A CELLULAR AUTOMATA MODEL OF ACTIVATION PROCESS IN VENTRICULAR MUSCLE

Kye Rok Jun†, Yeong Rak Seong‡ and Tag Gon Kim‡

† Department of Biomedical Engineering
Pusan National University Hospital
Pusan 602-739, Korea.

‡ Department of Electrical Engineering
Korea Advanced Institutes of Science and Technology
Taejon 305-701, Korea.

ABSTRACT

Using electrocardiography is a common method to diagnose heart disease. Modeling and simulation of activation process for the heart system is useful to understand electrocardiography. This paper proposes a two-dimensional cellular automata model for the activation process of the ventricles. The model represents the geometry of the ventricles by the ellipsoidal shape in two dimension. In the model, ventricles are divided into four layers, each of which has a set of cells with preassigned properties. The proposed model takes into account the local orientation of the myocardial fibers and their distributed velocity, and refractory period. Simulation experiment is performed to measure activation potential for each cell in each layer within the ventricles.

1 INTRODUCTION

The heart is a special subsystem in a cardiovascular system. Two basic functions of the heart are generation of rhythmical impulses to cause rhythmical contraction of the heart muscle, and conduction of these impulses rapidly throughout the heart. Unfortunately, the heart is very susceptible to damage by heart diseases. Ischemia of the heart tissues, resulted from poor coronary blood flow, may be fatal. Using electrocardiography is a common method to diagnose such disease.

Quantitative knowledge about the activation process of the ventricular muscle is essential to the understanding of electrocardiography. Such knowledge can be obtained by the detail study on the course of the cardiac impulse through the heart and times of its appearance in each separate part of the heart. Simulation modeling for activation process in the heart system may be a good approach to studying such course.

Many researchers has experimentally studied the ventricular activation process of animals by inserting multiple "plunge-type" electrodes inside the heart(Durrer *et al.* 1970; Huiskamp and Oosterom 1988; Robert, Hersh, and Scher 1969; Robert and Scher 1982). A simple depolarization model was first presented in(Okajima *et al* 1968; Solomon and Silvester 1973). Van Capelle and Durrer conducted simulation of a arrythmia on excitable cells connected in two dimension(Van Capelle and Durrer 1980). Based on Durrer's experimental result, Miller and Geselowitz proposed a three dimensional depolarization model(Miller and Geselowitz 1978). Being adopted passively activation process, the model was proved to be inaccurate in abnormal propagation of the heart.

This paper proposes a two-dimensional cellular automata model for the activation process of the ventricular muscle. The geometry of the ventricles is represented by ellipsoidal shaped cells located in two dimension. Ventricles are divided into four layers, each of which has a set of cells with preassigned properties. The proposed model takes into account the local orientation of the myocardial fibers and their distributed velocity, and refractory period. Simulation experiment is performed to measure activation potential for each cell in each layer within the ventricles.

We organize this paper as follows. Section 2 gives a brief description of a cellular automata model. Activation process of the ventricles is outlined in section 3. Section 4 develops a cellular automata model for the activation process of the ventricles. An efficient technique for simulating the cellular automata model is presented in section 5. Section 6 concludes our discussion.

2 CELLULAR AUTOMATA MODEL

A cellular automata model consists of spatially distributed cells, each having local and uniform computational laws and the uniform connection pattern to its neighborhood cells. Cellular automata are the discrete dynamic system's counterpart to continuous dynamic system's partial differential equations. Cellular automata models are very powerful to characterize discrete natural systems in natural science, combinatorial mathematics, and computer science. A fascinating example for cellular automata is the Game of Life in *Scientific American*(Gardner 1970).

The main advantage of cellular automata modeling is the uniformity property in state transitions and the interconnection patterns. The property enables us to specify model components in local and simple manner. In other word, we specify the model components only with a single prototypic description rather having to specify each one separately. Another advantage of cellular automata models is ease in visualization of the system's dynamics, which results from the spatial invariance property of cellular models.

