A coupled bulk-surface model for cell polarisation

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In this talk we will present a model describing the GTPase cycle between its active membrane-bound and inactive cytosolic form. Rho GTPases are key players in cell polarisation, which is required in several cellular activities, such as migration. The intricate reactions network of such proteins can lead to very complex mathematical models that are hard to analyse. Here, we present a simple basic interaction model of the same Rho GTPase protein in three-dimensional geometries, taking into account the different spatial compartmentalisation through the maturing theory of coupled bulk-surface semilinear parabolic equations.

In this work the bulk-surface model is a substantial extension of the wave pinning model first proposed by Mori et al (2008, Biophys J.). To understand the theoretical behavior of the model, we carry out detailed asymptotic and local perturbation analysis, which helps to find parameter regions in which polarisation occurs. The geometry effects are naturally taken into account and with the emergent property that polarisation regions become bigger when a cell increases its surface. This last result is particularly meaningful since surface increase typical occurs during cell migration. To provide validation and confirmation of the theoretical results, we proposed and implemented a corresponding bulk-surface finite element method which we use to solve the system of coupled bulk-surface reaction-diffusion equations. Simulation results are shown over simple and more complex three-dimensional geometries and the pattern generation mechanism is in line with theoretical predictions.