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Hardware Acceleration for Real Time Simulation of Physiological Systems

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Abstract— Testing of medical equipment such as pacemakers is a critical task, because any malfunction may cause patient death or serious and long-lasting health consequences. Thus, device behavior under normal functioning conditions as well as under faulty conditions should be tested as thoroughly as possible under the project's budget.

This paper presents a real-time digital simulator (DRTS) for possible use in testing of medical devices. The simulator runs a model of a physiological system (an organ or a group of organs) in real time and uses A/D and D/A cards to interface the simulation results to real medical equipment. With this simulator, the tests can be made as thorough as needed without much increase in cost.

I. Introduction

IT is expected that large-scale/ high detail computational simulation of cells, tissues and organs of human body will involve both open source and proprietary code of universities, research centers, and commercial providers. In this presentation, we discuss how to achieve highly detailed and scalable real-time simulation of nonlinear physiological systems such as found in the human body.

The simulation flow starts by creating a library of electrical equivalent models of the organs under study using the SimPowerSystem blockset from Matlab [5]. These models include linear devices (R, L, C, voltage and current controlled sources, etc.) as well as non-linear devices (switches, diodes, hystheresis, etc.).

A proprietary tool called GenVhdl analyses the Matlab model and generates three sets of files that store the representation of the model: a discrete state-space C-code model representing the linear part of the model; a C-code wrapper that instantiates the C-models picked from the library; and a VHDL wrapper that instantiates and interconnects the VHDL-models picked from the library.

The VHDL-generated code is passed to a commercial HDL Design Tool to be synthesized, placed, routed and uploaded to the FPGA card [6]. The generated C-code is compiled and loaded into the microprocessor.

Depending on the complexity of the model of the physiological system, the C-code state space model running in the microprocessor may not be able to attain the minimum timestep required for the simulation. GenVhdl can also generate a synthesizable VHDL model for the state space solver capable of sustaining more than 4.5 GFlops occupying about 50% of a Xilinx 2VP30 Virtex II Pro FPGA.

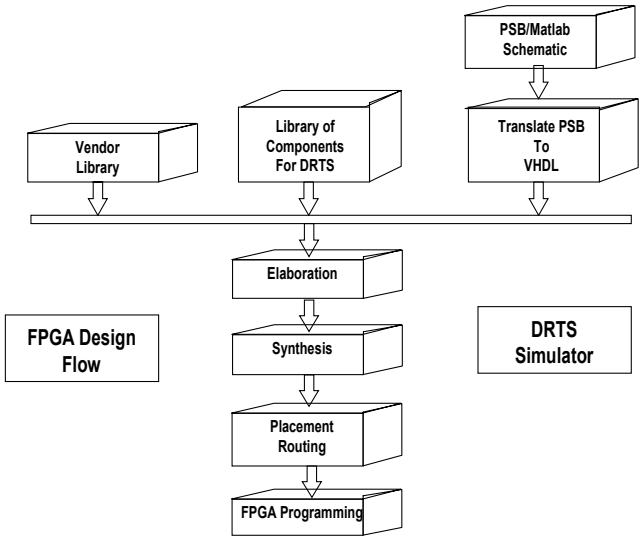

Fig. 1 – FPGA Implementation Flow

II. Simulator Architecture

The general architecture of the DRTS consists of a library of non linear models, a personal computer, interface A/D and D/A cards and FPGA cards. The non-linear models can be coded in C for implementation in a PC or in VHDL (VHASIC Hardware Description Language) to be implemented on a FPGA card. The VHDL/FPGA implementation is intended for real-time simulation of very complex models, possibly including many organs (e.g. detailed heart-lung system) or fine-grain tissue modeling of an organ (e.g. heart).

At the beginning of every timestep, the simulator acquires new data from the interface inputs through digital channels or through the A/D interface cards, and sends out the simulated physical variables through output digital channels

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or the D/A interface cards. It is important to note that this sequence introduces a two timestep delay between the simulator and the device under test, which can affects the accuracy of the simulation and in certain cases cause it to become instable.

Special care was taken in the development of the library of non-linear models as well as in the design of the simulator itself to reduce the occurrence of these unrealistic oscillations. Also, the simulation becomes more stable as the time step decreases in comparison to the circuit natural frequencies.

