Mathematical Modelling of Pattern Formation in Biological Systems

15 September 2025

Zeeman Building, University of Warwick

A one-day workshop to discuss the latest advances in the modelling of pattern formation phenomena in biology

Time	Activity	Title
09:45 - 10:40	Arrival and coffee	
10:40 - 10:45	Welcome	
10:45 - 11:30	Jonathan Sherratt (Heriot-Watt)	Understanding Spatiotemporal Patterns Using Absolute Stability
11:30 - 12:15	Valeria Giunta (Swansea)	Self-organisation in nature: patterns and bifurcations in nonlocal advection-diffusion models
12:15 - 13:45	Lunch	
13:45 - 14:05	Markus Kirkilionis (Warwick)	Stochastic Pattern Formation
14:05 - 14:25	Magnus Haughey (QMUL)	Extrachromosomal DNA driven oncogene spatial heterogeneity and evolution in glioblastoma
14:25 - 14:45	Mohit Dalwadi (Oxford)	Emergent and intrinsic dynamic robustness in pattern formation
14:45 - 15:15	Coffee break	
15:15 - 16:00	Philip Maini (Oxford)	Modelling collective cell motion in development
16:00 - 16:45	Lukas Eigentler (Warwick)	Can we predict wavelength changes of patterned ecosystems?
16:45 - 17:00	Closing	
17:00 - late	Social dinner	

All talks in Zeeman B3.03

Funders:

- London Mathematical Society Celebrating New Appointments - Scheme 9
- Mathematics Research Centre, University of Warwick

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Abstracts

Plenary talks:

Jonathan Sherratt

Heriot-Watt University

Title: Understanding Spatiotemporal Patterns Using Absolute Stability

Abstract: TBC

Valeria Giunta

Swansea University

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

Abstract: Understanding the mechanisms behind 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 real-world phenomena more faithfully, nonlocal models also display richer dynamical behaviours, 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 behaviours, including segregation, aggregation, time-periodic dynamics, and chase-and-run phenomena. I will also discuss parameter regimes with 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 behaviours in nature.

Philip Maini

University of Oxford

Title: Modelling collective cell motion in development

Abstract: TBC

Lukas Eigentler

University of Warwick

Title: Can we predict wavelength changes of banded vegetation patterns?

Abstract: Banded vegetation patterns are a common feature in drylands. The ability to self-organise into alternating stripes of vegetated and bare soil areas is thought to be a resilience mechanism that prevents catastrophic tipping of dryland plant ecosystems. Several mathematical models exist that describe the dynamics of dryland vegetation bands as periodic travelling waves (PTWs). Models predict that if environmental stress increases, dryland vegetation bands undergo cascades of wavelength changes that progressively increase the characteristic distances between stripes before a transition to desert. It is thus of crucial importance to understand when (i.e., at what parameter values) and how (i.e., to which new wavelength) PTW wavelength changes occur.

In this talk, I show that the traditionally used method of using Busse balloon boundaries to predict parameter values at which wavelength changes occur is often insufficient. Instead, I show that model solutions enter a (potentially long) transient after crossing a stability boundary and present a method to estimate the order of magnitude of the length of this transient. I further review our current knowledge of PTW wavelength selection, a problem that remains unsolved except for special cases, and will present new numerical evidence of selection principles in the context of dryland vegetation patterns.

Contributed talks

Markus Kirkilionis

University of Warwick

Title: Stochastic Pattern Formation

Abstract: I will give a multi-scale particle-based approach to pattern formation, taking no continuum limits. Particles in a biological setting can be molecules or cells, making the multi-scale approach clearly necessary. On a molecular level I will mainly discuss spatial Gillespie algorithms, on the cellular levels modern numerical methods for structured population models, i.e. we will attach internal state spaces as well as the external spatial states to cell populations.

Magnus Haughey

Queen Mary University of London

Title: Extrachromosomal DNA driven oncogene spatial heterogeneity and evolution in glioblastoma

Abstract: Extrachromosomal DNA (ecDNA) oncogene amplification is associated with treatment resistance and shorter survival in cancer. At present, the spatial dynamics of ecDNA, and the impact on tumor evolutionary trajectories, are not well understood. Here, we investigate ecDNA spatial-temporal evolution by integrating computational modeling with samples from 94 treatment-naive human *IDH*-wildtype glioblastoma patients. We developed a spatial-temporal computational model of ecDNA positive tumours that integrates whole-genome sequencing, multi-region DNA FISH, and nascent RNAscope, to provide unique insight into the spatial dynamics of ecDNA evolution. Random segregation in combination with ecDNA-conferred fitness advantages induce predictable spatial patterns of cell-to-cell ecDNA copy number variation that are highly dependent on ecDNA oncogenic makeup. *EGFR*-ecDNAs often reach high mean copy number (mean of 50 copies per tumour cell), confer strong fitness advantages and do not co-amplify other oncogenes on the same ecDNA particles. In contrast, *PDGFRA*-ecDNAs reach lower mean copy number (mean of 15 copies per cell), confer weaker fitness advantages and frequently co-amplify other oncogenes on the same ecDNA. Evolutionary modeling of*EGFR*-ecDNAs suggest ecDNA accumulation prior to clonal expansion, which we validate biologically in *MYC*-ecDNA induced mice. *EGFR* structural variants occur exclusively on ecDNA, arise from and are intermixed with wild-type *EGFR*-ecDNAs. Modeling suggests wild-type and variant *EGFR*-ecDNAs often accumulate before clonal expansion, even in patients co-amplifying multiple ecDNA species. In the first systematic study of the spatial dynamics of ecDNA, our results suggest a potential time window in which early ecDNA detection may facilitate more effective intervention.

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Mohit Dalwadi

University of Oxford

Title: Emergent and intrinsic dynamic robustness in pattern formation

Abstract: In this talk, we investigate an overarching question in developmental biology: how are cells able to decode spatio-temporally varying signals into functionally robust patterns in the presence of confounding effects caused by unpredictable or heterogeneous environments? By considering the effect of general spatio-temporal input variations on the outputs of pattern forming systems, we use multiscale mathematics to show how general biological pattern forming systems can generate non-standard dynamic robustness for 'free' over physiologically relevant timescales. This involves developing methods to deal with rate-induced bifurcations ("R-tipping") in PDEs. As such, this work also has applications in pattern formation more generally.

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