

# Abstracts

IGTC workshop at UBC, July 24-26, 2009

Author	Sandi Merchant <a href="mailto:merchant@math.ubc.ca">merchant@math.ubc.ca</a>
Title	Spatiotemporal patterns behind predator invasions in a model with non-local prey competition
Abstract	Reaction-diffusion systems are commonly used to model predator invasions on a spatial domain. In such models, the only spatial process is the diffusive movement of individuals and the interactions between individuals are assumed to be purely local. Here, I study a model where prey instead compete with each other over a spatial neighbourhood, and illustrate some of the effects this may have on a predator invasion, with particular focus on the spatiotemporal patterns that arise behind the invasion.

Author	Jaime Ashander <a href="mailto:ashander@ualberta.ca">ashander@ualberta.ca</a>
Title	Pink salmon and sea lice as a host-parasite system with host age-structure: implications for salmon farming and chemical resistance development in lice
Abstract	Sea lice parasitize both wild salmon and sea-cage farm salmon. Outbreaks on farms can result in economic costs to aquaculture and spread to wild populations, raising serious conservation concerns. In many salmon-farming regions parasites are currently controlled via integrated pest management (IPM) strategies that rely on chemical treatment. Long-term effectiveness of chemical management requires understanding pest evolutionary response. These include resistance, which is likely influenced by connections between lice populations on wild and farm salmon. However, the coupled population dynamics of sea lice, farm salmon and wild salmon are not yet understood in sufficient detail to permit exploration of resistance-emergence. Here I present a step toward this understanding: a model for a host-parasite system of pink salmon and sea lice. I also describe model dynamics and steps toward validation and incorporation of farm salmon populations.

Author	Jennifer Lindquist <a href="mailto:jenl@uvic.ca">jenl@uvic.ca</a>
Title	A mathematical model of syringe-sharing partnerships and the transmission of blood-borne infections.
Abstract	Persons who use injection drugs (PWUID) in Victoria, BC were interviewed regarding injection equipment sharing practices. Survey data indicate that PWUID who share syringes do so with a single person; there are no concurrent sharing relationships. As long as an infectious individual's pairing is stable, infection does not spread to the population at large. When a partnership involving an infectious person ends, this individual may enter a fresh relationship; if the new partner is susceptible, disease transmission can occur. Here we formulate a model of pair formation and break-up dynamics, and model disease transmission within the constraints of the pairing

	process. Analysis and parameters pertaining to the survey data are presented.
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Author	Jennifer Morrison <a href="mailto:morrison@math.ubc.ca">morrison@math.ubc.ca</a>
Title	Quantifying transient directed motion in single particle tracks using a hidden Markov model
Abstract	Single Particle Tracking (SPT) is a widely used biophysical technique whereby a biomembrane component is fluorescently or optically tagged and its trajectory is observed. Analysis of SPT data has led to investigations of the different modes of particle motion, the binding kinetics of specific proteins and the underlying structure of the plasma membrane. Quantification of a protein's interactions with the cytoskeleton and identification of directed motion provides insight into the spatiotemporal organization of the signaling pathways involved. I will present a method to identify transient directed motion in tracks of membrane-bound proteins using a hidden Markov model. As shown with simulated data, we can accurately estimate the diffusion coefficients and directed velocities of a particle in each state as well as the transition rates between each state. I will also discuss our attempts at analyzing particle tracks on T Cells using this method.

Author	Hannah McKenzie <a href="mailto:hmckenzie@math.ualberta.ca">hmckenzie@math.ualberta.ca</a> (HW McKenzie, MA Lewis, and JT Jacobsen)
Title	R0 analysis of spatial population models
Abstract	It is often of interest for biological control and conservation purposes to know under what environmental conditions populations will persist or go extinct. One approach to studying such questions is through the basic reproductive number $R_0$ , which is defined as the expected number of offspring produced by an individual over its lifetime. Typically a threshold exists such that if $R_0 < 1$ the population will go extinct, while if $R_0 > 1$ the population will persist. In this talk I will formulate an $R_0$ for a spatiotemporal model for populations in streams. I will show how one can view $R_0$ as the spectral radius of a certain operator and discuss the insights the model gives into population persistence in streams.