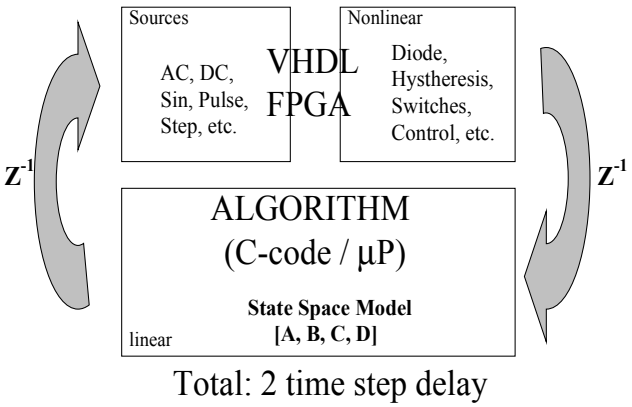

Fig. 2 – Decoupling linear and nonlinear sub networks

III. SIMULATION ALGORITHM

Physiological models vary according to level of granularity. Basically, we can capture the behavior of physiological models at cell, tissue and organ levels. Of course, a coarse granularity setting may not yield such good simulation results as a finer one. Sometimes a multilevel model may be necessary as a tradeoff between computational complexity and speed.

Cell level models can be captured by Maxwell equations. For example, let there be a bidomain cell model for the heart tissue [10], with two continua: intracellular and extracellular.

$$\nabla\bullet\left(\hat{\sigma}_i\nabla\Phi_i\right)=I_m+I_{in,i}=\beta_{sv}\left(I_{ion}+C_m(t)\frac{\partial V_m}{\partial t}+I_{tm}\right)$$

$$\nabla\bullet\left(\hat{\sigma}_e\nabla\Phi_e\right)=-I_m-I_{in,e}$$

$$=-\beta_{sv}\left(I_{ion}+C_m(t)\frac{\partial V_m}{\partial t}+I_{tm}\right)-I_{ec}$$

$$V_m=\Phi_i-\Phi_e$$

Where

Φ_i, Φ_e and V_m correspond to the intracellular, extracellular and transmembrane potentials,

σ_i and σ_e are the intracellular and extracellular conductivity tensors,

I_m, $I_{in,i}$, I_{ion}, I_{tm}, $I_{in,e}$, I_{ec} are current volumes

This type of bidomain model can be mapped to a bi-dimensional (2D) or tri-dimensional (3D) equivalent circuit involving R, C, L elements, which can be linear or nonlinear, as well as time independent or not.

Lumped R,L,C models can be also used to represent a section of a vessel (e.g. artery) or the full circulatory system [11-17], as for example this 10-layer model for the left ventricle blood circulation [17].

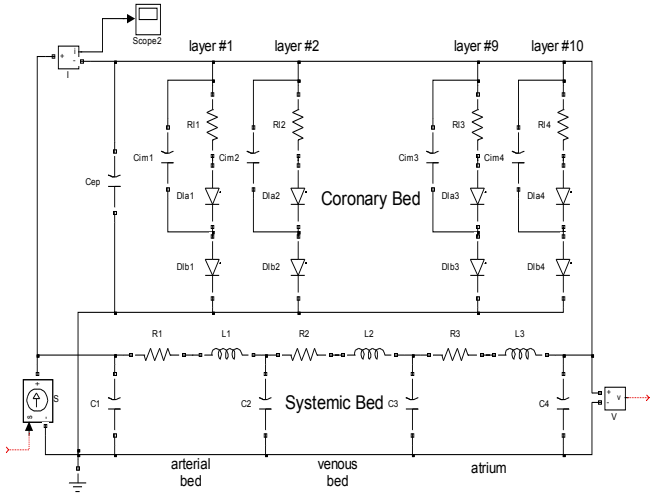

Fig. 3 – Analog electric model for the left ventricle blood circulation [17].

