A Procedural Method for Modeling the Purkinje Fibers of the Heart

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Abstract: The Purkinje fibers are located in the ventricular walls of the heart, just beneath the endocardium and conduct excitation from the right and left bundle branches to the ventricular myocardium. Recently, anatomists succeeded in photographing the Purkinje fibers of a sheep, which clearly showed the mesh structure of the Purkinje fibers. In this study, we present a technique for modeling the mesh structure of Purkinje fibers semiautomatically using an extended L-system.

The L-system is a formal grammar that defines the growth of a fractal structure by generating rules (or rewriting rules) and an initial structure. It was originally formulated to describe the growth of plant cells, and has subsequently been applied for various purposes in computer graphics such as modeling plants, buildings, streets, and ornaments. For our purpose, we extended the growth process of the L-system as follows: 1) each growing branch keeps away from existing branches as much as possible to create a uniform distribution, and 2) when branches collide, we connect the colliding branches to construct a closed mesh structure. We designed a generating rule based on observations of the photograph of Purkinje fibers and manually specified three terminal positions on a three-dimensional (3D) heart model: those of the right bundle branch, the anterior fascicle, and the left posterior fascicle of the left branch. Then, we grew fibers starting from each of the three positions based on the specified generating rule.

We achieved to generate 3D models of Purkinje fibers of which physical appearances closely resembled the real photograph. The generation takes a few seconds. Variations of the Purkinje fibers could be constructed easily by modifying the generating rules and parameters.

Key words: Purkinje fibers, L-System, heart simulation.

INTRODUCTION

A three-dimensional (3D) virtual heart model is often used for computer simulations and visualizations. Computer simulation is one way to understand the electrophysiological properties of the heart or to figure out the mechanisms of fatal arrhythmias [1-4]. Effective visualization of a 3D heart model is also a useful tool for education and communication between doctors and patients [1, 5]. However, the creation of a 3D heart model is difficult and time-consuming because the heart has intricate structures containing various tissues, such as the atrioventricular node, bundle of His, Purkinje fibers, and contractive myocardium. Our goal was to facilitate this process by providing effective modeling tools. In this study, we focused on the construction of Purkinje fibers.

The Purkinje fibers are part of the ventricular conduction system and were originally discovered by Tawara [6]. These tissues conduct excitation (electrical activation) rapidly from the bundle of His to the ventricular myocardial tissue. The Purkinje fibers are located in the ventricular walls of the heart, just beneath the endocardium. Figure 1 is a PAS-stained stereomicrograph of a sheep heart provided by Shimada *et al*. [7], which shows the closed mesh structure of the Purkinje fibers. Since the Purkinje fibers play a key role in the conduction system, many simulation studies have taken them into account. In such simulation-based systems, the fibers are usually constructed manually. In [2, 8, 9], authors drew a simplified
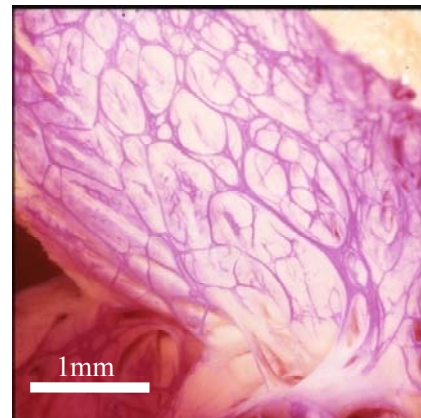

Fig. 1. A photograph of the Purkinje fibers of a sheep [7].

two-dimensional (2D) shape of the Purkinje fibers manually on the flatten endocardium and then mapped the 2D shape onto a 3D heart model. However, it is still difficult to manually create detailed structures as shown in Fig. 1. It also takes time to generate various Purkinje fiber patterns which are sometimes required to perform simulations using various models.

