Uduak George
Department of Mathematics, University of Sussex, Brighton, BN1 9QH, UK
e-mail: ude20@sussex.ac.uk
Angélique Stéphanou
IN3S, Faculté de Médecine de Grenoble, 38706 La Tronche cedex, France
e-mail: angelique.stephanou@imag.fr
Anotida Madzvamuse
Department of Mathematics, University of Sussex, Brighton, BN1 9QH, UK
e-mail: a.madzvamuse@sussex.ac.uk

Mathematical and numerical modeling of cell membrane deformations as a consequence of actin dynamics

Actin is a molecule that exists in two different forms which can be monomeric as globular actin (G-actin) or assembled into the polar filamentous form (F-actin). It resides in the cell cytoskeleton and plays an important role in controlling cell motility and maintaining cell shape [3]. Cell motility consist of numerous highly coordinated events which involve a combination of chemical kinetics and physical forces, transport and movements of a polymer protein network interacting with a vast number of other proteins. These events can be treated mathematically by combining models of continuum mechanics and biochemical kinetics [2]. These models have proven to be useful for decoding cell motility processes [1]. The model we consider is a system that consists of a force balance equation and a reaction-diffusion equation describing the mechanical properties and biochemical kinetic of actin respectively. We solve the model equations by use of the moving grid finite element method whose key advantage is in its ability to treat moving boundary problems with pronounced curvature and is very beneficial in the accurate representation and approximation of the shape of the cell. Assuming slow domain evolution we validate the numerical results by comparing the finite element solutions to those predicted by linear stability theory. We show that the numerical scheme computes spatially inhomogeneous steady state solutions which coincides with those predicted by linear stability theory close to bifurcation points [4].
Far away from instability, we show that this model is able to describe the intracellular actin dynamics and the resulting shapes and movements of the membrane. In particular, by varying the pressure coefficient and the measure of the contractile tonicity parameter, the model behaviour gives uniform expansions, contractions and irregular deformations of the cell membrane with the cell centre staying mostly unchanged in the majority of the cases considered. The model also allow us to compare the actin distribution at the vicinity where large deformations occur and the results we obtain are found to be consistent with those observed experimentally.

References

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