Mathematical Biology
Biologie mathématique
(Org: **Gerda de Vries** (Alberta) and/et **Frithjof Lutscher** (Ottawa))

CAROLINE BAMPFYLDE, University of Alberta, Department of Mathematical & Statistical Sciences, 632 Central Academic Building, Edmonton, AB, T6G 2G1, Canada
Biological control through intraguild predation: what is the most efficient control method?

Rusty crayfish (*Orconectes rusticus*) are aggressive invaders of the Great Lakes ecosystem. They interact with indigenous smallmouth bass (*Micropterus dolomieu*) through intraguild predation. Mature bass are predators of rusty crayfish, but predation is gape-limited, with the largest crayfish escaping predation. These individuals are the most fecund and compete with juvenile bass, causing a "juvenile competitive bottleneck". We use a stage-structured model to explore the dynamics of the interacting species and the possible biological control of rusty crayfish by smallmouth bass. The modelling framework can also be used to evaluate the most efficient method of mechanical control of crayfish using either trapping or trawling or a combination of both.

Smallmouth bass is a sport fish in many of the invaded lakes, and lakes with smallmouth bass have high recreational value. The impact of different fishing regulations on crayfish control can also be assessed. We use the framework to suggest methods for socially and cost-effective control.

JACQUES BELAIR, Université de Montréal, CP 6128, Succ. centre-ville, Montréal, QC, H3C 3J7
Stability in an Epidemiological Model with Two Transmission Rates and Application to Antibiotic Resistance in Commensal Bacteria

Drug-resistant bacteria often emerge when antibiotics are employed, including for prophylactic use in livestock feed. We derive a deterministic compartmental model to analyze the spread of resistance in swine population of constant size. We separate the uninfected from the infected, dividing the latter according to the consequences of the infection on the individual behaviour, and thus on the transmission rate of the disease. The specificity of the model resides in the separation of the infected individuals depending on whether there occurs a transformation in the behaviour of either the individual or the disease itself, thus affecting the transmission of the disease. A global stability result is obtained using Lyapunov techniques. Convergence to the stable equilibrium is shown to depend on the value of a parameter associated to a reproduction number. The model is applied to the epidemiology of bacterial resistance in commensal bacteria, relating colonized individuals to the infected class, with antibiotics modifying the incidence rate of resistant mutants.

The objective of such formulation is to provide epidemiologists with a tool to analyze and control the impact of the two transmission rates on the dynamics of the disease.

LUCIANO BUONO, University of Ontario Institute of Technology
Delays, Oscillations and Hopf Bifurcations in Drug Delivery Systems

Drug therapies are sometimes designed to reproduce the physiological fluctuations in normal biological agents, such as hormones, which entails the need for a periodic, yet sustained administration. The generation of oscillatory variations in concentrations is thus desirable in this context. We present such a system containing explicit time delays, in which the oscillations are generated by the delayed response of the permeability of a membrane at the boundary of a reaction chamber. We completely analyse the stability of the equilibrium, and present conditions under which Hopf bifurcations are present. We also provide further conditions for multiple mode instabilities to occur, by the occurence of double Hopf bifurcations, and present evidence of highly nonsinusoidal oscillations.

ERIC CYTRYNBAUM, Department of Mathematics, University of British Columbia, 1984 Mathematics Road, room 121
Connections between a 1D-spiral wave, fast and slow pulses

In this talk, I will discuss the dynamic properties of a novel unstable 1D spiral wave that sits on the boundary between the stable rest solution and the stable traveling pulse solution to the FHN equations. Some connections will be made to reflections, propagation failure and formation of spiral waves in inhomogeneous excitable media.

RALUCA EFTIMIE, University of Alberta, Edmonton, AB, T6G 2G1
Modelling complex spatial animal group patterns: the role of different communication mechanisms

Signal reception is essential for the formation and movement of animal groups. I will present a one-dimensional hyperbolic model for group formation that incorporates different mechanisms for the reception of signals emitted by group members. Numerical simulations reveal a wide range of spatial patterns that can form. Some of these are classical patterns, such as traveling waves, or stationary pulses. There are also new patterns, such as breathers, ripples zigzag pulses, or semi-zigzag pulses.

KEVIN HALL, NIH, Washington DC

FRANK HILKER, University of Alberta, Centre for Mathematical Biology, Mathematical & Statistical Sciences, 501 CAB, Edmonton, AB, T6G 2G1
Dynamical behavior of a population with nonlinear growth and fatal disease

We consider a population with strong Allee effect (i.e., negative population growth at small densities) that is subject to an infectious disease. The disease is of SI type (susceptible – infected) and induces an additional disease-related mortality. This is a reasonable model for some animal diseases with an infected period that is long compared to the life time. Mathematically, the model is composed of two ordinary differential equations with cubic nonlinearity. We show that the system can have six stationary states, three of which can be locally stable simultaneously. The bifurcation behavior is investigated numerically and exhibits the occurrence of Hopf, fold and homoclinic bifurcations, all of them meeting in a codimension-two Bogdanov–Takens bifurcation point. We discuss the implications of this surprisingly rich dynamics for management in conservation biology and biological control.

