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Boundary integral discretization of the cell-to-cell bidomain model of cardiac electrophysiology

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At cellular scale, the cardiac tissue is composed by tightly coupled myocytes, embedded into an extracellular matrix and surrounded by other cells. The cell-to-cell bidomain model is a system of partial differential equations describing the spatio-temporal evolution of the electric potential within each cell and in the extracellular space. The model accounts for the cellular membrane dynamics and the cell-to-cell coupling at fine scale.

From a numerical perspective, the cell-to-cell bidomain model poses a number of difficulties: the cellular subdomains are separated by a sharp interface, the cellular membrane; the temporal dynamics, dictated by the membrane ionic model, is confined on such interfaces; and the membrane dynamics is typically very stiff in time. Therefore, the electric potential is globally discontinuous and the PDE is degenerate in time, due to the elliptic constraints.

In this work, we recast the problem to a boundary integral formulation. The main advantage it that in this formulation all equations are confined on the cellular membrane, on which the temporal dynamics take place. We recover a reaction-diffusion model with a non-local diffusion operation stemming from the boundary integral formulation. The equation closely resembles the monodomain equation, routinely solved in the cardiac electrophysiology community. We analyze the local well-posedness of the reaction-diffusion system. Furthermore, we present some numerical experiments to compare the boundary element formulation to a more standard finite element approach. We also consider the feasibility of the approach towards the application to large scale models. Finally, we discuss various time discretization schemes, e.g., implicit-explicit schemes and Rush-Larsen scheme, and propose new ones, based on stabilized Runge-Kutta methods.

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