Title: A partitioned solver for Purkinje-muscle coupling in cardiac electrophysiology

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We present a computational methodology for simulating cardiac electrophysiology with an explicit representation of the Purkinje network. The method is based on coupling a three-dimensional eikonal-diffusion model in the myocardium to a one-dimensional eikonal model in the network, and allows to reproduce antidromic muscle-Purkinje reentries by means of iterations between the two solvers, thus leading to a partitioned solver for the 3D-1D coupled problem. The use of the eikonal-diffusion model in this context requires the introduction of a dedicated solver, based on a discrete pseudo-time formulation that can distinguish between active and inactive stimuli in correspondence of the Purkinje-muscle junctions. We present the results of simulations in a realistic model of the human ventricles, under healthy conditions as well as in pathological scenarios including the Wolff-Parkinson-White syndrome, a bundle branch block, and a bundle branch block treated with CRT. These results demonstrate how the proposed framework can correctly reproduce both orthodromic and antidromic propagation, and allow the identification of regions where antidromic reentries occur.