YU JIN, Memorial University of Newfoundland
Spatial Dynamics of a Periodic Population Model with Dispersal

This paper is devoted to the study of spatial dynamics of a class of periodic integro-differential equations which describe the population dispersal process via a dispersal kernel. By appealing to the theory of asymptotic speeds of spread and traveling waves for periodic semiflows, we establish the existence of the spreading speed c^* and the nonexistence of traveling wave solutions with the wave speed $c < c^*$. Then for the autonomous case we use the method of upper and lower solutions to obtain the existence of monotone traveling waves with the wave speed $c \geq c^*$. It turns out that the spreading speed coincides with the minimal wave speed for monotone traveling waves.

ANMAR KHADRA, Department of Mathematics, The University of British Columbia, Room 121, 1984 Mathematics Road, Vancouver, BC, Canada, V6T 1Z2
Robust Rhythmogenesis in Endocrine GnRH Neurons via Autocrine Regulations in a Common Pool of Extracellular Hormone

Gonadotropin-releasing hormone (GnRH) is a decapeptide hormone secreted by GnRH neurons located in the hypothalamus. It is responsible for the onset of puberty and the regulation of hormone release from the pituitary. There is a strong evidence suggesting that these GnRH neurons are intrinsically capable of generating pulsatile and episodic neurosecretion of this hormone. However, the underlying mechanism for the GnRH-pulse generator remains obscure. The discovery of GnRH receptors allowing GnRH to exert autocrine regulation on its own release, led several experimentalist in NIH to propose in 2003 a mechanism underlying this effect. We developed in 2006 a mathematical model describing the proposed mechanism, then we extended it to explain synchrony observed in GnRH neurons by incorporating the idea of a common pool of GnRH hormone.

In this talk, we shall present this model and analyze several aspects of it, especially robustness. We shall show that the coupling of a heterogeneous family of GnRH neurons will not significantly alter the general dynamics of the pulse generator. Indeed, we shall establish that no more than 50% of these coupled neurons must be active participants in the process to generate pulsatility. The effects of requirement and averaging in parameter-values will be also discussed. Several model predictions explaining the type of behaviour observed experimentally upon the injection of exogenous GnRH will be stated. These results will further demonstrate the essential properties of synchrony observed and the robustness of the model proposed.

FRITHJOF LUTSCHER, University of Ottawa
The effect of foraging patterns on population dynamics for central place foragers

Central place foragers are individuals living in a larger population at a central place from which they emerge to forage and to which they return to reproduce. Examples include ants, bats, colonial seabirds, and cave crickets. Foraging area and foraging behavior may influence population dynamics at the central place where reproduction occurs.

Typically, deterministic models for population dynamics consider either a nonspatial setting (e.g. ODEs or difference equations), or a spatial setting in which the species in question can reproduce anywhere in the domain (e.g. PDEs and integrodifference equations). Since neither of these two frameworks is suited for a central place forager population, we introduce a system of two equations in discrete time, one for the spatial distribution of resources and one for the (nonspatial) density of consumers at the central place. The two equations are connected via a 'foraging kernel' that captures the foraging behavior of individuals.

We study the resulting dynamics in two different cases.

(1) We assume a fixed foraging behavior in time and consider the minimal patch size required to sustain a population. We show how different foraging behaviors give qualitatively different population dynamics.

(2) We assume that individuals forage in such a way that the population-level food intake is maximized at each time step, i.e., the foraging kernel depends on the resource distribution. Several new dynamical behaviors arise with this simplistic implementation of optimal foraging: the minimal patch size becomes zero, and different bifurcations occur.

Typically, optimal foraging has a stabilizing effect on the population dynamics.

FAHIMA NEKKA, Université de Montréal
Impact of Drug Intake Variability on Therapeutic Outputs

Variability in drug intake is increasingly recognized as a major source of variability in drug response. This topic, known in human medicine as patient compliance with drugs is an old problem, dating back to Hippocrates. This old interest has produced an overwhelming literature on the subject, mainly from the behavioural aspect and patient managements. However, until recently, the topic has been mainly descriptive and suffered from a lack of real new ideas and breakthroughs. This has been attributed to the absence of reliable measurement techniques, methodological flaws of compliance and lack of a conceptual rigor. With the aim to build a theoretical framework of drug intake variability, we have conceptually formalized compliance in different therapeutic contexts. We have used probabilistic and stochastic approaches to reproduce the main characteristics and attributes of drug-intake patterns and to investigate their responsibility in the pharmacokinetic/pharmacodynamic (PK/PD)

variability. Using these approaches, we have shown that inclusion of random drug-intake features can generate a dramatic influence on the PK/PD variability that we properly characterized.

