

# The Construction of a Volumetric Cardiac Model for Real-time ECG Simulation

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## ABSTRACT

We present a novel approach for producing a real-time simulation of the 3D phenomenon of the electrocardiogram. Techniques are borrowed from the fields of computer vision and computer graphics to create a volumetric heart model that can be fine-tuned to illustrate a variety of electrophysiological situations. The activation sequence that occurs in the heart model is choreographed to coincide with the progression of a recorded ECG.

## Keywords

ECG, ECG simulation, cardiac modeling, volumization, texture mapping

## 1. INTRODUCTION

The electrocardiograph is one of the most useful diagnostic medical devices ever created. It offers a real-time non-invasive technique for monitoring cardiac activity. Figure 1 illustrates the heart's electrical conduction system and also describes the typical arrangement of the 3 standard ECG leads (I, II, III). Each edge of *Einthoven's triangle* is a *lead vector*, which indicates the direction in which current flow is being recorded for each of the standard leads. The output of the electrocardiograph, the electrocardiogram (ECG), sometimes referred to as EKG, is a set of 2D waveforms (one for each lead) that represent the electrical activity from different viewpoints in the human heart over time. The translation of the electrocardiogram into 3D is often unintuitive and a cause of confusion for students of medicine and physiology. Although many detailed ECG simulators exist [Ces02, Koh01, Por00, Gha95a, Nob91], few are suitable for undergraduate educational purposes and fewer still offer full real-time interaction on a commodity PC platform. Our

cardiac model has been designed specifically for the depiction of whole heart electrical activation and can be generated to various levels of detail allowing the model to be tailored to suit the performance capabilities of the host machine.

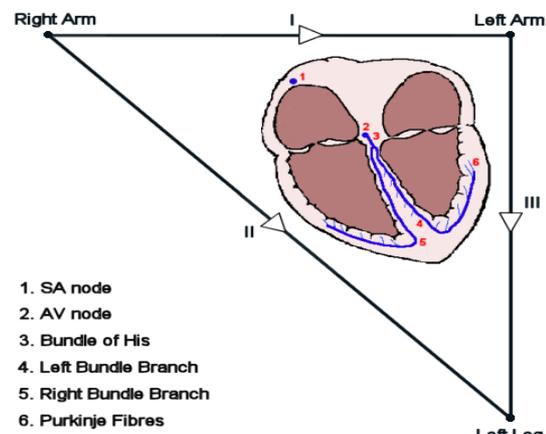


Figure 1 Einthoven's Triangle and the cardiac conduction system.

## 2. PREVIOUS WORK

Most cardiac simulation systems are based upon an interpretation of the bidomain model [Por00, Sa195, Plo89, Tun78], which separates the myocardial volume into an intracellular and extracellular space, separated by a membrane. Perhaps the most advanced cardiac model to date has been that produced by the *Cardiome Project*, a subproject of the *Physiome*

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*Project.* Generated through an international collaboration between physiologists and biomedical engineers in Oxford University, Johns Hopkins University and the University of Auckland among others, this virtual heart model consists of approximately  $10^6$  individual cells each controlled by a set of differential equations that govern its electrical excitability [Koh01]. Although this model is certainly a highly accurate representation of a functioning heart, its complexity makes it unsuitable for use on a typical workstation.

Recently the CESLAB system has been developed as a freeware application for commodity workstations and combines an interactive user environment with a high level of customizability [Ces02]. The environment allows cells to be configured to exhibit physiological defects such as branch blocks and Wolff-Parkinson-White syndrome. The cardiac model used is created within the CESLAB system environment and is generated by defining a set of contours that are extruded to create a 3D heart model.

### Model Acquisition

The initial polygonal cardiac model used in the system was created in New York University's School of Medicine. The model was designed through collaboration between consultant cardiologists and graphical designers for the specific purposes of interactive learning and VR teaching aids. However, in its initial state it was unsuitable for use within our system since it lacked many of the important features in the heart's electrical network i.e. SA node, AV node, left and right bundle branches. The SA node and AV node were added to the polygonal model using a commercial editor and were each represented by a single spherical primitive. Surface representations for the bundle branches and purkinje network were also added at this stage. However, the creation of a necessarily dense purkinje network proved to be cumbersome. Therefore, the bundle branches and purkinje system were later replaced by translating texture maps into 3D.

### Volumization

In order to illustrate the progression of the activation wave front across the inside of the heart, it was necessary to create a volumetric model from the edited cardiac model. The polygonal model was segmented into a number of constituent meshes and each was closed in order to cap any holes that existed as a result of the separation process. This segmentation allows a rough voxel classification to occur during the volumization process.

Volumes are generated by firstly creating an octree for each mesh. The depth of the octree represents the

resolution of the volume buffer e.g. depth  $n$  yields a lattice of  $2^n$  in each dimension. Random rays are then cast from the center of each node and the number of triangle crossings is recorded.

