

# Predicting Plausible Human Purkinje Network Morphology from Simulations

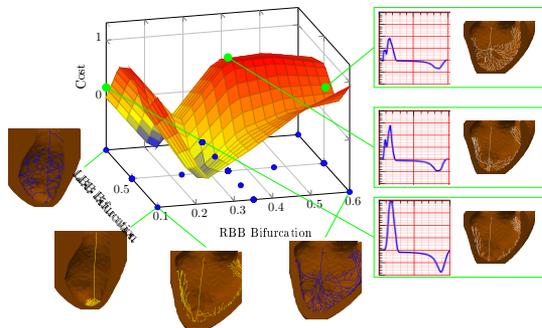
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The Purkinje Network (PN) varies between species and in particular from animals to humans. Nevertheless, the majority of morphological and physiological knowledge of the PN arises from animal studies. Thus, it is unclear how the PN morphology may be adopted to human heart shape. Therefore, we propose a virtual population study of human hearts investigating the PN morphology.

To this end, an automatic pipeline for the creation of physiological heart shapes and the electrophysiology simulations is developed. The automatic pipeline generates heart shapes from a statistical shape model, based on one shape parameter, then adds a deterministic generated PN depending on four Purkinje parameters, and calculated the myocardial fiber orientation. This is used to estimate the activation times based on the Eikonal model, which feed a forward ECG solution giving a 12 lead surface ECG.

The automatic pipeline is then used to systematically explore the shape and Purkinje parameter space leveraging a sparse grid algorithm. In most cases, the ECG showed a double spiked R-wave, commonly associated with bundle branch (BB) block. To characterise this, an energy function was developed which has increasing energy with R-spike separation, the function is based on two Gauss functions.

Our model favoured left BB bifurcation point near the base or near the apex. For the right BB bifurcation point, a strong favour close to the apex is observed. Both optimal bifurcation points are slightly impacted by the heart shape. However, the largest correlation can be observed between the BB bifurcation points them-self, only if both bifurcation parameters are chosen optimally an ECG with a single R-spike is produced. Further investigation of that relationship is being performed.



Cost function in relation of right and left bundle branch bifurcation point.