Modelling and Inference of the Robustness of Collective Cell Migration by Self-Generated Chemotaxis

John Mackenzie

Abstract:
Self-generated chemotaxis is a fundamental biological process wherein biological cells modulate their own chemical environment to guide movement. Traditional models often assume homogeneous populations, overlooking the potential impact of phenotypic variation in cellular behaviour. However, real biological systems exhibit variability in factors such as receptor sensitivity, motility, and enzyme degradation rates, which may significantly influence chemotactic efficiency and collective dynamics.

We consider the role of phenotypic variation in self-generated chemotaxis using a hybrid discrete-continuum model using stochastic differential equations for the movement of individual cells and a partial differential equation model to represent the chemoattractant concentration. Based on realistic parameter variability, simulations will be presented to determine which processes are most important to the robustness of self-generated population chemotaxis. We will also consider the inverse problem to determine distributions of model parameters from cell trajectory data.

Mech(n)anobiology of immune cells: architecture and dynamics of actin-rich podosomes

Alessandra Cambi

Tissue stiffness is altered in many pathologies, including pulmonary fibrosis, atherosclerosis, and cancer, disrupting mechanical homeostasis. Dendritic cells (DCs), key immune sentinels involved in these diseases, encounter extracellular environments with widely varying mechanical properties. However, how mechanical cues regulate DC function remains poorly understood. DCs rely on podosomes—mechanosensitive, actin-rich structures—to generate forces, migrate, and capture large antigens. Individual podosomes probe their surroundings through cycles of protrusion and retraction, while podosomes within clusters exhibit coordinated wave-like dynamics. The mechanisms underlying this collective behavior remain largely unknown.

To address this, we combined advanced quantitative bioimaging, biomimetic 2D and 3D substrates with tunable stiffness, immunological assays, and chemo-mechanical modeling. We show that podosome wave dynamics emerge from coupling between chemo-mechanical signaling and actin diffusion, establishing a mechanistic role for podosome clusters in DC mechanosensing. Furthermore, perturbation of the septin network, the fourth cytoskeletal filament system, altered podosome architecture and dynamics, revealing a previously unrecognized interplay between septins, myosin IIa, and actin. Finally, super-resolution imaging of DCs migrating along collagen bundles in decellularized dermis provides the first glimpse of podosome nanoscale organization and dynamics in a semi-physiological 3D environment. These findings highlight the need for dedicated image-analysis approaches and more advanced mathematical models to capture the complexity of DC mechanobiology in three dimensions.

Self-Organisation of Migrating Multicellular Communities

Giulia Celora

Abstract: Collective cell migration underlies many biological processes, including morphogenesis and cancer metastasis, yet the mechanisms governing emergent collective motion remain poorly understood. In this talk, I will present our recent advances in modelling the spatiotemporal dynamics of migrating cell collectives. In particular, I will discuss how mathematical theory and analysis, combined with experimental data, has helped us uncover key mechanisms of migration in two distinct systems: mixed dilute populations of immune cells and dense homogeneous groups of amoeba cells. Overall, our work offers a new perspective on collective migration by highlighting the fundamental role of physical interactions in shaping the emergent dynamics of cell groups.

Mathematical Oncology: Could We Cure Cancer with Calculus?

Mark Chaplain

Cancer is one of the major causes of death in the world, particularly the developed world, second only to cardiovascular disease. Over 10 million people throughout the world died from cancer in 2020 i.e. globally, almost 1 in 6 (16-17%) deaths can be attributed to cancer. In the UK between 2022 and 2024, the number of deaths was around 170,000. The latest data from the World Health Organisation show that approximately 20 million new cases were recorded in 2022 with this figure expected to increase to 32.6 million by 2045. There are few individuals whose lives have not been touched either directly or indirectly by cancer.

