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A PRACTICAL ALGORITHM TO BUILD GEOMETRIC MODELS OF CARDIAC MUSCLE STRUCTURE

Mark Potse[1], Luca Cirrottola[2] and Algiane Froehly[3]

[1] IHU Liryc, Université de Bordeaux, Campus Xavier-Arnozan, Avenue du Haut-Lévêque, 33600 Pessac, France, mark@potse.nl, https://www.potse.nl
[2] INRIA, Univ. Bordeaux, CNRS, Bordeaux INP, IMB, UMR 5251, 200 Avenue de la Vieille Tour, 33405 Talence cedex, France, luca.cirrottola@inria.fr, https://lcirrottola.github.io/
[3] Service d'expérimentation et de développement, Inria Bordeaux – Sud-Ouest, Pau, France, algiane.froehly@inria.fr, https://www.linkedin.com/in/algiane-froehly-3a247987/

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Cardiac muscle tissue has a unique, network-like structure, consisting of elongated cells that are mechanically and electrically connected to several neighbours. Large-scale three-dimensional models of this structure are needed for simulations of the electrophysiology and mechanics of the heart. Since reconstructions from imaging data are limited to a small number of cells we developed an algorithm to produce such models artificially. We define the outer membranes of the muscle cells in terms of an implicit surface. This implicit surface is expressed on a tailored unstructured multi-domain mesh which allows to define multiple cells and boundaries between the connected cells.

The algorithm first creates a random network of cell centers, observing angle and distance criteria inferred from real tissue. The space around the network edges is assigned to the cellular domains based on the nearest half-edge. The network is then immersed in a regular tetrahedral mesh which is refined to fit the domain boundaries and to offer sufficient density around the cell membrane. Successive refinement steps resolve the edges and corners where multiple cell domains meet. When necessary, the refinements are alternated with basic mesh improvement operations to maintain an acceptable mesh quality. On the refined mesh a level-set function is expressed that defines the cell membrane, respecting a minimum distance between cells and a maximum cell diameter. The remeshing code `Mmg3d` is then used to discretize the level set while retaining the domains, and to improve the quality of the final mesh.

A serial implementation of the algorithm was able to produce meshes of a few hundreds of cells in 15 minutes. Discretization of the level set worked correctly. However, the resulting meshes presented difficulties for the remesher. We hypothesize that these complex meshes trigger bugs that rarely pose a problem in simpler cases, and we are currently investigating these issues. It was still possible, however, to correctly mesh a network of a handful of cells that was designed to be replicated by successive mirroring. This allowed us to build models of upto $1\,\mathrm{cm}^3$ of tissue (11 million cells and 370 billion tetrahedra) that now serve in performance tests of a large-scale simulation code.