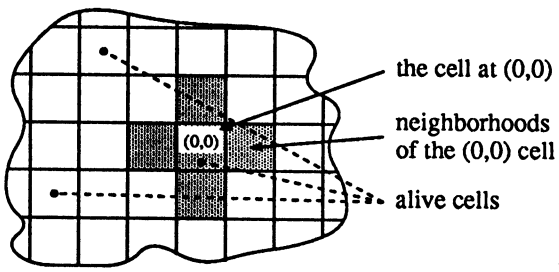


Figure 1: A Two-Dimensional Cellular Automata Model

A cellular automata model can have an infinite number of cells in any dimension. Here, we consider a finite number of cells in a two dimensional as shown in Figure 1. A two-dimensional cellular automata model CA is defined as a structure(Zeigler 1984):

$CA =< S, N, T >$: discrete time system
S: the set of states
N: the neighborhoods pattern at (0,0)
T: the transition function

subject to the following constraints:
$N \subseteq I^2$
T: $S^{|N|} \rightarrow S$

To consider the automaton specified by CA, let Q and f be a global state and the global transition function of CA, respectively. Then, $Q = \{q | q : I^2 \rightarrow S\}$ and $f(q(i,j)) = T(q|N + (i,j))$ for all q in Q and (i,j) in I^2.

3 ACTIVATION PROCESS OF VENTRICLES

The special excitatory and conductive system of the heart consists of the S-A node, the internodal pathways, the A-V node, the A-V bundle, and the left and right bundles of Purkinje fibers.

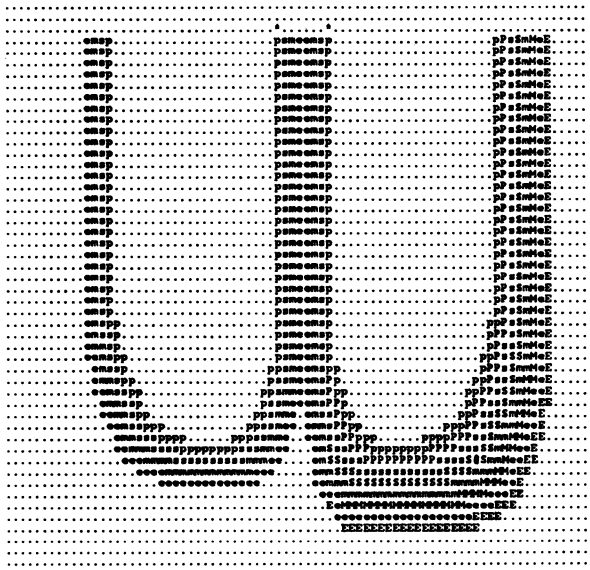
Originated from the A-V node the Purkinje fibers form the A-V bundle. The A-V bundle splits almost immediately into the left and right bundle branches lying beneath the endocardium of the respective sides of the septum. Each of these branches spreads downward toward the apex of the respective ventricles. The terminal Purkinje fibers penetrate about one third of the way into the muscle mass to terminate on the muscle fibers.

Upon reaching at the ends of the Purkinje fibers, the cardiac impulse is transmitted through the ventricular muscle mass by the ventricular muscle fibers themselves. The cardiac impulse entering the bundle spreads rapidly through the Purkinje fibers to the entire endocardial surfaces of the ventricles. The impulse then spreads slowly through the ventricular muscle to the epicardial surface.

The electro-physiological characteristics of the ventricular muscle is high sensitivity to electric stimuli and transmission of activation through cardial cells. To be detail, the activation of a cell in the muscle mass causes neighborhood cells to be activated, each of which then causes its neighborhood cells to be activated, and so on. Such transmission of activation results in contraction and relaxation of the ventricular muscle. To explore the transmission process requires electronic probes be instrumented at hundreds of locations in the ventricular muscle to detect variation of electric potential and activation time. Isochrones map is very important to recognize the course of cardiac impulses in the heart.

4 MODELING ACTIVATION PROCESS IN VENTRICULAR MUSCLE

The ventricular muscle system for activation process is modeled in cellular automata by discretizing the process with the spatially decomposed ventricular muscle.



p purkinje fiber
s subendocard layer
m midlevel layer
e epicardial layer
. empty space
* normal activation source
@ ectopic activation source

Figure 2: Geometry of the Modeled Ventricular Muscle

Table 1: Modeling Parameters of Cells(Adam 1991)

Ventricular layer	Long. Vel. (cm/s)	Norm. Vel. (cm/s)	RP (ms)	AT (ms)
Purkinje fibers	225	75	130	38
Subendocardial layer	66	22	120	38
Midlevel layer	84	28	105	32
Epicardial layer	84	28	90	28