While treatment for cancer is continually improving, alternative approaches can offer even greater insight into the complexity of the disease and its treatment. In this talk, we will present an overview of the contribution mathematical modelling is playing in the fight against cancer, and highlight recent multiscale modelling that is giving real insight into several key processes involved in solid tumour growth and progression. The development of quantitative, predictive models (based on sound biological/clinical evidence and underpinned and parameterised by biological/clinical data) has the potential to have a positive impact on patients suffering from the disease through improved clinical treatment and optimised personalised medicine.

Self-similar fast-reaction limits of reaction-diffusion systems with nonlinear diffusion

Elaine Crooks

This talk is concerned with the characterisation of fast-reaction limits of systems with nonlinear diffusion, when there are either two reaction-diffusion equations or one reaction-diffusion equation and one ordinary differential equation, on unbounded domains. The ideas used extend previous results in the linear diffusion case and show that in the fast-reaction limit, spatial segregation leads to the two components of the original systems each converging to the positive and negative parts of a self-similar limit profile that satisfies one of four ordinary-differential systems. The position of the free boundary separating where such self-similar profiles are positive from where they are negative provides information on the rate of penetration of one substance into the other and for specific forms of nonlinear diffusion, some results will be presented on the relationship between the form of the nonlinear diffusion and the position of this free boundary. This is joint work with Yini Du.

Asymptotic behaviour of integral mutation equations

Marie Doumic

Abstract: In this talk, we introduce integral equations to model bacterial mutations, in order to model experimental results obtained in (Robert et al., Science, 2018).
We obtain criteria to avoid instantaneous blow-up, and study the long-time behaviour in the case of deleterious mutations.
This is a joint work with Miguel Escobedo and Guillaume Garnier.

This Orchard is on Fire: Travelling Waves in a PDE-ODE Coupled Model of Blossom Blight

Hermann Eberl

Fireblight is a bacterial disease of apple and pear trees and other plants in the roseca family. It can wipe out an entire orchard in a single growing season. Depending on the part of the plant that it affects it sometimes goes by various names, such as trunk blight, shoot blight or blossom blight. We present a model for fireblight during blooming season consisting of two semilinear PDEs for the pathogen and 3 ODEs for the stationary host. Numerical simulations suggest the formation of travelling wavs which we then set out to prove. We determine the minimum wave speed and give conditions on parameters that guarantee the existence of such TWs that can be biologically interpreted, with implications for orchard management. Our results are sub-optimal in the sense that TWs can also be obtained for parameter combinations that do not satisfy our conditions.

On a Thermodynamically Consistent Diffuse-Interface Model for Incompressible Two-Phase Flows with Chemotaxis

Andrea Giorgini

We consider a hydrodynamic system of Navier–Stokes/Cahn–Hilliard type, which describes the motion of a two-phase flow of two incompressible fluids with unmatched densities coupled with a soluble chemical species. This thermodynamically consistent diffuse-interface model incorporates both the chemotaxis effects induced by the chemical species and the mass transport processes within the mixture. For the two-dimensional initial-boundary value problem, we will discuss the existence of global finite energy solutions and global weak solutions, as well as the existence and uniqueness of global strong solutions for sufficiently regular initial data. In particular, we show that the density of the chemical substance stays bounded for all time if its initial datum is bounded. This implies a significant distinction from the classical Keller–Segel system: diffusion driven by the chemical potential gradient can prevent the formation of concentration singularities.

Self-organisation in nature: patterns and bifurcations in nonlocal advection-diffusion models

Valeria Giunta

Understanding the mechanisms underlying the self-organisation of mobile organisms is a central question in ecology and biology. In nature, individuals - whether cells or animals - sense their environment before moving. This process is typically nonlocal, as information is gathered from a wider region rather than just the immediate surroundings. Empirical studies highlight nonlocality as a key feature of movement, and mathematical models that incorporate it are increasingly used to describe self-organisation in biological systems. Beyond capturing some real-world phenomena more faithfully, nonlocal models also exhibit rich dynamics, making them of interest to both modellers and analysts.

