INTEGRATION OF DIFFERENT CARDIAC ELECTROPHYSIOLOGICAL MODELS INTO A SINGLE SIMULATION PIPELINE

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Clinical translation of computational models of the heart has been hampered by the absence of complete and rigorous technical and clinical validation, as well as benchmarking of the developed tools. To address this issue, a dataset containing the cardiac anatomy and fibre orientations from magnetic resonance images (MRI), as well as epicardial transmembrane potentials from optical mapping acquired on *ex-vivo* porcine hearts, have previously been made available to the community. Image processing techniques were developed to integrate MRI images with electrical information. Different models were tested and compared with the integrated data [1], including: i) a new methodology to customize and regularize heart shape and myocardial fibre orientation to predict activation waves in these personalized meshes with generic conduction parameters; ii) a statistical model-constrained framework to produce *maximum a posteriori* (MAP) estimation of the 3D distribution of transmembrane potential; iii) a personalized simplified reaction-diffusion 3D electrophysiological model; iv) a personalized fast conduction Purkinje system with a simple Eikonal-based electrophysiological model.

The main goal of this work is to present initial developments of an integrated system that combines these different model and personalization strategies. The proposed model pipeline propagates personalized material parameters extracted from images and signals and boundary conditions derived from simple models to customize more biophysically detailed models. The first stage is the MAP state estimation to generate volumetric isochrones considering a simple model and incomplete data uncertainties from the available 2D optical measurements at the epicardium. Subsequently, the optimization of the Purkinje tree with a fast electrophysiological model based on Eikonal equation, is applied to personalize the fast conduction system. The following step uses the personalized Purkinje tree to initialize the personalization of conductivity/diffusion parameters of a simple phenomenological model (PM). Resulting personalized conductivity/diffusion maps are then incorporated into a detailed generic biophysical ionic model (IM) as boundary conditions. We designed a strategy that relies on a calibration of conductivity parameters between the different models in order to re-use the parameters estimated with one model for simulations based on a different model. The last step using an ionic model provides the most personalized and complete simulation results. It combines personalized parameters extracted with the simplest models, which were embedded in an optimization procedure with reasonable computational costs, together with a detailed ionic model. This pipeline illustrates the complementary roles of statistical, phenomenological and biophysical approaches.

The prediction capabilities of the integrated pipeline are assessed by estimating the activation time errors obtained in one pacing configuration with parameters learned in a different pacing scenario at every stage of the pipeline. An IM with generic parameters taken from the literature obtained average errors of 16.25ms. Estimation of the Purkinje system based on a simple model reduced the error to 14.04ms, and a regional estimation of local conductivities with a PM reached an error of 6.87ms. These esults demonstrate an improvement for the prediction of depolarization isochrones using the integrated pipeline. Nevertheless, results also illustrate that further investigations are needed regarding the increase of model complexity and the parameter uniqueness and identifiability.

[1] Details about these models can be found in Camara et al., PBMB'11 or in the proceedings of the STACOM-CESC'10 workshop (LNCS 6364).