Models of Motion in Biology (CAIMS)
Modéles pour les mouvements en biologie (SCMAI)
(Org: **Dan Coombs** (UBC))

CATHERINE BEAUCHEMIN, Ryerson University, Toronto, ON
Capturing the Mechanisms Guiding T Cell Motion within Lymph Nodes

The recent application of two-photon microscopy to the visualization of T cell movement has presented trajectories of individual T cells within lymphoid organs both in the presence and in the absence of antigen-loaded dendritic cells. Remarkably, even though T cells largely move along conduits of the fibroblastic reticular cell (FRC) network, they appear to execute random walks in lymphoid organs rather than chemotaxis. Here, we will present results from our analysis of experimental trajectories of T cells using computer simulations of idealized random walks. Comparisons of simulations with experimental data provide estimates of key parameters that characterize T cell motion in vivo. For example, we find that the distance moved before turning is about twice the distance between intersections in the FRC network, suggesting that at an intersection a T cell will turn onto a new fibre about 50% of the time. Finally, recent, more detailed models from other groups will also be discussed. [Talk presented at CMS/MITACS 2007.]

GUSTAVO CARRERO, Athabasca University, Centre for Science, Edmonton, Alberta, Canada T5J 3S8
Studying nuclear actin and histone H1 dynamics using FRAP experiments

Fluorescence recovery after photobleaching (FRAP) has become a common fluorescence microscopy technique for measuring the mobility of proteins within the cell nucleus. By photobleaching a region of a cell nucleus populated with a specific fluorescent fusion protein, recording the fluorescence recovery of the region over time, and interpreting this recovery with a mathematical model it is possible to extract in vivo kinetic properties of the protein under investigation.

Experimental FRAP recovery curves of two nuclear proteins, namely actin and histone H1, exhibit two distinct types of behaviour. To characterize these types of behaviour mathematically and to obtain information on the dynamics of the proteins, FRAP data are interpreted with a linear reaction-diffusion system of equations. The kinetic analysis of the model and the data

(i) enables us to understand that the two distinct types of behaviour correspond to two asymptotic cases of the reaction-diffusion model,

(ii) supports the relevant biological fact that actin exists in the nucleus in both monomeric and polymeric forms, and

(iii) allows us to conclude that histone H1 can have both high and low binding affinities to the chromatin structure.

DANIEL COOMBS, University of British Columbia
Models of motion in biology

Understanding motion of biological objects (molecules, cells, organisms, populations) is of fundamental importance in biology. This minisymposium will showcase recent work on biological motion at every scale, from nanometer-sized proteins to collections of large animals. Common themes and questions emerge. For instance, to what extent can we approximate biological motion by diffusive motion? How can we model interactions between large numbers of moving objects that each obey simple physical rules of behaviour? How can experimental time-courses for individual objects reveal the laws of motion? In this introduction talk I will outline some of the challenges and possibilities in this field.

RAIBATAK DAS, University of British Columbia
The motion of cell-surface proteins analyzed with a hidden Markov model

Single particle tracks of tagged cell-surface proteins frequently show deviations from random Brownian diffusion. Such deviations are usually transient and are variously attributed to membrane heterogeneities, the presence of rigid obstacles, or interaction with other membrane-bound or cytosolic proteins. We analyze the dynamics of a diffusing cell-surface protein that interacts with a homogeneously distributed binding partner, such as intracellular cytoskeletal tethers. The system is parametrized by 2D diffusion coefficients of the protein in its free and bound states, and transition probabilities between the two states. Tracks of single protein molecules are considered to be the outcome of a hidden Markov model, whose underlying Markovian state sequence (free or bound) is not observable, while the particle position at each observation time is recorded. In this formulation, the likelihood of the observed sequence of displacements in a track is a function of the four model parameters. We maximize this likelihood function with respect to the model parameters to estimate their best-fit values and assign statistical error bounds to these estimates. Our analysis reveals important kinetic parameters for the underlying physical system that are not easily discernible with a traditional single particle tracking analysis. We apply our analysis to experimentally observed tracks of the adhesion molecule LFA-1 on the surface of T cells.