In this report, we present a semiautomatic system for modeling the mesh structure of the Purkinje fibers by applying the L-system. The user manually specifies the endocardial regions that the Purkinje fibers will cover, sev-

eral positions from which fibers will grow (e.g., the terminal positions of the right bundle branch, the left anterior fascicle, and the left posterior fascicle on the endocardium), and the parameters of the L-system. Then, the growth simulation of L-system generates 3D mesh structures that cover the specified regions. This process takes only a few seconds and the user can generate various Purkinje fiber models by simply changing the generation parameters.
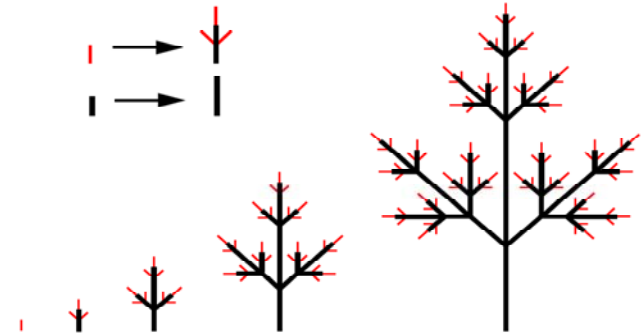

Fig. 2. A simple example of the L-system (compound leaf) [12]. Beginning with the initial structure (leftmost thin red line), the system generates a complicated structure by applying two generating rules (top-left) sequentially.

L-system: The L-system is a formal grammar originally introduced by Lindenmayer to formalize the development of multicellular plants [10] and was subsequently expanded to represent higher plants and complex branching structures [11-13]. The framework of the L-system consists of an initial structure and rewriting rules (or generating rules). The essence of development is parallel replacement using the rewriting rules. Starting from the initial structure, the L-system replaces each part of the current structure by applying the rule sequentially. Figure 2 shows a simple example, the development of a compound leaf [12]. This includes two module types: the apices (thin red lines) and the internodes (thick black lines). This example has two rewriting rules (Fig. 2, top-left): one replaces an apex with an internode, two lateral apices, and a top apex, while the other replaces an internode with a longer one. The initial structure is a single apex. Using these simple rules, the system develops an intricate branching structure over several replacing steps. An interesting aspect of the system is that each replacement process corresponds to the growth of part of the plant. Therefore, the L-system is not only a heuristic technique that creates fractal-like shapes, it is also a simulation of real-world plant growth. Karch *et al.* presented a similar method to generate vessel tree patterns [14]. However, the L-system and the method of Karch *et al.* [14] are designed for open tree structures and cannot be applied directly for the closed mesh structures seen in Purkinje fibers.

METHODS

In contrast to existing approaches that create Purkinje fibers on flattened 2D endocardium [2, 8, 9], we generate them directly in 3D space to achieve the detailed 3D overlapping structures of Purkinje networks. Our system loads a 3D polygon model of the heart and generates Purkinje fiber models just beneath the endocardium. We
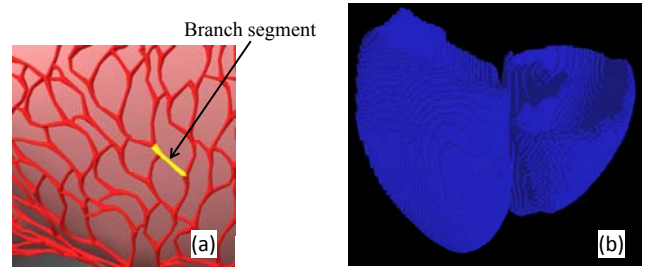

Fig. 3. Branch segments of the Purkinje fibers (a) and volume representation of the Purkinje layer (b).
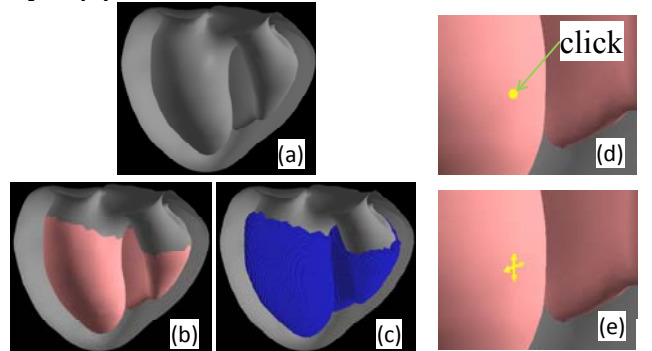

Fig. 4. Overview of the modeling process. The user specifies endocardial regions (b) on a 3D heart model (a) so as to create the Purkinje layer (c). The user also specifies the initial points by clicking (d,e).
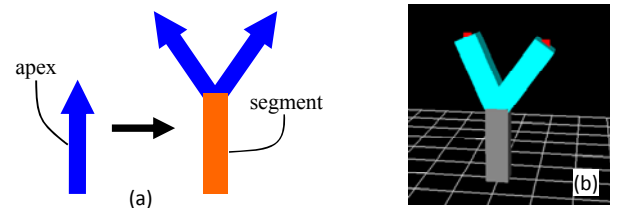

