The Role of Myocardial Fiber Direction in Epicardial Activation Patterns via Uncertainty Quantification

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Introduction: Myocardial fiber structure governs the spread of excitation in the heart; however, little is known about the effects of physiological variability in the fiber orientation on epicardial activation patterns. Knowledge of how physiological changes in fiber orientation alter electrical propagation is necessary to interpret activation patterns to localize sources of arrhythmias.

Methods: To investigate these effects, we used bi-ventricular Eikonal simulations to compare ventricular activation sequences initiated from stimulus sites located in the epicardium and endocardium. We implemented rule-based fibers, which were varied using modern uncertainty quantification techniques to encompass a large range of physiological values. Specifically, we implemented polynomial chaos expansion which allows for robust exploration with reduced computational demand by implementing an emulator function to approximate the underlying forward model.

Results: Our results showed that physiological variation in fiber orientation does not impact the overall location of activation features; however, variation in fiber orientation does impact the overall spread of activation. Specifically, such variability has a higher presence on the left ventricle for epicardial stimulation sites whereas the right ventricle has a higher degree of variability for endocardial stimulation sites.

Discussion: The sensitivities we observed may have minimal impact on clinical procedures such as the localization of premature ventricular contractions, which relies primarily on the identification of sites of early activation. In this context, we saw little difference in our model output that would alter the location of the site of early activation. On the other hand, we did observe a larger degree of variability in relation to the activation sequence as a whole. Such variability may have an impact on modeling reentrant arrhythmias as changes in the activation sequence based on fiber orientation may cause differences in the site of reentry, or even the presence of any reentry in the simulation.