A flux-corrected finite element method for chemotaxis problems

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Chemotaxis, an oriented movement towards or away from regions of higher concentrations of certain chemicals, plays a vitally important role in the evolution of many living organisms. The chemotactical response gives numerous creatures, ranging from bacteria and protozoa to tissue cells, a chance to find more favourable locations in their environments. This feature improves their ability to search for food, detect the location of mates or escape danger. Chemotaxis is encountered in many medical and biological applications, including bacteria/cells aggregation and pattern formation processes, tumour growth, etc.

A representative class of chemotaxis models based on advection-reaction-diffusion equations can be written as follows:

$$u_t = \nabla \cdot (D(u)\nabla u - A(u)\, B(c)\, C(\nabla c)) + f(u), \tag{1}$$

$$c_t = d\Delta c - s(u)\, c + g(u)\, u \qquad \text{in} \quad \Omega, \tag{2}$$

where $u(\boldsymbol{x}, t)$ denotes the cell density and $c(\boldsymbol{x}, t)$ is the chemoattractant concentration. The functional dependence of the involved coefficients on u and c defines a particular model.

It is known that for some parameter setting the pure Galerkin scheme may give rise to nonphysical oscillations in the cell density. Therefore without proper stabilization techniques the corresponding numerical simulation is often not possible. We propose an implicit flux-corrected transport (FCT) algorithm for the general form of chemotaxis models (1)–(2). Coefficients of the Galerkin finite element discretization are adjusted in such a way as to guarantee mass conservation and keep the cell density nonnegative. The numerical behaviour of the proposed high-resolution scheme is tested on the blow-up problem for a minimal chemotaxis model with singularities. It is also shown that the results for an *Escherichia coli* chemotaxis model are in good agreement with experimental data reported in the literature. The certain generalization of the considered chemotaxis model makes it possible to extend the proposed algorithm to more complex real-life problems in medicine and biology for two- and three-dimensional domains.

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