Tailoring Process for the Regional Personalization of Atrial Fibrillation with a Novel Cardiac Model

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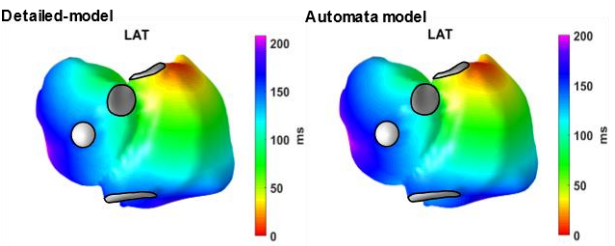
Background. Personalization of mathematical models has the goal to help in the identification of optimal antiarrhythmic therapies for each patient. Nevertheless, their need of high computational resources and long running times move them far away from real-time clinical practice.

Methods. In this study, a novel cellular automata model is presented. This model captures the essential dynamics seen in real myocardium tissue while requiring low computational resources and short simulation times. Moreover, we present a tailoring process based on regional regression curves which allow the regional personalization of some of the automata parameters thus it can mimic a desired electrophysiological behavior. These regression curves linked the wished electrophysiological properties (the regional conduction velocities and the duration of action potentials) with their corresponding adjusted automata parameters.



The local activation time (LAT) maps of the detailed-model and the cellular automata model for a sinus rhythm simulation.

Results. Both the automata and the tailoring procedure have been compared against an already validated detailed-mathematical during diverse cardiac rhythms. A high performance was obtained for regular rhythms simulations (as sinus rhythm and Atrial Flutter (AFL) cases). During Atrial Fibrillation (AF) same general dynamics (similar regional location of singularity points) than the reference model were obtained.

A systematic comparison between the detailed-model and the CA indicate that mean absolute relative error of CV were 5.56%, 11.73% and 37.96% for the sinus rhythm, AFL and AF models respectively. Regarding the mean absolute relative error of APD_{80}, errors were 1.02% for sinus rhythm, 5.17% for AFL and 9.63% for A.F.

Conclusion. This novel automata model and its personalization framework may be applied to produce fast and personalized simulations from clinical data.