The number of ray crossing tests can be reduced by inheriting node classification from parent nodes i.e. nodes that are not leaf nodes but are inside the mesh assign all their child nodes to be inside also. Surface nodes are obtained from leaf nodes that intersect the mesh's triangles. In this way a trinary dataset (inside, outside, surface) for each mesh is generated efficiently. The volumization process is complicated by the preceding segmentation of the cardiac mesh. Boolean operations were applied to the voxel classifications of the mesh-set and the voxels representing the myocardium were extracted.

### Electrical Network Construction

The heart's electrical conduction system consists of six major parts, Figure 1. The voxels that define the SA and AV nodes are determined from the volumization process, and are typically represented by a single or small group of cells. However, the complicated network that follows the AV node could not be derived during volumization since a reasonable surface representation could not be designed. Therefore, a technique for the creation of the tree-like networks of the left and right branch complexes for the myocardial voxel-set was required.

Firstly a reference image was created using commercial image editing software. This image is composed of a set of easily identifiable regions e.g. a grid of numbers. Using a spherical projection, the reference image is texture mapped onto the surface of each of the ventricles. In this way, texture coordinates are created and the way in which an image will wrap around the ventricular surface can be viewed.

Using snap shots of the ventricles texture mapped with the reference image, another 2D image is created that describes the branch on the ventricle. The branch image can now be easily created to map onto the desired ventricle in a way that is physiologically plausible. The branch texture is a trinary image containing one color for background pixels and two for foreground pixels (branch cells and junctional cells). The foreground pixels are extracted from the branch image and their corresponding UV texture coordinates are computed. Taking the UV coordinates of each triangle's vertices,  $\{(u_1, v_1), (u_2, v_2), (u_3, v_3)\}$ , and the UV coordinates of the pixel  $(u_0, v_0)$ , we calculate the barycentric coordinates  $b_1, b_2, b_3$  as:

$$b_0 = (u_2 - u_1) * (v_3 - v_1) - (u_3 - u_1) * (v_2 - v_1) \quad (1)$$

$$b_1 = ((u_2 - u_0) * (v_3 - v_0) - (u_3 - u_0) * (v_2 - v_0)) / b_0 \quad (2)$$

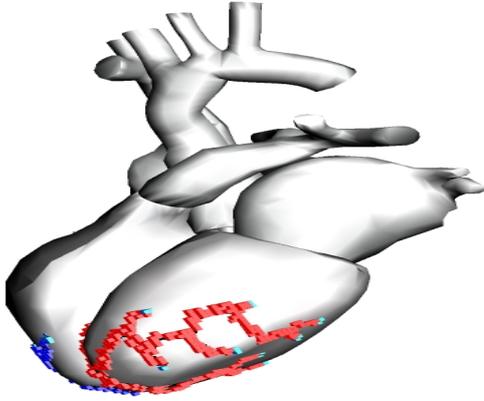
$$b_2 = ((u_3 - u_0) * (v_1 - v_0) - (u_1 - u_0) * (v_3 - v_0)) / b_0 \quad (3)$$

$$b_3 = ((u_1 - u_0) * (v_2 - v_0) - (u_2 - u_0) * (v_1 - v_0)) / b_0 \quad (4)$$

If the barycentric coordinates  $b_1, b_2, b_3$  are positive then the foreground pixel is inside the triangle. If  $b_i=0$  and  $b_j, b_k$  are positive then the foreground pixel lies on the edge opposite vertex  $i$ . Furthermore if  $b_i$  and  $b_j$  are equal to zero then the pixel lies on vertex  $k$ . Once a pixel is determined to be inside the triangle it is translated into XYZ coordinates as follows:

$$(x, y, z)_{pixel} = (v_1 * b_1) + (v_2 * b_2) + (v_3 * b_3) \quad (5)$$

where  $(x, y, z)_{pixel}$  represents the Euclidean coordinates of the pixel and  $v_1, v_2, v_3$  are the 3D coordinates of the triangle containing the pixel. Then the closest surface voxel to the pixel's 3D coordinates is chosen to represent it in the volume buffer.

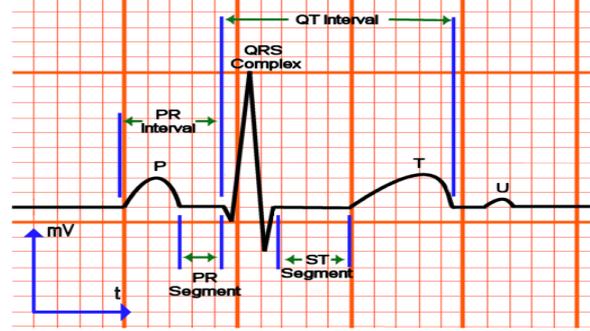


**Figure 2 Left ventricle with volumetric network after 2D branch texture translation.**

One shortcoming of this approach is that, although the 2D texture represents an unbroken ventricular branch, the 3D translation does not. The problem is solved by exploiting our knowledge of each pixel's neighboring pixel in the branch texture. For each foreground pixel the neighboring foreground pixels are recorded. Therefore, voxels can be connected in the same way as the pixels that they represent. Once discovered, gaps can be joined by finding the shortest path between two supposedly connected voxels.