In this talk, I will present a class of advection–diffusion equations modelling population movement driven by nonlocal species interactions. Using analytical and numerical techniques, I will show that these models support a wide range of spatio-temporal patterns, including segregation, aggregation, time-periodic dynamics, and chase-and-run phenomena. I will also discuss parameter regimes exhibiting multiple stable solutions and hysteresis effects.

Overall, I will highlight methods for analysing bifurcations and pattern formation in these models, which provide essential mathematical tools for understanding self-organisation and emergent phenomena in nature.

How cells steer themselves by making and breaking attractants

Robert Insall

Cells do not simply follow external chemical cues; they actively shape them. This is turning out to be almost universally true - passive responses are rare and self-steering is seen in immune cells including neutrophils, macrophages and dendritic cells, neural crest, amoebas and bacteria. Self-steering is also a potent driver of collective migration - an attractant for one cell is an attractant for its neighbours. I will talk sbout how migrating cells generate, degrade, and recycle attractants to create self-generated gradients that steer movement with robustness and precision. By coupling signal breakdown, secretion, and endocytosis to actin dynamics, cells control when and where they sense, enabling reliable navigation in complex and changing environments.

Regulation and interpretation of morphogen signaling in spinal cord development

Anna Kicheva

In the developing vertebrate neural tube, opposing morphogen gradients regulate dorsoventral patterning and tissue growth. We combine quantitative assays in embryos and organoids with biophysical modeling to investigate the control and interpretation of morphogen signaling dynamics in the neural tube. In recent work, we developed geometrically constrained two-dimensional organoids in which dorsal neural tube patterning self-organizes. Pattern formation depends on the emergence of BMP and Wnt signaling gradients with characteristic biphasic temporal dynamics. We show that these dynamics arise from coupled negative and positive feedback on ligand production. Cells interpret the resulting signaling trajectories to specify distinct cell fates at defined developmental times. Our results reveal regulatory principles governing morphogen-producing domains in the neural tube and demonstrate how temporally ordered pattern formation can emerge from dynamic signaling.

Communicating Nonlinear Dynamics Across Boundaries via Interactive Simulations

Andrew Krause

This talk will be a mix of "communicating" and "doing" science in different ways, aided by modern conceptual and computational tools. I will demonstrate the value of communication across disciplinary boundaries using real-time interactive simulations through VisualPDE.com. I will describe how past and ongoing work with developmental biologists, geographers, ecologists, and microbiologists can be enriched with these tools, and in particular how deep insights can be rapidly communicated without the need for vast disciplinary expertise. Among other examples, I will discuss stochasticity in 2D Rayleigh-Bénard convection, as well as the role of subcritical diffusion-driven instabilities in oncological, ecological, and embryological settings, demonstrating the ease with which nuanced and technical theoretical ideas can be illustrated and explored in real-time. I will end by discussing fundamental limitations of phenomenological dynamical systems modelling in general, giving rise to the need for better frameworks to do science.

A sharp mass threshold for boundedness in a critical quasilinear chemotaxis model with indirect signal production: the radially symmetric case

Philippe Laurencot

A critical quasilinear chemotaxis model with indirect signal production in dimensions higher than two is studied under radial symmetry. Exploiting the variational structure of the system, the existence of a sharp mass threshold $M_c>0$ is established: solutions with mass below M_c are global and bounded, while those with mass above M_c and sufficiently negative energy are global but unbounded.

Spatial phase transition in collective dynamics

Sara Merino-Aceituno

The emergence of bands in simulations of the Vicsek model is still a poorly understood phenomenon in collective dynamics. The model is rather simple, yet this pattern is surprisingly difficult to explain and characterise mathematically. These spatial phase transitions can be at least partially explained when deriving continuum equations from the corresponding discrete dynamics. In this talk, I will report on recent progress on simulating and characterizing this phenomenon at the continuum level.
This is a collaboration with Pierre Degond (University of Toulouse, CNRS) and Léo Meyer (University of Vienna).