Fig. 5. A generating rule (a) and its handle (b). The user can modify the growth directions of two child apices by manipulating the control points.

represent the mesh structure of the Purkinje fibers with a number of *branch segments* connected to each other (Fig. 3a). Each branch is represented as a curved polyline and constructs cylindrical objects along the polyline for effective visualization. We also create a volume representation to compute a distance field to guide the growth of the Purkinje fibers. We prepare $128 \times 128 \times 128$ volume data that cover the entire heart model, and activate voxels just beneath the endocardium where the Purkinje network is located (we call this the *Purkinje layer*; Fig. 3b).

User interface: After loading a 3D heart model, the user first specifies endocardium surface regions on the heart model. We provide a sketch-based interface that allows the user to specify polygons by painting. The specified surfaces are highlighted in red (Fig. 4b). The system then generates the Purkinje layer by activating voxels that are inside the 3D heart model and close to the specified endocardium surface (we used $3r$ as a threshold, where r is the voxel width; Fig. 4c). Next, the user specifies initial points from which the Purkinje fibers will grow by clicking on the heart model directly. The system places four initial apexes radially at each specified position (Fig. 4d, 4e). Finally, the user sets the growth parameters of the generating rule by manipulating the control points directly [15] (Fig. 5). When all of the parameters

are set, the user pushes the "growth button" to start the growth simulation of the L-system.

The actual photograph of Purkinje fibers (Fig. 1) shows that most of the branch segments are divided into two child branches. Based on this observation, we provide a simple generating rule in Fig. 5. This generating rule contains two module types, apices (blue arrow) and internodes (orange bar), and replaces one apex with an internode and two new child apices. The system allows the user to modify directions of the two child apices by manipulating a handle (Fig. 5b). The user can also set branch length l_{bra}. We introduce a randomness to the length by using Gaussian random number: $l_{bra}' = l_{bra} + \text{random}(\mu, \sigma^2)$. We set mean value $\mu = 0$, and standard deviation $\sigma^2 = 0.4 \times l_{bra}$ for generating the results in this paper.

Creation of Purkinje Network: When the growth button is pressed, our system runs a growth simulation to create a Purkinje network. The growth simulation uses an iterative algorithm similarly to the standard L-system. Each iteration process consists of two steps. In the first step, we randomly shuffle the order of all apices and insert them into a queue. (Note that there are 4 apices for each user-specified initial point at the beginning.) In the second step, we grow all apices in the queue one by one. Differently from the standard L-system in which all branch segments have straight shapes (Fig. 2), we grow an apex to be a curved branch segment so as to obtain a uniform distribution (see the next paragraph). If a growing apex steps out of Purkinje layer or collides to an existing branch, we stop the growth of the apex. If not, we add two new apices based on the generating rule (Fig. 5). These new apices will grow in the next iteration. Their directions and lengths are determined by the user-specified parameters. We stop the growth iteration when no new apices are generated.

Extended L-system: The branch segments of Purkinje fibers are curved and distributed uniformly, as shown in Fig. 1. To generate such mesh structures, we introduce two extensions of L-system: one is for generating uniform distributions and the other is for constructing closed mesh structures.

To generate uniform branch distributions, we grow and bend a new branch to keep away from all existing branches. Our system approximates the curved shape of a branch with a simple polyline consisting of five line segments. During the growth process, the system first constructs a distance field from all existing branches and calculates the gradient of the distance field (Fig. 6a). We compute only this distance field and the gradient field at the voxel grids for fast calculations. The system then grows a new branch that curves along the gradient. We define the direction of each line segment of a branch as;

$$d = \frac{d_{original} + w_I * d_{gradient}}{\| d_{original} + w_I * d_{gradient} \|} \quad . \quad (1)$$

where $d_{original}$ is the direction of the previous segment, $d_{gradient}$ is the gradient direction at the terminal point of the previous segment, and w_I is a user-specified weight. Figure 6b shows a simple example: a new branch is growing from bottom to top in a gradient field that slants from left to right. The branch curves gradually in the direction of the gradient. We also project the direction d parallel to the endocardium surface so that the growing branch does
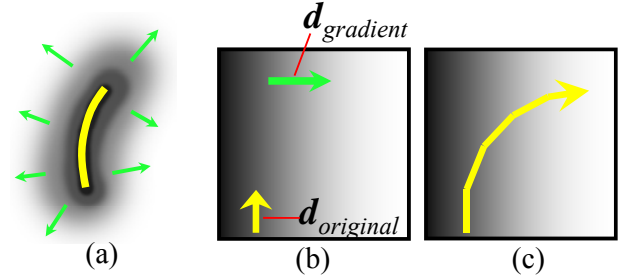

