From single to collective cell migration: A geometric multi-physics bulk-surface PDE approach
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An Asymptotic Analysis of Spike Self-Replication and Spike Nucleation of Reaction-Diffusion Patterns on Growing 1-D Domains

Pattern formation on growing domains is one of the key issues in developmental biology, where domain growth has been shown to generate robust patterns under Turing instability. In this work, we investigate the mechanisms responsible for generating new spikes on a growing domain within the semi-strong interaction regime, focusing on three classical reaction-diffusion models: the Schnakenberg, Brusselator, and Gierer-Meinhardt (GM) systems. Our analysis identifies two distinct mechanisms of spike generation as the domain length increases. The first mechanism is spike self-replication, in which individual spikes split into two, effectively doubling the number of spikes. The second mechanism is spike nucleation, where new spikes emerge from a quiescent background via a saddle-node bifurcation of spike equilibria. Critical stability thresholds for these processes are derived, and global bifurcation diagrams are computed using the bifurcation software pde2path. These results yield a phase diagram in parameter space, outlining the distinct dynamical behaviors that can occur.

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Travelling waves and wave pinning (polarity): Switching between random and directional cell motility

We derive a simple model of actin waves consisting of three partial differential equations (PDEs) for active and inactive GTPase promoting growth of filamentous actin (F-actin, F). The F-actin feeds back to inactivate the GTPase at rate sF, where $s \geq 0$ is a "negative feedback" parameter. In contrast to previous models for actin waves, the simplicity of this model and its geometry (1D periodic cell perimeter) permits a local and global PDE bifurcation analysis. Based on a combination of continuation methods, linear stability analysis, and PDE simulations, we explore the existence, stability, interactions, and transitions between homogeneous steady states (resting cells), wave-pinning (polar cells), and travelling waves (cells with ruffling protrusions). We show that the value of s and the size of the cell can affect the existence, coexistence, and stability of the patterns, as well as the dominance of one or another cell state. Implications to motile cells are discussed.

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Symmetry-Breaking in Compartmental-Reaction Diffusion Systems with Comparable Diffusivities

Since Alan Turing's pioneering publication on morphogenetic pattern formation obtained with reaction-diffusion (RD) systems, it has been the prevailing belief that two-component reaction diffusion systems have to include a fast diffusing inhibiting component (inhibitor) and a much slower diffusing activating component (activator) in order to break symmetry from a uniform steady-state. This time-scale separation is often unbiological for cell signal transduction pathways. We modify the traditional RD paradigm by considering nonlinear reaction kinetics only inside compartments (cells) with reactive boundary conditions to the extra-compartmental space which diffusively couples the compartments via two (chemical) species. The construction of a nonlinear algebraic system for all existing steady-states, or quasi-steady-states, enables us to derive a globally coupled matrix eigenvalue problem for the growth rates of eigenperturbations from the symmetric steady-state in 1-D, 2-D, and 3-D. We show that the membrane reaction rate ratio of inhibitor rate to activator rate is a key bifurcation parameter leading to robust symmetry-breaking of the compartments. Illustrated with Gierer-Meinhardt, FitzHugh-Nagumo and Rauch-Millonas intra-compartmental kinetics, our compartmental-reaction diffusion system does not require diffusion of inhibitor and activator on vastly different time scales. Our results reveal a possible simple mechanism of the ubiquitous biological steady and oscillatory cell specialization observed in nature. (This is joint work with Michael J. Ward.)

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A Closest Point Method for PDEs on Manifolds with Interior Boundary Conditions for Geometry Processing

Solving partial differential equations (PDEs) on manifolds is fundamental to many geometry processing tasks, such as diffusion curves on surfaces, geodesic computations, tangent vector field design, and reaction-diffusion textures. These PDEs often involve boundary conditions prescribed at points or curves on the manifold's interior or along the geometric boundary of an open manifold.

We present a robust extension of the closest point method (CPM) for handling interior boundary conditions. The CPM reformulates the manifold PDE as a volumetric PDE in the Cartesian embedding space, requiring only the closest point representation of the manifold. This approach inherently supports open or closed manifolds, orientable or not, and of any codimension. To address interior boundary conditions, we derive a technique that implicitly partitions the embedding space

across interior boundaries, modifying finite difference and interpolation stencils to respect these partitions while preserving second-order accuracy.

Our method includes an efficient sparse-grid implementation and scalable numerical solver capable of handling tens of millions of degrees of freedom, enabling solutions on complex manifolds. We demonstrate the convergence and accuracy of our approach using model PDEs and showcase applications to a range of geometry processing problems.

This is joint work with Nathan King (University of Waterloo), Haozhe Su (Lightspeed Studios), Mridul Aanjaneya (Rutgers University), and Christopher Batty (University of Waterloo).

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