
New Mathematical Tools for the Modeling of Cellular Processes
Nouveaux outils mathématiques pour modélisation des processus cellulaires
(Org: **Thomas Hillen** (Alberta))

DANA COBZAS, University of Alberta

Tumor Invasion Margin on the Riemannian Space of Brain Fibers

Glioma is one of the most challenging types of brain tumors to treat or control locally. One of the main problems is to determine which areas of the apparently normal brain contain glioma cells. Gliomas are known to infiltrate several centimetres beyond the clinically apparent lesion that is visualized on standard CT or MRI scans. To ensure that radiation treatment encompasses the whole tumor, including the cancerous cells not revealed by MRI, doctors treat the volume of brain that extends 2 cm out from the margin of the visible tumor. This approach does not consider varying tumor-growth dynamics in different brain tissues, thus it may result in killing some healthy cells while leaving cancerous cells alive in the other areas. These cells may cause recurrence of the tumor later in time, which limits the effectiveness of the therapy.

Knowing that glioma cells preferentially spread along nerve fibers, we propose the use of a geodesic distance on the Riemannian manifold of brain diffusion tensors to replace the Euclidean distance used in the clinical practice and to correctly identify the tumor invasion margin. This mathematical model results in a first-order PDE that can be numerically solved in a stable and consistent way with.

To compute the geodesic distance, we use actual Diffusion Weighted Imaging (DWI) data from 11 patients with glioma and compare our predicted growth with follow-up MRI scans. Results show improvement in predicting the invasion margin when using the geodesic distance as opposed to the 2 cm conventional Euclidean distance.

ADRIANA DAWES, University of Alberta

*Cortical thickening and negative curvature may position the Par protein boundary in the early *C. elegans* embryo*

Many cell types have the capacity to polarize by segregating specific proteins to opposite ends of the cell. In embryos of the nematode worm *C. elegans*, the proteins of interest are the Par proteins. The Par proteins bind to the actin cortex, a thin structure just below the cell membrane consisting of polymers of the protein actin which are crosslinked by the contractile protein myosin. Shortly after fertilization, the single cell embryos stably polarize, with distinct Par proteins occupying opposite ends of the cell, and the boundary between the Par domains is placed near the centre of the embryo. In this talk, I will discuss possible mechanisms for spatial positioning of the Par protein boundary and demonstrate how the boundary position may depend on both cortical thickening and negative curvature during polarization. This work is joint with David Iron (Dalhousie University)

GERDA DE VRIES, University of Alberta

Quantitative Analysis of Single Particle Tracking Experiments: Applying Ecological Methods in Cell Biology

A commonly used experimental technique to study the movement of biomolecules in the cell membrane is Single Particle Tracking (SPT). SPT involves tagging biomolecules with a fluorescent label and observing and recording their trajectories over time. A diffusion coefficient then can be extracted from the data from mean square displacement calculations. Although the diffusion coefficient provides an overall measure of mobility, it does not provide insight into the underlying heterogeneity of the membrane environment.

Since the method of data collection from individual biomolecules is analogous to that from individual animals, we propose to use methods from ecology to provide spatial insight. Ecologists regularly quantify animal movement using the concepts of correlated random walk, net squared displacement, and first-passage time. In this talk, we will demonstrate the applicability of these methods in the context of cell biology. In particular, we will show how we can distinguish biomolecule trajectories

undergoing a correlated random walk from those that do not, and how we can identify the presence of transient confinement zones in molecular diffusion.

PETER HINOW, University of Wisconsin - Milwaukee
A Kinetic Model for Cell Movement in Network Tissues

Mesenchymal motion describes the movement of cells in biological tissues formed by fibre networks. An important example is the migration of tumour cells through collagen networks during the process of metastasis formation. We investigate the mesenchymal motion model proposed by T. Hillen (J. Math. Biol. **53**:558-616, 2006) in higher dimensions. We formulate the problem as an evolution equation in a Banach space of measure-valued functions and use methods from semigroup theory to show the global existence of classical solutions. We investigate steady states of the model and show that patterns of network type exist as steady states. For the case of constant fibre distribution, we find an explicit solution and we prove the convergence to the parabolic limit.

JOHN LOEWENGRUB, UC - Irvine

ZHIAN WANG, Hong Kong Polytechnic University
Stochastic and deterministic models of chemotaxis

In this talk, we shall discuss a Langevin type stochastic chemotaxis model which assumes that the statistical increment of cell motion results from the fluctuation of cell velocity. Our main goal is to derive the well-known Keller-Segel model of population chemotaxis from the proposed stochastic model and establish the connection between the stochastic and deterministic chemotaxis model. We first derive the mean field chemotaxis model (i.e. Fokker-Planck equation) corresponding to the Langevin stochastic chemotaxis model by means of the mean field theory. Then based on the mean-field chemotaxis model, we derive the classical Keller-Segel model by using the minimization principle, moment closure approach, approximation technique and scaling argument. The relationship between microscopic and macroscopic parameters is explicitly identified. Moreover an analytical approximation of the probability density function of the Langevin stochastic chemotaxis model is found by minimizing the free energy of the mean-field model. The biological implications will be discussed.