### 3. 3D ECG Simulation

Once a classified volumetric model has been created the cellular activation is calculated so that it corresponds with the progression of a recorded ECG. The ECG is captured using the standard 12 leads and is saved to a file that relates the reading on each electrode to a single time value. Figure 3 shows the typical ECG waveform as recorded by standard lead II for a single sinus rhythm.



**Figure 3 ECG standard lead II output.**

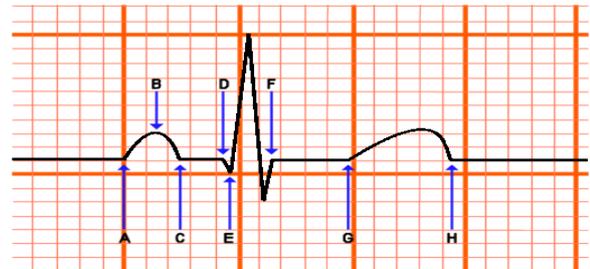
### ECG Components

The *P wave* is denoted by the first positive deflection around the isoelectric line. It begins when the SA node initiates the atrial depolarisation sequence. AV nodal activation occurs within the P wave, although the exact time at which this occurs is not discernable from the ECG. The *PR segment* represents the slow conduction through the AV node and Bundle of His to the first injection of activation into the interventricular septum. The *PR interval* is the time between the start time of atrial depolarisation and the beginning of ventricular depolarisation.

The *QRS complex* represents complete ventricular depolarisation. It consists of three consecutive waveforms i.e. they are not separated by intervals, or segments. The *QT Interval* denotes the time from the beginning of the *QRS complex* to the end of the *T wave*. However, where a *U wave* is present the interval is delimited by the end of the U wave. The *ST segment* denotes the duration of the isoelectric line between termination of the S wave and the beginning of the *T wave*, where complete ventricular repolarisation is represented. Although rarely seen in clinical recordings, the *U wave* represents late Purkinje fibre repolarisation.

### ECG Tagging

In order to synchronize the spread of current in the 3D model with the recorded ECG, it is necessary to extract the points of interest from the wave. These points are time values at which the total or partial state of the system can be deduced. In our system there are 8 such time points (tags), Figure 4.



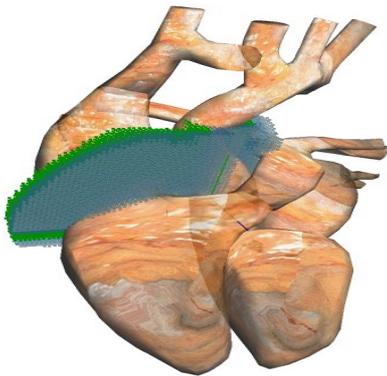
**Figure 4 Tagged output from standard lead II.**

All but one of the tags can be obtained from examination of the ECG, since the tag representing AV nodal activation can only be obtained through simulation. The system does not use the U-wave since it does not contribute significantly to the ECG.

Taking atrial depolarization as an example, times  $A$  and  $B$  are extracted from the ECG recording and used to calculate the interval in which full atrial depolarization must occur. Then beginning at the SA node, an isotropic activation sequence is simulated. On each iteration of the activation the newly activated cells are stamped with a value representing the number of iterations since the interval began. Once every cell has been stamped, atrial depolarization is complete and the activation time of each cell can be calculated as follows:

$$T_i = I_s + ((I_e - I_s) / N) * N_i, \quad (6)$$

where  $T_i$  is the timestamp for the cell,  $I_s$  and  $I_e$  are the start and end times of the interval respectively,  $N$  is the total number of activation iterations in the interval and  $N_i$  is the iteration when the isotropic activation reaches the cell. In this way, the activation for each interval will begin and end at exactly the right time. Figure 5 illustrates the progression of the depolarization wave front across the atria.



**Figure 5 The atrial depolarization wave front.**

Unfortunately this method cannot be used to generate activation times for the ventricular cells, because during ventricular activation current is injected into the myocardium in a number of different locations each with its own activation time. We solve this problem by considering each junctional cell as a current source in isolation. For each junctional cell we simulate an isotropic activation sequence on the complete set of ventricular cells. Once this is completed we examine the list of possible activation times for each cell and extract the minimum time.

#### 4. CONCLUSIONS & FUTURE WORK

We have described a set of graphical techniques that can be used to create a plausible cardiac model for volumetric ECG simulation. Although the initial surface model used in this research was not derived from medical imagery, the techniques described are applicable to any cardiac model.

Since the simulation sequence is timed against the start and end point of each wave, our techniques provide no way to ensure that the 3D activation corresponds to the ECG recording between wave intervals. Despite this we believe that we have generated a convincing depiction of the whole heart activation and that the resulting system offers students a useful real-time ECG visualization environment.

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