Fig. 6. The distance field of one branch (a) and the growth of a branch in a gradient field (b, c).
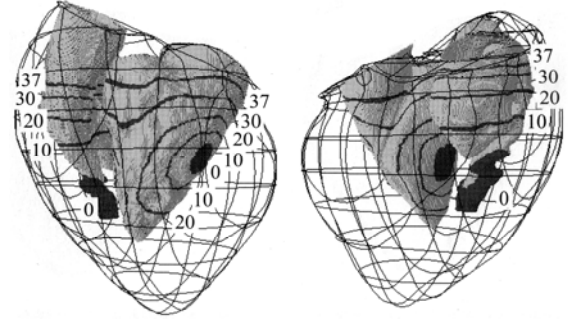

Fig. 7. Excitation sequence on the ventricular endocardium. The numbers are the times in milliseconds when stimuli occur at points [16].

not pop out from the thin Purkinje layer:

$$d' = d - (d \cdot n)n \quad . \quad (2)$$

where n is the normal vector of the nearest polygon on the endocardium surface. When a growing branch steps out of the user-specified endocardial region, the system stops its growth.

To generate a closed mesh structure, we add a simple rule to the L-system. If a growing branch collides with an existing branch, the system connects the growing branch to the collided branch and stops the growth of the branch. Since thin branches rarely collide with each other in 3D space, we use a threshold k. If the distance between growing and existing branches is less than k, we detect a collision. We set $k = 0.2 \times l_{bra}$.

RESULTS AND DISCUSSION

Based on a photograph of actual Purkinje fibers, we designed a generating rule (Fig. 5a) and set branch length $l_{bra} = 1.8$ mm. The branch length is ~10-times the actual one since the Purkinje network has self-similarity as shown in Fig. 1. The conduction velocity in the Purkinje fibers is ~2 m/s and thus the activation time along the branch is estimated as ~0.9 ms, which is markedly shorter than the action potential rising phase (several milliseconds). Therefore, we strongly believe that this degradation of the Purkinje network scale does not alter the physiological role in the simulated 3D ventricles. Next, we specified 3 initial growth points based on a map of excitation sequence on the endocardium that was modeled based on measured data (Fig. 7) [16]. These 3 initial growth points (Fig. 8a) correspond to the 3 earliest stimuli regions (0 ms regions in Fig. 7); distal ends of the right bundle branch, the left anterior fascicle, and the left posterior fascicle. Figure 8b shows a generated Purkinje model, demonstrating that our system can capture the detailed mesh structure. The growth simulation takes less than 10
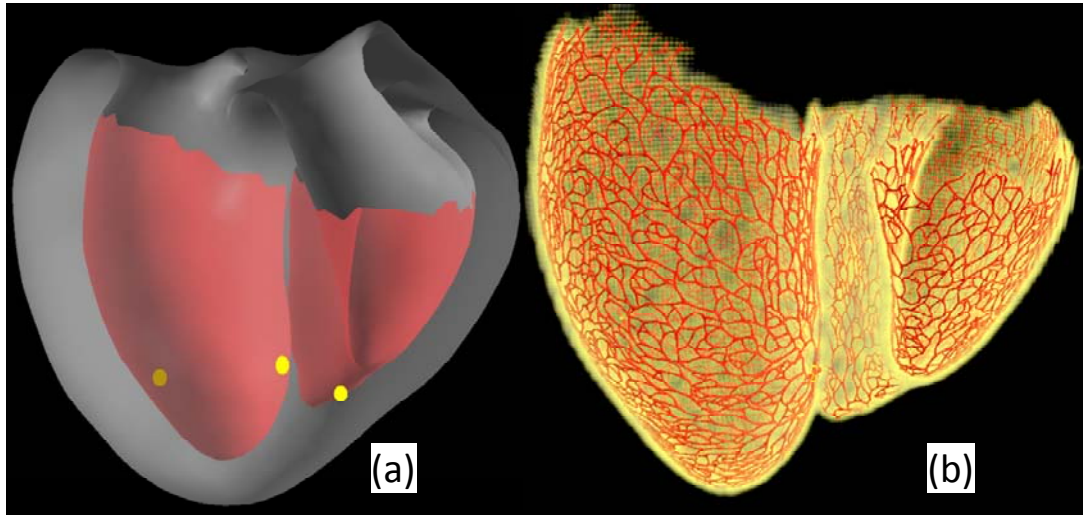
Fig. 8. The 3D heart model (a) and 3D Purkinje fibers created by our system (b). In (a), the endocardial regions are highlighted in red and the initial points of growth are in yellow. The resulting model, whose physical appearance closely resembles that of the actual Purkinje fibers, is generated by our system.
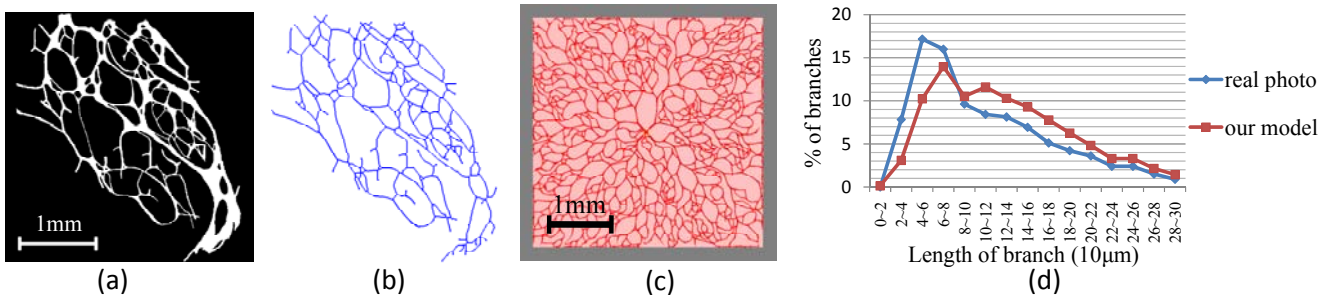

