

HKU Workshop on Mathematical Biology

Date: 15 June, 2026

Venue: Rm 210, Run Run Shaw Building, HKU

9:50--10:00	Opening
10:00--11:00	<p>Prof. Jiandong Huang (HKU)</p> <p><i>Sequential Symmetry Breaking in Expanding Cell Populations: A Synthetic Biology Approach to Periodic Stripe Formation</i></p>
11:00--11:20	Coffee break
11:20--12:20	<p>Prof. Zhiwen Zhang (HKU)</p> <p><i>Stochastic Interacting Particle Field Methods in the Computation of Chemotaxis and Haptotaxis PDEs</i></p>
12:30--14:30	Lunch
14:30--15:30	<p>Prof. King-Yeung Lam (Ohio State U)</p> <p><i>When Distant Regions Drive Invasion: Nonlocal Pulling in Heterogeneous Media</i></p>
15:30--15:50	Coffee break
15:50--16:50	<p>Prof. Zhian Wang (HK PolyU)</p> <p><i>Boundary layer problem for the Keller-Segel Model</i></p>
16:55--17:55	<p>Dr. Lingyu Li (HKU)</p> <p><i>From Gene Regulatory Dynamics to Spatial Cellular Phenotypes: Learning and Modeling Across Scales</i></p>
18:00--18:30	<p>Mr. Chen Yang (HKU)</p> <p><i>On the Cucker-Smale Model</i></p>

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Jiandong Huang (HKU LKS Faculty of Medicine and School of Biomedical Sciences)

Title: Sequential Symmetry Breaking in Expanding Cell Populations: A Synthetic Biology Approach to Periodic Stripe Formation

Abstract: Periodic pattern formation is a fundamental feature of biological morphogenesis, yet the underlying regulatory networks often obscure the core physical principles at play. In this work, we present a synthetic gene circuit that couples local cell density to motility, providing a minimal model for the autonomous generation of sequential stripe patterns. By engineering an expanding population of cells where motility is suppressed at high densities, we demonstrate the emergence of crisp, periodic spatial structures in a growing domain.

From a mathematical perspective, we analyse this system as a density-dependent reaction-diffusion process. Our theoretical framework reveals that the stripes arise from a recurring instability at the leading edge of a traveling-wave front. Rather than relying on a global pacemaker or a fixed morphogen gradient, the system utilizes the non-linear coupling between growth and transport to drive a sequence of aggregation events. We demonstrate that the spatial frequency of these stripes can be precisely tuned by varying the kinetic parameters of a single promoter, consistent with our model's bifurcation analysis. These results illustrate how synthetic systems can serve as tractable experimental platforms for validating theoretical models of spatially extended systems and provide a potent route for generating regular structures through simplified motility control.

King-Yeung Lam (The Ohio State University)

Title: When Distant Regions Drive Invasion: Nonlocal Pulling in Heterogeneous Media

Abstract: Propagation in heterogeneous and shifting environments is a central problem in ecology and reaction–diffusion theory. Motivated by classical conjectures of Shigesada–Kawasaki and recent works on shifting habitats, we study invasion phenomena in competition systems and their reduction to scalar KPP-type models.

We develop a Hamilton–Jacobi framework based on viscosity solutions to characterize spreading speeds and front dynamics. In particular, we derive a variational formula for the propagation speed and identify regimes where invasion exhibits nonlocal pulling, whereby the spreading speed is determined by distant favorable regions rather than local conditions near the invasion front.

We further extend this framework to non-monotone environments, where the limiting problem may have non-unique solutions. This issue is resolved by introducing appropriate junction conditions and flux-limited solutions in the sense of Imbert–Monneau.

This project is a joint work with Gregoire Nadin, Chang-Hong Wu and Xiao Yu.

Lingyu Li (HKU School of Biomedical Sciences)

Title: From Gene Regulatory Dynamics to Spatial Cellular Phenotypes: Learning and Modeling Across Scales

Abstract: Understanding cellular behavior requires linking gene regulatory mechanisms, dynamic cell-state transitions, and spatial localization within tissues. In this talk, I will present three projects that bridge these scales through dynamical and data-driven modeling. First, **LogBTF** infers gene regulatory network (GRN) from single-cell RNA-seq data by integrating Boolean network (BN) with elastic net regression, enabling interpretable regulatory logic learning. Second, **CellLand** compares BN- and diffusion-based models for analyzing cellular dynamics on energy landscape, highlighting how model choice and network structure influence attractor detection. Finally, **FineST** integrates spatial transcriptomics (ST) with histology images via contrastive learning to enable nuclei-resolved gene expression imputation and ligand-receptor interaction analysis, overcoming the resolution limitations of current 10x Visium ST platforms for studying cell-cell communication. Together, these works provide a unified perspective connecting regulatory logic, dynamical landscape, and spatial phenotype for studying complex biological system.

This talk is based on joint work with Profs. Wai-Ki Ching and Yuanhua Huang.

Zhian Wang (The Hong Kong Polytechnic University)

Title: Boundary layer problem for the Keller-Segel Model

Abstract: In this talk, we shall discuss the boundary layer problem of the singular Keller-Segel model with physical boundary conditions in any dimensions. First, we obtain the existence and uniqueness of boundary-layer solution to the steady-state problem and identify the boundary-layer profile and thickness near the boundary. Then we find the asymptotic expansion of boundary-layer profile in terms of the radius for the radially symmetric domain, which can assert how the boundary curvature affects the boundary-layer thickness. Finally, we establish the nonlinear stability of the unique boundary-layer steady state solution with exponential convergence rate for the case of radially symmetric domain, we prove that the model is uniformly persistent and admits a positive (coexistence) steady state.

Chen Yang (HKU)

Title: On the Cucker-Smale Model

Abstract: Many biological systems such as the flocking of birds, the schooling of fish, and the swarming of insects are captured by the famous Cucker-Smale model, in which a large population aligns its velocities through pairwise interactions. A natural question is how an external agent can drive the system toward consensus, giving rise to optimal control problems whose numerical solution is hampered by the $O(N^2)$ cost of pairwise interactions. The Cucker-Smale model is numerically challenging, especially when N is large. In this talk, I will present an efficient algorithm for solving large-scale cases of the Cucker-Smale model, prove its convergence, and estimate its convergence rate. This talk is based on joint work with Profs. Xiaoming Yuan, Yongcun Song, and Hangrui Yue.

Zhiwen Zhang (HKU)

Title: Stochastic Interacting Particle Field Methods in the Computation of Chemotaxis and Haptotaxis PDEs

Abstract: In this talk, I will present the latest advances in stochastic interacting particle field (SIPF) methods. This methodology originates from the Lagrangian framework and is applied to compute the asymptotic behavior of PDEs, including effective diffusivities and KPP front speeds. First, I will illustrate the SIPF methods for solving parabolic-parabolic Keller–Segel chemotaxis equations. Then, I will extend the SIPF framework to solve haptotaxis equations. Additionally, I will introduce the DeepParticle method for learning and generating aggregation patterns in Keller–Segel chemotaxis systems, and elaborate on the connection between these developments and generative modeling.