Machine Learning Based Cell Model for fast approximation of cellular action potential to enable clinical translation

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Motivation: Simulations of cardiac arrhythmias have shown great potential to plan and optimize therapies. However, biophysical models are complex and involve a high computational cost that poses a problem for their clinical translations. Alternative methods such as eikonal based simulations can help to reduce the cost at the expense of not considering an action potential model.

Aims: In this work, we aimed to develop a methodology to perform the simulation of the action potential of a myocyte in the tissue with a low computational cost that could be coupled with a fast Eikonal diffusion solver to provide more realistic results.

Methods: We modelled the cell dynamics as a transition between states represented by the action potential curves. We performed a batch of biophysical simulation and segmented the transition between two different AP curves (see Figure 1, train). The AP curves were encoded by a vector formed by 4 characteristic points in 2D (t, ap(t)). Then, given an initial state and a succession of activation times, the simulation of the cell AP can be posed as the problem of predicting the successive states of the cell. To this end we used a k-Nearest Neighbours strategy to predict the states succession.

Results: We tested the results in two different scenarios to assess the capacity to generalize (see Figure 1, TEST). In both the geometry and the stimulus protocol were changed. The method presented bounded errors of approximation and realistic results. The main source of error came from punctual delays in the depolarization of the cell.

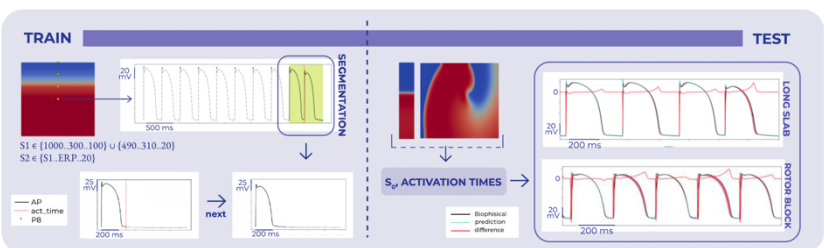

Figure 1. Pipeline for training and test the myocyte AP estimation model