RYAN LUKEMAN, University of British Columbia, 2329 West Mall Vancouver, BC, Canada V6T 1Z4
Collective Motion in Animals Groups from an Idealized Perspective

The collective motion of groups of animals often exhibits interesting patterns, both visually and mathematically. Common examples include schooling fishes and flocking birds. Often, individuals in such a group can only communicate locally (i.e., with nearest neighbours), yet the aggregate exhibits some global pattern. With such biological groups as motivation, an interacting self-propelled particle ODE model is used to study some idealized 'perfect school' formations. The regular geometry of such formations allows analytical insights on existence and stability that are not typically possible from numerical simulation alone. This approach allows one to make concrete connections between properties of individuals, and properties of the emergent pattern at the group level.

Although there has been quite a few modeling studies of such animal groups, there has been relatively little real data for comparison, typically owing to the difficulty of obtaining such data reliably. In this talk, I will discuss our modeling approach and results, and also briefly discuss some efforts in collecting field data on groups of aquatic diving ducks.

FRITHJOF LUTSCHER, University of Ottawa
The effect of landscape heterogeneity on spread and persistence in integrodifference equations

The spread of non-indigenous species and diseases poses a major risk to ecosystems and human health worldwide. The key challenges to management and control of such invasions are to understand the conditions of spread and the different factors influencing the speed of spread. Of particular interest is the effect of landscape heterogeneity on the spread of organisms. We formulate a discrete-time model for growth and dispersal, where both of these processes vary in space. We then present approximation formulas for the spread rate in such a heterogeneous landscape and demonstrate their validity by comparison with numerical simulation. We also give rules of thumb for the conditions under which a species is able to spread in a heterogeneous landscape. We separately consider the two cases with and without Allee effect in the population growth function. Our results provide simple recipes for calculation of spread rates in complex landscapes together with their limits of validity.

HANNAH McKENZIE, University of Alberta, Edmonton, AB, Canada
First passage time: insights into animal movement

Movement plays a role in structuring the interactions between individuals, their environment, and other species. First passage time is a novel way of understanding the effect of the landscape on animal movement and search time. In the context of animal movement, first passage time is the time taken for an animal to reach a specified site for the first time. We derive a

general first passage time equation for animal movement that can be connected with empirical data. This equation is related to the Fokker–Planck equation, which is used to describe the distribution of animals in the landscape. Drawing on examples of red fox movement within a home range and wolf movement in response to linear features, we use first passage time analysis to demonstrate the effect of spatial heterogeneity on the time required for a predator to locate prey. In addition, we discuss the effect of two different searching modes on the functional response and show that random searching leads to a Holling type III functional response. First passage time analysis provides a new tool for studying the influence of animal movement on ecological processes.

CHAD TOPAZ, Dept. of Mathematics and Computer Science, Macalester College, St. Paul, Minnesota 55105, USA
A model for rolling migratory locust swarms

We construct an individual-based, kinematic model for rolling migratory locust swarms. The high-dimensional ODE model incorporates pairwise social interactions of attractive-repulsive type, gravity, wind, and the impenetrable boundary formed by the ground. The parameters controlling the social interactions determine whether the group is in the H-stable or catastrophic statistical mechanical regime. We simulate both cases. In free space, an H-stable group forms a crystalline lattice of individuals and with gravity it forms a grounded lattice.

Wind smears the swarm out along the ground until all locusts are stationary. In contrast, a catastrophic group forms a densely packed structure in free space. With gravity, the swarm forms a bubble-like shape with a group of airborne locusts and a dense layer of grounded locusts below them. With wind, the swarm migrates in a rolling motion.

The rolling structure is similar to that observed by biologists, and includes a takeoff zone, a landing zone, and a stationary zone where grounded locusts can rest and feed. To further understand the vertical structure of the swarm, we formulate a one-dimensional continuum problem describing a vertical slice. We use variational methods to minimize the energy for this problem and find exact solutions of the resulting integral equation. These exact solutions agree closely with simulations of the discrete problem.