This work is in collaboration with Dr. Jun Li.

ALEX POTAPOV, University of Alberta, Edmonton, AB, T6G 2G1
Modeling aquatic invasions and control in a lake system: principles and approaches

Bioeconomic approach to biological invasions requires accounting for a number of processes and combining several analysis techniques: models of establishment, population dynamics and control from invasion biology; transportation models for invader flow between the lakes; cost-benefit analysis and discounting from economics; and methods of optimization and optimal control. Each side of the problem can be considered with a different degree of detailization, therefore it is possible to build a collection of models of different complexity. I will describe four models and most important results about the lake invasions, which were obtained with the help of these models.

ROBERT SMITH, The University of Ottawa, 585 King Edward Ave
The basic reproductive ratio: does the emperor have no clothes?

The basic reproductive ratio, R_0, is defined as the number of secondary infections arising from a single individual during his or her entire infectious period, in a population of susceptibles. This concept is fundamental to the study of epidemiology and within-host pathogen dynamics. Most importantly, R_0 often serves as a threshold parameter that predicts whether an infection will spread. Related parameters which share this threshold behaviour, however, may or may not give the true value of R_0. We give a brief overview of common methods of formulating R_0 and surrogate threshold parameters from deterministic, non-structured models. We also review common means of estimating R_0 from epidemiological data. Finally, we survey the recent use of R_0 in assessing emerging diseases such as SARS and avian influenza, a number of recent livestock diseases, and vector-borne diseases malaria, dengue and West Nile Virus.

PHILIPPE TRACQUI, CNRS, Lab. TIMC–IMAG/DynaCell, IN3S, Pavillon Taillefer, Domaine de la Merci, 38706 La Tronche Cedex, France
Proteolytic control of the mechanical switch leading to in vitro morphogenesis of capillary-like networks: a theoretical analysis

In vivo morphogenesis of capillary networks, or angiogenesis, is closely mimicked by in vitro models of endothelial cells (ECs) cultured on extracellular matrices, such as fibrin biogels with tunable stiffness. Indeed, under specific microenvironmental conditions, randomly seeded ECs self-organize into capillary-like structures (CLS). Traction forces exerted by ECs affect the initiation and progression of the biogel patterning and remodeling. Considering the well-documented mechanosensitivity of endothelial cells, and especially the suggested role of secreted matrix metalloproteinases, we develop and analyze a mathematical model of this morphogenetic process which is able to reproduce several qualitative and quantitative features of our in vitro experiments. The results of the theoretical analysis show how CLS result from an autobaric-driven instability and appear for a well-defined critical traction force that is a function of the proteolytic ECs response to extracellular stresses. This model also provides a basis for a theoretical analysis of the anisotropic mechanical sensing of ECs and its functional inter-dependence with ECs migration and CLS formation. We additionally illustrate how the simulated model behaviors contribute to define a model-driven data acquisition framework that is necessary to increase our understanding of angiogenesis both in physiological and pathological contexts.

REBECCA TYSON, UBC Okanagan, 3333 University Way, Kelowna, BC, V1V 1V7
Modelling the swimming behaviour of the nematode

The swimming behaviour of biological organisms is a spatio-temporal pattern which arises through the complex interactions of the swimmer's nervous system and musculature, and the hydrodynamics of the surrounding fluid. The entire system is enormously complex to describe both mathematically and through simulations. Models of swimming have traditionally focussed on one or perhaps two aspects of the full swim-system, and generally are restricted to one hydrodynamic regime: either low- or high-Reynolds number flow. We present a brief overview of models of swimming, and our results using a promising modelling approach based on the immersed boundary method.

ALLAN WILLMS, University of Guelph, Guelph, ON, N1G 2W1
A Geometric Comparison of Hodgkin–Huxley and Multi-State Models

Multi-state models of ion channel gating have been used extensively, but choosing optimally small yet sufficiently complex models to describe particular experimental data remains a difficult task. In order to provide some insight into appropriate model selection, we present some basic results about the behaviour of solutions of multi-state models, particularly those arranged in a chain formation. Some properties of the eigenvalues of constant-rate multi-state models are presented, and an expression for the product of the eigenvalues of a coupled chain is developed in terms of those of its constituent chains. We look at a geometric description of a three-state chain and in particular, analyze differences between a chain equivalent to a Hodgkin–Huxley model and a chain with identical rates. One distinguishing feature between these two types of chains is that decay from the open state in the Hodgkin–Huxley model is dominated by the most negative eigenvalue while the identical rate chain displays a mix of modes over all eigenvalues.