Figure 2 shows the spatial decomposition. The shape of two ventricles is to be mosaic over a square block constructed with 80×50 cells. The left and right ventricles are defined by two ellipsoids, each composed of four layers. There are 6 types of cells in Figure 2; '.', 'p', 's', 'm', 'e', and '*', representing empty space, a purkinje fibers cell, a subendocard layer cell, a midlevel layer cell, an epicardial layer cell and an activation source, respectively. The activation source is used for starting simulation. The longitudinal and normal propagation velocities, refractory period, and activation time for each type of cells are given in Table 1.

Although the ventricular muscle system is composed of heterogeneous cells, the cellular automata model of the muscle system, CM_{CA}, is characterized with no dependencies on the type of cells. CM_{CA} is defined as follows:

FUNCTION NEXT($s_{i,j}, s_{i+1,j}, s_{i-1,j}, s_{i,j+1}, s_{i,j-1}$)
switch $s_{i,j}$
  case ACTIVE:
    return REFRACTORY;
  case REFRACTORY:
    return PASSIVE;
  case PASSIVE:
    if any one of $s_{i+1,j}, s_{i-1,j}, s_{i,j+1}, s_{i,j-1}$ is ACTIVE
      return ACTIVE;
    else
      return PASSIVE;
    end if
end switch

Figure 3: Function NEXT

$CM_{CA} =< S, N, T >$
$S = \{\text{ACTIVE}, \text{PASSIVE}, \text{REFRACTORY}\};$
$N = \{(0,0),(1,0),(-1,0),(0,1),(0,-1)\};$
$s'_{i,j} = s_{i,j}(t+1)$
$= T(s_{i,j}, s_{i+1,j}, s_{i-1,j}, s_{i,j+1}, s_{i,j-1})$
$= \text{NEXT}(s_{i,j}, s_{i+1,j}, s_{i-1,j}, s_{i,j+1}, s_{i,j-1});$
where,
$s_{i,j}$ denotes the state of the cell located at (i,j) and NEXT is a function for the next state to be defined in Figure 3.

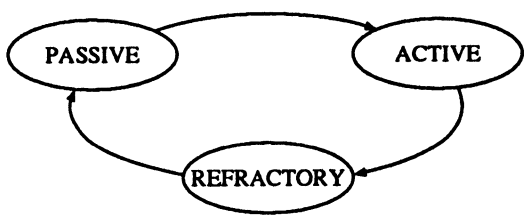


Figure 4: State Transition of a Cell

Each cell in the ventricular muscle should have one of the following states. Initially, all cells are in PASSIVE state. In this state, a cell is discharged electrically and has no influences on its neighbor cells. When simulation starts, a ventricular impulse enters a cell, then the cell would be charged and eventually activated(ACTIVE state). Now, the cell transmits the ventricular impulse to its neighbor cells. Eventually, the ventricular impulse is transmitted to all cells in the ventricular muscle. After an activation, the cell would be discharged and enter the REFRACTORY state in which the cell cannot be reactivated. After a moment, the cell changes its state to the PASSIVE state, in which the cell awaits next impulse. Figure 4 depicts state transition of a cell.

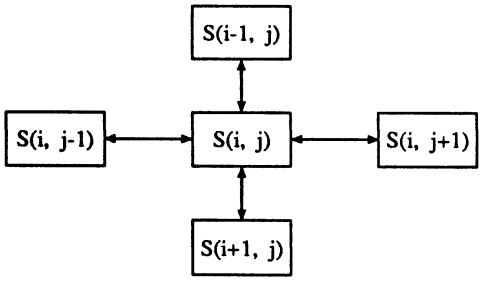


Figure 5: Neighbors of S(i, j)

The neighbors of the cell located at (i, j) are defined by translating the neighborhood template N to (i, j). Indeed, the neighbors are obtained by vector addition, i.e. adding (i, j) to each pair of N. Figure 5 shows the result. Note that the neighbor set of a cell also includes the cell itself.