Degenerate & singular mixed dimensional diffusion systems: A journey from modelling, and numerical methods, to well-posedness

Koondanibha Mitra

Nonlinear, degenerate, and coupled (mixed-dimensionally) systems arise in various applications of societal relevance, such as biofilm growth, reactive transport in fractured porous media, and cellular biology. For such problems, the biomass or the main-substrate is restricted to a lower-dimensional manifold embedded in a domain in d-dimensional space, and the evolution of the biomass density/substrate concentration exhibits degenerate and singular diffusion behaviour (possibly even cross-diffusion). The other equations (for nutrients/reagents) are defined on the bulk, and are of linear advection-reaction-diffusion type.

In our analysis, we propose a backward Euler time-discretisation of the problem where the reactive terms coupling the equations are estimated semi-implicitly. Thus, the equations are dimensionally decoupled and can be solved sequentially. A bulk-surface finite element method is used to discretise the system in space. Then, an iterative linearisation algorithm is proposed to solve the fully-discrete nonlinear problem on the discretised interface. It is proven that the iterations converge unconditionally even for degenerate/singular cases and for curved interfaces, thus, showing the existence of a solution to the fully-discrete nonlinear problem. Then, for a flat interface, the convergence of the fully-discrete solutions to the time-discrete solution is shown, and the order of convergence with respect to mesh size is estimated. Properties such as well-posedness, boundedness, and positivity of the time-discrete solutions are proven, and the existence of the time-continuous solutions is shown by passing the time-step size to zero. Uniqueness is proven by a contraction argument, and blow-up of solutions is investigated for homogeneous Neumann conditions. Numerical results validate the theoretical predictions. They also reveal a rich source of pattern formations exemplified by biofilm and skin-patterning cases.

Existence of blow-up solutions to a chemotaxis system with logistic term

Masaaki Mizukami

In the study of chemotaxis-growth systems, existence of blow-up solutions is known to be a challenging problem. In the previous results, the results on existence of blow-up solution are only for some simplified problem, and there do not seem to be any results concerning fully parabolic systems. The purpose of this work is to show existence of blow-up solutions and their properties. This is a joint work with Dr. Mario Fuest (Leibniz University Hannover) and Prof. Johannes Lankeit (Leibniz University Hannover).

A zoo of dynamical patterns: Uncovering response complexity of small gene regulatory circuits

Ruben Perez-Carrasco

Small gene regulatory networks are often viewed as simple motifs whose behaviour is fixed by their wiring. In this talk, I will argue that this picture is far too limited. Even minimal circuits can generate a rich zoo of dynamical patterns, including long-lived transients, hybrid switching–oscillatory behaviour, critical slowing down, and strong history dependence.

Using concrete examples, I will show how this complexity arises and how it can be systematically uncovered. A minimal three-gene AC/DC circuit, for instance, can realise more than forty distinct bifurcation diagrams, allowing oscillations, multistability, and hysteresis to coexist within a single topology. In contrast, mushroom bifurcations in even simpler circuits reveal how extrinsic noise can be exploited to stabilise decision timing without sacrificing precision. Bayesian inference provides a unifying framework to disentangle these behaviours and identify the dynamical rules governing timing, reversibility, and robustness.

Together, these results highlight small gene regulatory networks as powerful generators of flexible, tunable behaviour, with implications for cell-fate decisions, synthetic circuit design, and how we interpret regulatory dynamics in living systems.

Deriving subdiffusion equations

Benoit Perthame

It is widely used that super-diffusions can be derived from jump processes. Eventhough Caputo derivatives are widely used, the derivation of sub-diffusion equations is not very much studied mathematically.

After some motivations, we show the equations for sub-diffusions and derive them from an age structured equations with small jumps. The methodology allows us to obtain the same derivation from a wider class of waiting time processes.

This is a work with Min Tang (SJTU).

