colonies
Wang, Yafei	A multi-model investigation of mechanobiologic effects on cancer metastases in the liver
Windecker, Richard	A Model for How a Foraging Animal Might Determine Step Lengths in a Random Walk
Yu, Na	Simple Walking in 2-dimensional Space: Model and Experiment
Zhelezov, Gleb	Being Post-Punc: Localising Evolutionary Pulses on Phylogenetic Trees