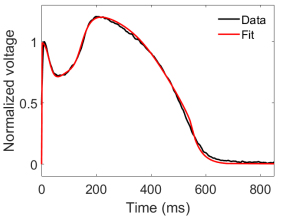
Automated Customization of Cardiac Electrophysiology Models to Facilitate Patient-Specific Modeling

Darby I Cairns, Maxfield R Comstock, Flavio H Fenton, Elizabeth M Cherry

Georgia Institute of Technology
Atlanta, GA, USA

Introduction: Models of cardiac electrophysiology can be useful for assessing the behavior of the heart when subjected to interventions like pacing, defibrillation, or drugs. However, for patient-specific predictions, models must be customized to match the electrophysiological properties of individuals.

Methods and Results: We present a browser-based tool for customizing models of cardiac action potentials by fitting parameter values to user-provided datasets. The tool uses a particle swarm optimization algorithm accelerated by the user's graphics card, which can support a large particle population and typically finds a low-error solution within a small number of iterations (10-30), computed within seconds. Users can choose from several different models, including the Bueno-Orovio model et al., which can be used to fit action potentials from a variety of species, including the example shown in the figure of a Brugada-type action potential recorded from an explanted human heart. The interface allows all model parameters or a specific subset to be selected for fitting, and the user can set bounds for all parameters to constrain their values. Data from multiple pacing cycle lengths can be fit simultaneously to account for rate adaptation.



Example of Brugada action potential (black) from a human heart and a fit with the Bueno-Orovio et al. model (red).

Conclusion: Our browser-based automated fitting tool is capable of finding good parameter sets to match cardiac action potentials recorded from multiple species, including human hearts, under normal and diseased conditions. Harnessing the highly parallel capabilities of the user's graphics card allows the optimization algorithm to explore a large population simultaneously, allowing low-error customized sets of parameter values to be output within seconds. We expect this tool will be useful for tuning models to match data recorded from individual experiments and patients.