

Accelerating stabilization of whole-heart models after changes in cycle length

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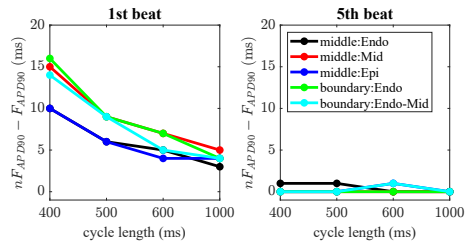
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Introduction Parameter changes in membrane models can cause long-term drift in model variables. To reduce the cost of whole-heart simulations with such changes one can perform the stabilization in models of isolated cells and then copy the state variables to the full model, but it can then still take many beats to stabilize. We hypothesized that differences in activation time leading to cycle length (CL) variability before the first beat contribute to this. To remove this variability we froze most state variables of the model until the sodium current activated.

Methods Simulations were performed with CL 400, 500, 600 and 1000 ms in a modified Ten Tusscher-Panfilov 2006 model. Isolated cells parameterized to mimic endocardial, mid-myocardial, and epicardial myocytes were simulated for 1000 beats. Their final state was then copied to all nodes of the corresponding type in a model of the whole human ventricles, which was run for 5 beats, with and without freezing. Model stability was evaluated in terms of action potential duration at 90 % repolarization (APD₉₀).

Results Stabilization of the whole-heart model took three to four beats. Differences between the first and 5th beat were larger at shorter CL. Freezing of the membrane state accelerated stabilization in some cell types but caused opposite drifts in others. Drifts were largest in the epicardial and mid-myocardial layers, and not in particular at their interfaces.

Discussion Freezing of membrane state may help to accelerate stabilization but in our scenarios other types of drift dominated and may in fact be aggravated by freezing, as it inhibits electrotonic interactions between different cell types before the first activation.



Differences in APD₉₀ with (F) and without (nF) freezing for 1st and 5th beat at different CL.