

# International Graduate Training Center (IGTC)

## Mathematical Biology Summer Course:

### May 11-June 11, 2008

Instructor: Leah Edelstein-Keshet and Visiting Lecturers

April 7, 2008

## 1 The IGTC Summer course

The International Graduate Training Center (IGTC) is a new program sponsored by the Pacific Institute for Mathematical Sciences (PIMS) to train graduate students in interdisciplinary research. The first IGTC graduate course in Mathematical Biology will be held at UBC over a one month period (May 11-June 11) in the summer of 2008. The course is open to current UBC students (as a normal three-credit course) as well as to incoming students from elsewhere. It would be equivalent to a three-credit graduate course. Students from Western Canada provinces should be able to get credit for this course based on the Western Dean's agreement.

## 2 Course number and other details

The IGTC summer course is equivalent to UBC Mathematics 561, "Topics in Mathematical Biology", a regular full-credit UBC graduate course. (Usual number of lecture hours per semester: 39; anticipated number of lecture hours in summer school: 40-50). Students at UBC, SFU, U Vic, and U Alberta can arrange to transfer credit for the above course with agreement of their home institutions.

### 2.1 Prerequisites

Students would be expected to have background in differential equations, linear algebra, and introductory modelling. Experience with mathematical software, while useful, is not an essential prerequisite.

### 2.2 Instructors

The course will be taught by the following instructors:

- Leah Edelstein-Keshet (Dept. of Mathematics, UBC): full time instructor; will cover basic survey of "classic" Mathematical Biology, together with specific research interests of the UBC Math-Biology group.

- Prof Karl Hadeler (Dept. of Mathematics, Tübingen, and Visiting Professor, Arizona): two weeks visit, May 11-24. Prof Hadeler will present the mathematics of transport and diffusion equations, chemotaxis; his part of the course will be more specialized, dealing with the modeling and analysis based on partial-differential equation models.
- Prof Bard Ermentrout (Dept. of Mathematics, U Pittsburgh): one week, May 26-31. Prof Ermentrout will present specialized topics in mathematical neurosciences. He will also help with more advanced tutorials using the differential-equation and bifurcation analysis software, XPP.
- Prof Alex Mogilner (Dept of Mathematics, UC Davis): one week, June 4-10. Prof Mogilner will present advanced topics in mathematical cellular biology.

During the month-long course, there will be on average two to three hours of lectures every morning. (generally one lecture would be given by LEK and another by the visiting lecturer). There will be tutorials/ computer labs in the afternoon several days per week.

Approximately 4-5 other research-level seminars will be presented during the course of the Summer School, with local and near-by Math Biologists invited to present their research. This will diversify the offerings and allow students to learn about local research interests in Mathematical Biology.

Students will be exposed to interesting biological questions at the forefront of current scientific research. They will learn how to use simulation software (such as XPP), methods of modeling and analysis, as well as fitting models to data. The course will provide practice at verbal and written communication in the form of a project. Credit will be based on problem sets and on a final project.

## 2.3 Keshet's Syllabus (Tentative)

Cell biology offers a rich area where concepts and methods of applied mathematics can come into play. I plan to make this one central core of my own set of lectures in this course.

In my survey, I will first discuss chemical networks with specific dynamic properties (modeled by ODEs), focusing on recent applications to biochemical signalling in cells. I will review properties of several reaction-diffusion systems, illustrating both pattern and wave-based phenomena, with applications to the problem of gradient sensing and directional selection in a polarizing cell. I will survey recent work on cell motility modeling.

In a second part of my lectures, I will introduce a number of additional topics. These will include models for interacting individuals (PDE's, systems of ODE's, and non-local models), recent models for biomedical problems such as diabetes and Alzheimer's disease. Students will gain experience with stage-structured models, integro-PDE's, and both Lagrangian and Eulerian models for swarms and schools.

