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Exploring the spatial tissue environment: non-local modelling, applications, numerical challenges

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A partial differential equation (PDE) model of the spatio-temporal evolution of cell populations which interact in a spatially nonlocal fashion with and between themselves has been introduced in the landmark paper [1] by Armstrong, Painter, and Sherratt in 2006. Since then, their basic approach has been incorporated in numerous biomedical models and, along this way, it has been refined, extended, analysed, and implemented. The range of applications, to name a few, includes adhesion-driven pattern formation of cellular populations, tumour invasion of host tissue, wound healing dynamics, and neural crest cell dispersal in developmental biology.

In this presentation, we start from the basic model [1] and its mathematical properties, like mass conservation and non-negativity, and extend it to include volume filling terms as well as attracting and repelling interactions. A Turing-like analysis then sheds light on parameter ranges which allow for pattern formation starting from spatially perturbed homogeneous steady states. The consideration of cross-diffusion within such models is presented and gives rise to a further qualitative improvement of the model. The nonlocal nature of the model also necessitates a look at the formulation of suitable boundary conditions.

Spatially nonlocal terms in a PDE model constitute a computational challenge for model simulation, in particular for spatial dimensions higher than one. This challenge arises because the matrices representing the approximation of nonlocal terms are not sparse and thus, in general, computationally expensive. Here we present a finite volume framework which makes use of Fast Fourier Transform techniques to allow for an efficient treatment of these terms under some suitable side conditions. We also touch upon the issue of non-negativity preservation which is ensured by the scheme presented.

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References

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