Inferring rules of tissue organisation with neural cellular automata

Linus Schumacher

The dynamics of a biological tissue arises from the behaviour of its constituent cells and their interactions. Traditionally, in mathematical biology we have built models by combining individual components and interactions into, for example, differential equations or individual-based simulators, and adding further complications as required to describe experimental observations. In this talk I will offer a complementary approach in which we attempt to statistically learn cell-cell interaction models directly from data in interpretable ways. This approach builds on familiar concepts of cellular automata but makes the model differentiable and parameterises the update rule with a neural network, but with physically-informed constraints built in that leave open a path towards interpretation. We have tested this Neural Cellular Automata framework on well established reaction-diffusion models and are now applying it to learn the rules of multicellular pattern formation in vitro models of embryo development.

Starvation-driven cell patterning: integrating lab experiments and mathematical modelling

Cinzia Soresina

We present a reaction–diffusion model describing the interactions among cells, nutrients, and growth factors, aimed at capturing the emergence of starvation-driven cell pattern formation, a phenomenon recently observed in laboratory experiments under nutrient-limited growth conditions. Experiments and modelling were developed in parallel, enabling progressively more targeted experimental design while enhancing the biological realism of the model. This interdisciplinary feedback loop led to the formulation of new hypotheses and enabled the estimation of several key parameters. Numerical simulations show that the model reproduces pattern formation in both one- and two-dimensional spatial domains. To provide theoretical support for these findings, we performed a Turing instability analysis to investigate the potential for diffusion-driven instability. The analysis indicates that the observed patterns are not driven by chemotaxis; rather, they arise naturally under starvation conditions and display structural similarities to the Klausmeier model for vegetation pattern formation in semi-arid environments, suggesting the robustness of the underlying mechanism across biological scales.

Joint work with
Anna Bernardi-D'Agostini (CNR IMATI, Milano, Italy),
Giovanni Cappello (LIPhy, CNRS and Université Grenoble Alpes),
Simone Pezzuto (University of Trento, Italy)

Collective cell migration during gastrulation in the chick embryo

Kees Weijer

We investigate the mechanisms that control and integrate the behaviours of rapidly increasing numbers of cells that generate and shape the primitive streak in the chick embryo. We address this question using a combination of lightsheet microscope in combination with novel transgenic chick lines that allow the detailed visualisation and quantitative characterisation of up to several hundred thousand cells in the early chick embryo. A dedicated image processing and analysis pipeline allows linking individual cell behaviours to largescale tissue flows under conditions of normal and experimentally perturbed development. These data have led to the formulation of a mechano-chemical hypothesis to explain the coordination of critical cell behaviours into the large-scale tissue flows underlying the formation of the primitive streak in the early chick embryo. We are currently testing this hypothesis through a combination of detailed biophysical modelling and further experiments.

Modelling cell migration to understand cancer invasion

Luigi Preziosi

The talk will focus on modelling cell migration in confined environments and in particular on how to describe the presence of thin structures such as base membranes, cell lining and vessel walls. The method to identify the proper interface conditions is discussed for a cell population also in the case in which it is characterized by heterogeneous phenotypic characteristics regarding cell motility. In this latter case, the way in which the interface conditions depend on the phenotype is found, determining the ability to cross the thin structure. In this way the membrane can act as a selector of more invasive phenotypes with respect to more residential phenotypes.

From kinetic models to diffusion equations

Havva Yoldas

I will talk about a class of nonlinear BGK-type kinetic equations with density dependent collision rates that arise as simplified models of interacting particle systems and closely related to run and tumble equations. We establish global well-posedness and show exponential convergence to equilibrium using classical hypocoercivity methods adapted to the nonlinear setting. From the kinetic model under the diffusive scaling, we rigorously derive nonlinear diffusion equations including the porous medium and fast diffusion equations. I will also report on how we extend this result to derive anisotropic, heterogeneous diffusion equation from the corresponding kinetic model. The talk is based on joint works with Josephine Evans (Warwick), Daniel Morris (TU Delft) and Hoyoun Kim (KAUST).