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Geometric effects in bulk-surface dynamics

Reaction-diffusion equations with nonlocal constraints naturally arise as limiting cases of mathematical models of intracellular signaling. Among the interesting behaviors of these models, much has been made of their 'geometry-sensing' properties: the strong sensitivity of steady-state solutions to domain geometry is widely seen as illustrative of how a cell establishes an internal coordinate axis. In this talk, I describe recent efforts to formally clarify this geometry dependence through careful study of the long-time behavior of a popular model of biochemical symmetry breaking. Using the tools of formal asymptotics, calculus of variations, and a new fast solver for surface-bound PDEs, we study the formation and motion of interfaces on a curved domain across three dynamical timescales. Our results allow us to construct several analytical steady-state solutions that serve as counter-examples to received wisdom regarding the geometry-dependence of this class of model.