Personalization of ventricular cardiac conduction system models to reproduce patient electrocardiogram

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The application of computational electrophysiology simulations of the heart to diagnosis and therapy planning of arrhythmia has started to penetrate in advanced clinical environments over the last years. However, as a first step, it is key to be able to reproduce the patient's electrical sequence of activation by personalizing the models. The ECG is one of the most common sources of information to adapt the computational model to the clinical patient data. We present a methodology to estimate the full ventricular cardiac conduction system of a patient from electroanatomical maps (EAMs) to obtain personalized electrical activations that reproduce faithfully the patient's 12-lead ECG. We first annotate and filter the endocardial samples from the EAMs, fit them to the patient geometry, and estimate the Purkinje myocardial junctions (PMJ), and the underlying Purkinje network (PKN) associated to the PMJ locations and activation times. As a result, we obtain a minimal PKN that reproduces the electrical sequence of activation in the endocardium, provided an estimated global longitudinal conduction velocity in the myocardium and in the PKN. We have applied our methodology to 14 patient datasets that include EAMs for the right and left ventricle. The optimal CV for the PKN in simulations was 1.95 ± 0.25 m/s. Due to errors in EAMs samples, their local activation times (LAT) were not always in agreement with the simulated sequence of activation. Those cases with good agreement ($> 70\%$) showed an average LAT error of 6.1 ms, and had an average of 24 PMJs. The resulting simulated 12-lead ECGs showed a correlation higher than 0.8 in almost all leads. In addition, we compared personalized PKNs with a sequence of activation obtained from both Durrer's sequence and PKN automatically generated with Fractals, obtaining a better ECG correlation in the personalized cases (see Fig. 1, patient P12).