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A matrix-free solver for high-order discretization in cardiac electrophysiology

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Numerical models for cardiac electrophysiology have assumed a key role to investigate and better understand the whole cardiac function and to provide answers to clinical problems [3]. In this work we tackle the monodomain equation endowed with suitable ionic models [2], which describe the space and time evolution of the trans-membrane potential and of chemical species in myocardial cells; the solution to such problem exhibits sharp propagating wave fronts, which warrants for the investigation of high-order discretization techniques such as in the framework of *hp*-FEM or spectral elements with numerical integration (SEM-NI) [1]. We compare different numerical schemes and computational techniques on a set of benchmark problems, from idealized toy models to realistic simulations: we show that the SEM-NI method is more efficient due to a better conditioning number when fine time-discretizations are employed; then we propose a matrix-free solver, whose computational costs and memory footprint are proved to be overall more convenient than a standard *assemble-and-solve* finite element code; finally, we compare the two naivest approaches for increasing the accuracy of simulation results, *i.e.* choosing a smaller mesh size h or higher polynomial degree p, deducing that the latter leads to a more beneficial accuracy/cost ratio. The aforementioned methods have been implemented in `life`$^{\text{x}}$ (`https://lifex.gitlab.io/`), a new `C++` high-performance simulator of multi-scale and multi-physics problems. This work has been funded with the ERC Advanced Grant iHEART "An Integrated Heart Model for the simulation of the cardiac function", 2017-2022, P.I. Prof. A. Quarteroni (ERC-2016-ADG, project ID: 740132).

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