5 DISCRETE EVENT SIMULATION OF CM_{CA}

The activation process of the ventricular muscle is started with giving a cardiac impulse to a cell. Eventually, the cell would be activated and transmits the cardiac impulse to its neighbors. As repeating the process, the cardiac impulse is spread over entire cells in the system. At this time, by an observation of the scenario, we can find that state transition would be localized in some regions of the ventricular muscle at an instant. Although the ventricular muscle system is modeled as a discrete time system, the time at the state transition of a cell depends on the type of the cell. Discrete time simulation of such a model often suffers from extremely large time complexity. In this paper, a discrete event simulation paradigm for discrete time models is employed(Zeigler 1976). By such an approach, the simulation time could be reduced drastically.

For ordering the execution of events, i.e. state transition of cells, a global data structure, *event_queue*, is employed. In *event_queue*, pairs of an alive cell and its next state transition time are stored in the increasing order of time. A cell is said to be alive if the cell could change its state in finite time without an external impulse. So, in CM_{CA}, a cell is alive when it has at least one ACTIVE neighbor or its state is either ACTIVE or REFRACTORY. We implement *event_queue* by a binary heap. Initially *event_queue* contains only activation source cells.

Figure 6 shows the algorithm. For each step, the

```
1  repeat until event_queue is empty
       ▷ get the imminent event set
2      t := the minimum next event time;
3      while TIME.OF.FIRST(event_queue) == t
4          remove FIRST(event_queue) from event_queue
           and add the cell associated with the removed
           event to current_event_set;
5      end while

       ▷ determine the next state
6      for each cell in current_event_set
7          execute the state transition function and store
           the result;

       ▷ change the state
8      for each cell in current_event_set
9          change its state to the stored next state;

       ▷ schedule neighbor cells
10     for each cell in current_event_set
11         schedule state transitions of the neighbor cells
           which become alive now;

12     flush current_event_set;        ▷ for the next loop
13 end repeat
```

Figure 6: Simulation Algorithm

cells with the minimum next state transition time is removed from *event_queue* and added onto the set in *current_event_set*. After finding the set, each cell in the set executes the state transition function given in Figure 3 and stores the result as the next state. After the step, each cell in *current_event_set* changes its state to the stored next state. Since state transitions are separated from determination of the next state, the order executing events scheduled at the same time does not affect on the simulation result. As a result of the state transitions, some cells now enter the ACTIVE state. So, the neighbor cells of such cells would become alive. Therefore, the neighbor should be inserted to *event_queue*. At this time, the next event times for the neighborhoods are determined by the longitudinal/normal velocity of the influencer cells. This procedure is repeated until *event_queue* is empty.

6 DISCUSSION AND SUMMARY

The proposed cellular automata model are simulated for two activation processes: normal and abnormal. The simulation result shows states of each cells in the ventricles during the activation process. The result also shows the total times for all cells to be activated

completely.

The impulse transmits through the ventricular muscle by preassigned velocity. It spreads rapidly through the Purkinje fibers to the entire endocardial surface of the ventricles. Then the impulse spreads slowly through the ventricular muscle to the epicardial surface.

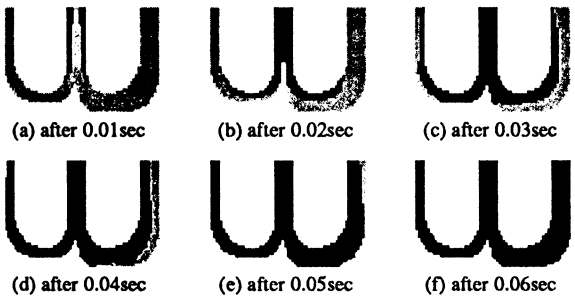


Figure 7: Normal Activation Process Observed at each 0.01sec.(Dark cells are activated.)

Figure 7 shows the normal activation process. For the process, an electronic stimulus is applied at the top of the left and right bundle branches marked by '*' in Figure 2. Figure 7 shows activation states of each cells in the ventricular muscle measured at each 0.01 sec. Note in Figure 7 that after 0.05 sec, all the cells in the right ventricle are fully activated, while those in the left ventricles are partially activated. It takes 0.06 sec for cells in the left ventricles to be activated completely.