## 2.4 Prof Mogilner's course description

In the last decade, cell biology has been undergoing revolutionary change, in no small part due to rapid accumulation of quantitative data and development of mathematical and computational models that helped to make sense of these data. As a result, mechanistic understanding of molecular processes in the cell increased dramatically. In the course of five lectures, we will use recent research

papers to examine a few cell biological phenomena (i.e. biochemical signaling, cell cycle, cell division, intracellular transport) to understand what was the logic of the controlled experiments, how the data was used to formulate and test the models, and how the models helped to make sense of the data. No prior biological knowledge will be needed. Basic applied mathematics tools will be used (ODEs, PDEs, elementary probability). The lectures will be followed by three problem solving sessions, during which we will work on an open modeling problem. Numerical simulations involved will be done using Matlab.

## 2.5 Prof. Haderer's Course description:

Bacteria perform peculiar movements and control size and shape of their colonies by "quorum sensing". They "want" to optimize their environment, e.g. by "chemotaxis", and they "want" to spread. What are the mechanisms? Are movements and growth patterns arbitrary or governed by laws for the individual and the population? Can we cast these laws into equations with few parameters which can be identified in experiments? Similar questions can be posed for animal and plant species and for the spread of infectious diseases (West Nile virus is a recent example).

A suitable framework are reaction diffusion equations which exhibit biologically and mathematically challenging phenomena: patterns, localization (spikes), blow up, fronts and pulses. These occur also in refined models like damped wave equations, reaction transport equations, and Langevin equations. We demonstrate phenomena and establish connections between levels of complexity, e.g. by diffusion approximation. We ask whether a species is stable within an ecosystem (persistence) and how a species like the zebra mussel can invade (it took 150 years to get from England to North America).

We ask whether the dynamics of a system is determined by its components, when all components are similar (lattice dynamics) and when components represent quiescent or dormant phases. Examples are microbes (spores), cells ("most cells in the body are quiescent"), plants (seed banks) and mammals (hibernation).

Rather than modeling the size of fishes or rodent colonies by size classes one can use first order partial differential equations which allow dependence on individual growth rates and total population size, but mostly not stochastic variation. We incorporate stochastic behavior by diffusion (mathematically: viscosity approach to conservation laws).

Delays often represent unknown transport or reaction processes. Relations between delay differential equations and structured population models have been known since long, but their true nature became clear only recently. They help us to understand delay equations as models in their own right and to justify neutral delay equations.

Modeling infectious diseases is a most important application: vaccination, education and quarantine policies, effect of social structure, core groups and small reservoirs, demographic impact, and spread in space, as well as parameter identification from field data.

## 2.6 Prof. Ermentrout's course description

In this set of lectures I will discuss the modeling and analysis of rhythmic phenomena in biology. I will start with models of oscillations including ODE models, PDE models and delay equations, laying out the necessary conditions that are required for oscillations. I will discuss the underlying geometry of mechanisms from which a system goes from a stable fixed point to a periodic orbit. I

will then switch to questions concerning the interaction of intrinsic oscillators, that is, what kinds of behavior can we expect when oscillators are coupled. My main approach will be the reduction to "phase models" in which each oscillator is reduced to a one-dimensional variable on a circle. The interactions between the oscillators as well as the topology of the connections determines the stable patterns which are possible. I will show how both the intrinsic properties as well as the time scales of interactions combine to determine the stability of patterns in networks. In addition to synchronization behavior, I will provide conditions for various types of wave-like behavior including target waves, spiral waves, and complex dynamics. Applications to neural and cellular phenomena will be provided as well as many computer exercises in XPPAUT or if the students want to write their own code, Matlab.

### **3 Course Credit and Grading**

As usual in graduate courses, tests and exams will be minimized, and grading (for students taking the course for credit) will be calculated as follows: 6 out of 8 hand-in assignments - 10% each (for a total of 60%), participation in discussions - 10%, oral presentation of research topic - 15%, submission of final report on research topic - 15 %. (Students will be expected to read and present papers, as well as work on a mini-project that they would present at the end of the summer school.)

### **4 Other details**

As the course evolves, more details will be posted at:

<http://www.pims.math.ca/science/2008/08ssigtcmb/>