Author	Jiafen Gong* ( <a href="mailto:jgong@math.ualberta.ca">jgong@math.ualberta.ca</a> ) and Thomas Hillen
Title	Mathematical Model for Optimizing Cancer Radiation Treatment Schedule
Abstract	In cancer radiation treatment planning, clinicians want to find an optimal schedule to kill as many cancer cells as possible while keeping the normal tissue damage at an acceptable level. Mathematical models to quantify cancer cell killing and normal tissue complication are needed for this optimization. In this talk, I mainly studied two pairs of models for regulating cancer cell killing and normal tissue complication, and want to use them to optimize realistic cancer radiotherapy treatment schedules in future. One approach is the total survival fraction for cancer killing and the cumulative radiation effect for normal tissue complication. The total survival

	fraction is a deterministic model derived from cancer cell growth laws and simple survival fraction models and the cumulative radiation effect is obtained from data fitting. The other pair of models is derived from birth-death processes: the tumor control probability and the normal tissue complication probability.
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Author	Justin Marleau <a href="mailto:jnmarlea@ualberta.ca">jnmarlea@ualberta.ca</a>
Title	Early Plant Primary Succession on Mount St. Helens: Mechanisms and Mathematical Models
Abstract	Understanding the mechanisms such as facilitation, competition and dispersal limitation that control the rate and trajectory of primary succession can greatly aid in ecosystem rehabilitation. To explore how these mechanisms can drive successional dynamics, we devised stoichiometric ecosystem-level models that considered the role of nutrient limitation and dispersal ability in plant primary succession. We applied these models to the well-studied primary plant community on Mount St Helens to check the importance of the proposed mechanisms. Our results demonstrate that the most competitive plants within the community are nitrogen-limited and that the presence of a nitrogen-fixing legume, <i>Lupinus lepidus</i> , can greatly enhance community biomass at the local scale. The presence of <i>Lupinus</i> within the community is highly dependent on seed dispersal and the survival of these seeds. These results confirm suggestions from previous studies that the presence of <i>Lupinus lepidus</i> , which thereby removes nitrogen-limitation, can influence primary succession. This study suggests that competitive and facilitative effects of plants can be examined within the framework of stoichiometry.

Author	Shaun Strohm <a href="mailto:shaun.strohm@gmail.com">shaun.strohm@gmail.com</a>
Title	Dispersal of Mountain Pine Beetle in Banff and Impacts of Management
Abstract	In this talk I will present a hybrid model for the Mountain Pine Beetle (MPB). The model is made up of diffusion and chemotaxis-based PDEs for the beetle flight period and discrete equations for the MPB overwintering stage. The model includes forest management activities such as tree baiting and removal of green attack trees. I will discuss the formation of beetle attack patterns in the PDE model. Ultimately, we wish to understand how the inclusion of management strategies alters the attack patterns of MPB. Lastly, I will discuss future research plans and how the model will be tested against data from Banff National Park.

Author	Ryan Lukeman <a href="mailto:lukeman@math.ubc.ca">lukeman@math.ubc.ca</a>
Title	Linking Empirical Data to Modeling of Collective Motion in Animal Groups
Abstract	Many modeling studies have been presented to understand mechanisms of group formation and motion in animal groups. Yet,

	<p>without empirical data to validate these models, the proposed models remain purely hypothetical. Obtaining reliable data on positions and trajectories of animals within large groups is complicated by a number of factors, limiting the available data, and thus, limiting model validation. In this talk, I'll describe our novel data set of flocks of a few hundred surf scoters swimming, for which we can entirely reconstruct individual trajectories. I'll then show how the empirical data can be synthesized to reveal structure within the data, providing a test for model validity. Using this test, we construct and optimize a self-propelled particle model from which we infer inter-individual interactions occurring between scoters.</p>
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Author	Vishaal Rajani <a href="mailto:vrajani@ualberta.ca">vrajani@ualberta.ca</a>
Title	Quantitative Analysis of Single Particle Tracking Experiments
Abstract	<p>A commonly used experimental technique to study the movement of biomolecules is Single Particle Tracking (SPT). SPT involves tagging biomolecules (such as proteins) with a fluorescent label and observing and recording their trajectories over time. A diffusion coefficient describing the movement of the biomolecules then can be extracted from the data from mean square displacement calculations. The method of data collection from individual biomolecules is analogous to that from individual animals. Ecologists regularly quantify movement from observation of animals moving in the field, using the concepts of net squared displacement and residence index. We (1) explore the quantitative methods used in ecology to characterize the movement of animals from tracking data, and (2) investigate the possibility of adapting these methods to characterize the movement of biomolecules.</p>