Fig. 9. An evaluation of the resulting model. A chart (d) compares a branch length distribution of real Purkinje fibers in the photograph and that of our resulting model.

seconds.

To evaluate the quality of Purkinje fiber model created by our method, we compared a distribution of branch lengths of our model and that of the real photograph in Fig. 1. First, we manually binarized the photograph (Fig. 9a) and extracted mesh structures by skeletonizing the binary image (Fig. 9b). Next, we generated real-scale Purkinje fibers on a plane surface by our method (Fig. 9c). We set l_{bra} = 0.18 mm. We then compared the distribution of branch lengths (Fig. 9d), and found that our created model has a similar length distribution to the real Purkinje fibers. In both cases (Figs. 9b and 9c), the mean length of branches is ~0.13 mm. In the generation process of Fig. 9c, we observed that ~45% apices collided to existing branches and stopped their growths. This causes that the number of shorter branches are more than that of longer branches. Figure 10 shows the growth iteration processes of the extended L-system on a plane surface. We can also generate variations of Purkinje fiber models by modifying the parameters of the L-system, as shown in Fig. 11.

We can also perform a simple simulation of excitation conduction on Purkinje fibers. First, we activate branches connected to the initial points. Then, we iteratively activate branches connected to the activated branches in each simulation step. Figure 12 illustrates the excitation conduction along the Purkinje fibers. We observe an excitation conduction pattern similar to the measured model (Fig. 7).

In contrast to existing methods that require the user to model the detailed mesh structures manually, our system allows the user to design variants of 3D Purkinje fiber models using simple interactions. Since the growth simulation using the extended L-system is rapid, the user can easily examine and tune parameters by trial and error. The resulting Purkinje fiber models have detailed mesh structures and their physical appearances closely resemble the photograph of the Purkinje fibers.

CONCLUSIONS

We present a semiautomatic system for creating 3D Purkinje fiber models and introduce two extensions to the L-system: collision avoidance and closed mesh structure creation. The user specifies the endocardial regions, initial points of growth, and generating rules of the L-system. Then, our extended L-system performs the growth simulation that constructs the 3D mesh structure of Purkinje fibers in a few seconds.

