Patterning and evolution of biological surfaces

Minisymposium ECMTB 2014 to take place between 14:00-19:00 on the 16th of June 2014.

The aim of this minisymposium is to foster the exchange of ideas by bringing together theoreticians, modellers and analysts who share an interest in the patterning and evolution of biological surfaces.

Talks

- 14:00-14:30. Anotida Madzvamuse (Sussex)
- 14:30-15:00. Colin Macdonald (Oxford)
- 15:00-15:30. Tom Ranner (Leeds)
- 15:30-16:00. Coffee break.
- 16:00-16:30. Chandrasekhar Venkataraman (Sussex)
- 16:30-17:00. John Mackenzie (Strathclyde)
- 17:00-17:30. Melda Tozluoğlu (UCL)
- 17:30-18:00. Frits Veerman (Oxford)
- 18:00-18:30. Linus Schumacher (Oxford)

Title and abstracts

- 14:00-14:30. Anotida Madzvamuse (Sussex)

  Title: Pattern formation in morphogenesis on evolving biological surfaces: Theory, numerics and applications

  Abstract: In this talk, I will present our most recent results based on two finite element formulations: (i) the surface finite element and (ii) the projected finite element methods applied to solving partial differential equations of reaction-diffusion type on arbitrary stationary and evolving surfaces. Reaction-diffusion equations on evolving surfaces are formulated using the material transport formula, surface gradients and diffusive conservation laws. The evolution of the surface is defined by a material surface velocity. The projected finite element method differs from the surface finite element method in that it provides a conforming finite element discretization which is "logically" rectangular. However, this property restricts the general applicability of the numerical method to arbitrary surfaces, a key advantage for the evolving surface finite element method. To demonstrate the capability, flexibility, versatility and generality of the numerical methodologies proposed, I will present various numerical results. This methodology provides a framework for solving partial differential systems on continuously evolving surfaces. Reaction-diffusion models have numerous applications in developmental biology, cancer research, wound healing, tissue regeneration, and cell motility.

- 14:30-15:00. Colin Macdonald (Oxford)

  Title: Simple numerical techniques for reaction-diffusion on general geometry.

  Abstract: The Closest Point Method is a set of mathematical principles and associated numerical techniques for solving partial differential equations (PDEs) posed on curved surfaces or other general domains. The method works by embedding the surface in a higher-dimensional space and solving the PDE in that space using simple finite difference and interpolation schemes. This presentation outlines some of the work we've done on reaction-diffusion equations on surfaces and other general domains, including bulk-coupling, curvature-dependence, point clouds and our Matlab/Python software for performing these calculations.

- 15:00-15:30. Tom Ranner (Leeds)

  Title: Solving diffusion equations on evolving surfaces defined by biological images

  Abstract: In many different application areas one wants to solve diffusion equations on an evolving curved surface. Modern cell microscopy has progressed significantly in recent years allowing high resolution three-dimensional time dependent images of cell migration to become available. This can be used to define the geometry for diffusion equations on the cell surface which can be solved using an Arbitrary Lagrangian-Eulerian finite element method formulation of the surface finite element method. Finally, we use this methodology to explore ligand-receptor models where bulk and surface terms are considered.

- 15:30-16:00. Coffee break.

- 16:00-16:30. Chandrasekhar Venkataraman (Sussex)

  Title: Moving interface and free boundary problems that arise in the study of cell motility

  Abstract: The mathematical modelling of cell motility naturally leads to free boundary and moving interface problems. One example is the case when the moving cell membrane is regarded as the unknown, for example as the solution to a geometric evolution law. Another scenario of interest is when a free boundary problem is posed on the, possibly evolving, cell membrane itself, such models arise in cell polarisation or cell adhesion. In this talk we focus on the modelling, simulation and analysis of such problems. Novel mathematical and numerical methods for the analysis and simulation of geometric evolution laws, free boundary problems and partial differential equations posed on moving interfaces will be discussed. Numerical simulations will also be presented.

- 16:30-17:00. John Mackenzie (Strathclyde)

  Title: A Computational Model for Eukaryotic Cell Migration and Chemotaxis

  J.A. Mackenzie*, M. Nolan* and R.H. Insall**

  Abstract: A computational framework is presented for the simulation of eukaryotic cell migration and chemotaxis. A pattern formation model, based on a system of nonlinear reaction-diffusion equations, is approximated in the evolving cell membrane using an arbitrary Lagrangian Eulerian surface finite element method (ALE-SFEM). The solution state is used to drive a mechanical model of the protrusive and retractive forces of the cell boundary. Movement of the cell is achieved using a parameterised finite element method. Building on an earlier model of ours, we extend our computational technique to include the coupling with two-dimensional intra and extra-cellular effects such as surface receptor ligand binding kinetics and cell adhesion. We will discuss the efficient grid generation for two-dimensional evolving domains and the solution of reaction-diffusion equations on the evolving cell membrane coupled to processes in the bulk. The capability of the numerical framework will be demonstrated in a range of biological simulations including chemotaxis.

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- 17:00-17:30. Melda Tozluoğlu (UCL)

  Title: Plasticity of cancer cell migration: Extracellular matrix derives the optimisation of blebbing, adhesions, and spreading.

  Abstract: The molecular requirements and morphology of migrating cells can vary depending on matrix geometry; therefore, predicting the optimal migration strategy or the effect of experimental perturbation is difficult. We present a model of cell motility that encompasses actin polymerisation based protrusions, actomyosin contractility, variable actin-plasma membrane linkage leading to membrane blebbing, cell-extracellular matrix adhesion, and varying extracellular matrix geometries. This is used to explore the theoretical requirements for rapid migration in different matrix geometries. Confined matrix geometries cause profound shifts in the relationship of adhesion and contractility to cell velocity; indeed cell-matrix adhesion is dispensable for migration in discontinuous confined environments. The model is challenged to predict the effect of different combinations of kinase inhibitors and integrin depletion in vivo and in confined matrices based on in vitro 2D measurements. Intravital imaging is used to verify bleb-driven migration at tumour margins, and the predicted response to single and combinatorial manipulations. Further, we investigate the ability of motile cells to adapt changing extracellular matrix geometries, and variable adhesion zones within the cell's path. Here, our model suggests the feedback mechanisms between the forces exerted by cells, and cell-ECM the adhesion strength allows the cells a higher adaptability, at the cost of peak cell velocities.

- 17:30-18:00. Frits Veerman (Oxford)

  Title: Pattern formation on curved surfaces: an analytical exploration

  Abstract: Patterned curved surfaces are ubiquitous in biology. In this talk, the extension of the Turing patterning mechanism to such curved surfaces is explored analytically. The effect of curvature on pattern shape is illustrated by a number of sample surfaces. The analysis pairs concepts and tools from differential geometry with classical ODE theory. The possibilities and challenges of general curved surfaces will be addressed, with possible extensions to surface growth.

- 18:00-18:30. Linus Schumacher (Oxford)

  Title: Power spectra of stochastic reaction-diffusion equations on stochastically growing domains

  Abstract: Being able to create and sustain robust, spatial-temporal inhomogeneity is an important concept in developmental biology. Generally, the mathematical treatments of these biological systems have used continuum hypotheses of the reacting populations, which ignores any sources of intrinsic stochastic effects. We address this concern by developing analytical Fourier methods which allow us to probe the probabilistic framework. Further, a novel description of domain growth is produced, which is able to rigorously link the mean-field

and stochastic descriptions. Finally, through combining all of these ideas, it is shown that the description of diffusion on a growing domain is non-unique and, due to these distinct descriptions, diffusion is able to support patterning without the addition of further kinetics.