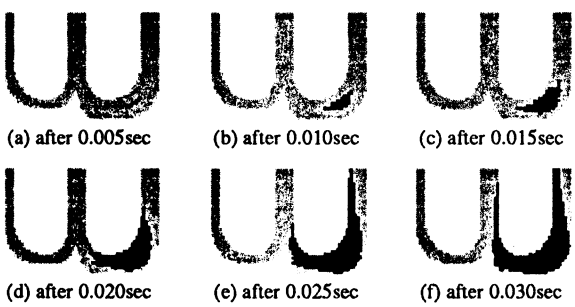


Figure 8: Abnormal Activation Process.(Ectopic stimulation is applied at the location marked '@' in Figure 2.)

Figure 8 shows an abnormal activation process. An ectopic stimulus is applied at the left bottom of the ventricles marked by '@'in Figure 2. Note that after 0.06 sec, the left ventricle is partially activated while no cells the right ventricle is in activation.

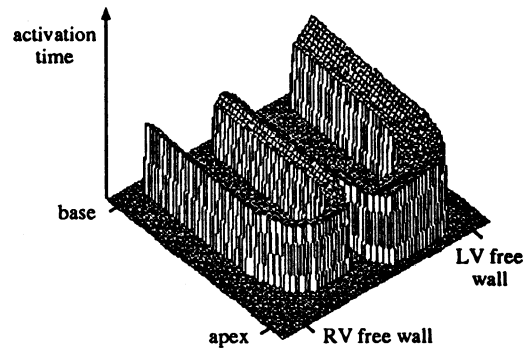


Figure 9: Activation Time for Normal Process

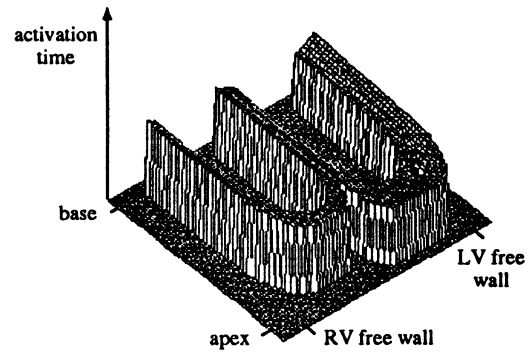


Figure 10: Activation Time for Abnormal Process

Figures 9 and 10 show the times of complete activation for the normal and abnormal activation processes, respectively.

REFERENCES

Adam, D.R. 1991, "Propagation of Depolarization and Repolarization Processes in the Myocardium an Anisotropic Model," *IEEE Trans. Biomed. Eng.*, 133–141.

Durrer, D.; Vandam, R.T.; Freud, G.E.; Janse, M.J.; Meigler, F.; and Arzbaecher. R. 1970. "Total Excitation of the Isolated Human Heart," *Circulation*, 899–912.

Gardner, M. 1970. "The Fantastic Combinations of John Conway's New Solitaire Game 'Life'," *Scientific American*, 23(4), 120–123.

Huiskamps, G.J.M and A. van Oosterom. 1988. "The Depolarization Sequence of the Human Heart Surface Computered from Measured Body Surface Potentials," *IEEE Trans. Biomed. Eng.*, 1047–1058.

Miller, W.T.III and Geselowitz, D.B. 1987. "Simulation Studies of the Electrocardiogram I: The Normal Heart," *Circ. Res.*, 301–315.

Okajima, M.; Fujino, T.; Kobayashi, T.; and Yamado, K. 1968. "Computer Simulation of the Propagation Process in Excitation of the Ventricles," *Circ. Res.*, 203–211.

Roberts, D.E.; Hersh, L.T.; and Scher, A.M. 1971. "Influence of Cardiac Fiber Orientation on Wavefront Voltage, Conduction Velocity, and Tissue Resistivity," *Circ. Res.*, 701–712.

Robert, D.E and Scher, A.M. 1982. "Effect of Tissue Anisotropy on Extracellular Potential Fields in Canine Myocardium in situ," *Circ. Res.*, 342–251.

Solomon, J.C. and Silvester, R.H. 1973. "Simulation of Measured Activation Sequence in the Human Heart," *Amer. Heart J.*, 518–524.

Van Capelle, F.J.L. and Durrer, D. 1980. "Computer Simulation of Arrythmias in a Network of Coupled Excitable Elements," *Circ. Res.*, 454–464.

Zeigler, B. P. 1976. *Theory of Modelling and Simulation*, John Wiley.

Zeigler, B. P. 1984. *Multifacetted Modelling and Discrete Event Simulation*, Academic Press.