One limitation is that our system requires users to tune the parameters based on their observations and experiments. We plan to extend this system so that rules and parameters can be estimated from anatomical photographs. Another future project is to apply our method to other targets such as airways and blood vessels.
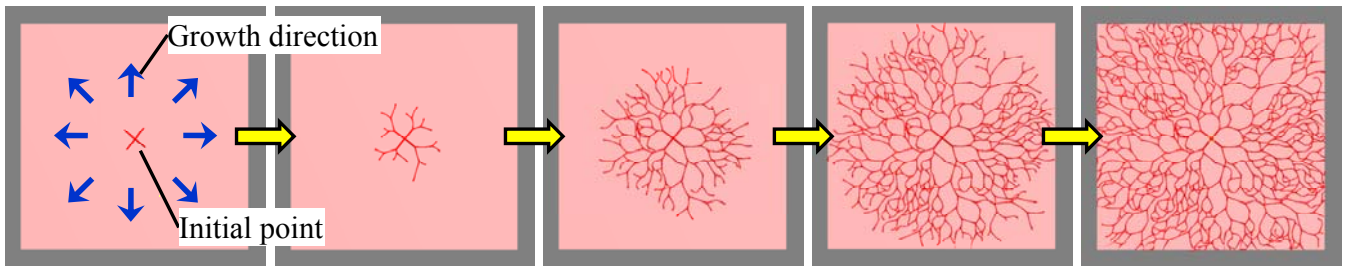
Fig. 10. Growth process of the extended L-system on a plane surface. These panels show the 1st, 3rd, 6th, 9th, and 12th iterations of the growth process from left to right. Starting from the center point, the Purkinje fibers grow to fill the pink region.
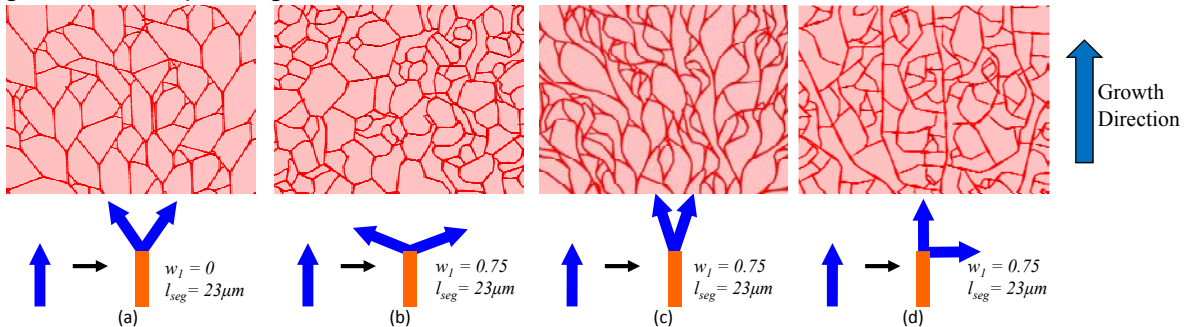

Fig. 11. Variations of Purkinje fiber models and their growth parameters. In example (a), we turn off the collision avoidance framework by setting $w_1 = 0$.
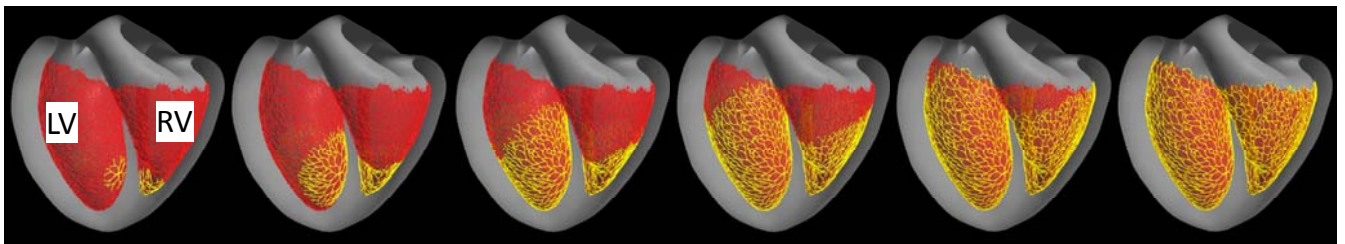

Fig. 12. Excitation conduction along the ventricular Purkinje fibers. The excitation conduction started from the initial points of growth, and we activated the connected branches iteratively. These panels show the 2nd, 6th, 10th, 14th, 18th, and 22nd iterations.

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