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Analysis of reaction-diffusion PDE models for localized pattern formation in cells

We study a system of reaction-diffusion PDEs, which models the dynamics of small GTPases, a family of signalling proteins. The system is composed of 3 fully coupled quantities, a fast-diffusing active protein, a slow-diffusing inactive form (with nonlinear interconversion term) and slow negative feedback from a and a non-diffusive quantity (F-actin). We explore the system's bifurcation behaviors using local perturbation analysis (a shortcut to probe the growth/decay of localized spikes), and look for spatio-temporal patterns using numerical simulations. The results have biological applications toward understanding cell motility phenomena.