A Machine Learning Approach to the Personalization of Atrial Electrophysiological Models

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Personalization of models for the evaluation of therapies may improve the efficacy of Atrial Fibrillation patients' management. Machine Learning (ML) may help in obtaining a cellular model that accurately represents a patient.

A tissue model (3x20x0.25mm, inter-node distance 0.25mm, a) was used to simulate a paced rhythm for 2100 different ionic profiles, generated by sampling random values between -75% and 150% of the original values for eight ionic currents (b). The simulated models were evaluated for propagability, and those able to propagate had six biomarkers (APA, RMP, V_{20}, $APD_{20,50,90}$) measured. With this dataset, three different shallow neural networks were trained to evaluate propagability, predict biomarker values based on ionic current (IC) values (b, up), and predict IC values from biomarkers (b, down).

When predicting biomarkers from IC (R^2:0.98±0.01), results were more accurate than when predicting IC from biomarkers (R^2:0.48±0.38, b), therefore, in this direction the problem is ill-posed. As an example, see the performance for RMP prediction, in contrast to the g_{Ks} prediction (c). To perform a further validation, 250 new ionic profiles were generated, leading to the following confusion matrix (d) for propagation viability predictions, along with similar performance in predicting biomarkers from IC. See the ability to develop new models with disperse biomarkers (e). Finally, it is important to highlight that the classification and estimation of biomarkers using a trained model is near instantaneous, while the simulation spanning 20s for 250 models took 13.5h.

Machine learning can accelerate the implementation of personalized ionic profiles by estimating biomarkers quickly and in mass for a wide range of currents and selecting those more representative for the patient.