In this work, we use the decoupling technique shown in Figure 4 to split the organ electric model into two parts: a linear sub network and a nonlinear one. The linear sub network is simulated using the state-space classical approach. The electrical network is represented by its continuous-time state space model as:

$$\frac{dX(t)}{dt} = A\,X(t) + B\,U(t)$$

$$\frac{dY(t)}{dt} = C\,X(t) + D\,U(t)$$

Or in the discrete-time linear form:

$$X(n+1) = A\,X(n) + B\,U(n)$$

$$Y(n) = C\,X(n) + D\,U(n)$$

Where: n is the time step number
X is the state variable
U is the input stimulus vector
Y is the output signal vector
and A, B, C and D are the state space matrix or nonlinear operators

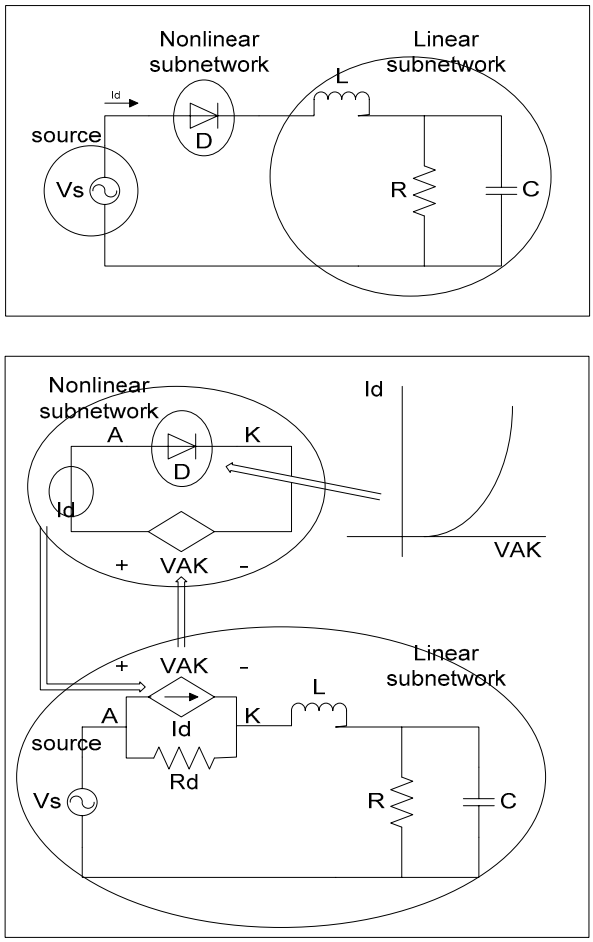

Fig. 4 Example of partition of a nonlinear circuit showing the Voltage/Current Source Decoupling Technique

Then, the discrete-time state space form is solved by a program running in the microprocessor. The equation of Figure 5 shows the state space representation of the linear part of the nonlinear circuit of Figure 1.

$$\frac{d}{dt}\begin{bmatrix} I_L \\ V_C \end{bmatrix} = \begin{bmatrix} \frac{-R_S}{L} & \frac{-1}{L} \\ \frac{1}{C} & \frac{-1}{RC} \end{bmatrix}\begin{bmatrix} I_L \\ V_C \end{bmatrix} + \begin{bmatrix} \frac{1}{L} & \frac{R_S}{L} \\ 0 & 0 \end{bmatrix}\begin{bmatrix} V_S \\ I_D \end{bmatrix}$$

$$\begin{bmatrix} V_C \\ I_A \\ V_{AK} \end{bmatrix} = \begin{bmatrix} 0 & 1 \\ 0 & 0 \\ R_S & 0 \end{bmatrix}\begin{bmatrix} I_L \\ V_C \end{bmatrix} + \begin{bmatrix} 0 & 0 \\ 0 & 1 \\ 0 & -R_S \end{bmatrix}\begin{bmatrix} V_S \\ I_D \end{bmatrix}$$

Fig. 5 State space representation of non linear circuit using Voltage/Current Source Decoupling Technique.

IV. FPGA IMPLEMENTATION

We are currently using a 2VP30 Virtex-II Pro, manufactured by Xilinx, as the target FPGA with about 136 multipliers. Our main module is a parameter-based pipelined vectorial add multiplier unit that can be configured to use 23 bits floating point representation (17 of mantissa and 6 bits of exponent) or 32 bits floating point representation (24 of mantissa and 8 bits of exponent). When configured for 23 bits floating point it is able to evaluate the scalar product of two vectors of 20 elements each in about 0.3 microseconds. When configured for 32 bits floating point it is able to evaluate the scalar product of two vectors of 20 elements each in less than 0.5 microseconds [18].

Assuming a physiological model with about n reactive elements (e.g. L or C), we can estimate that we would need about O(n) = k*n state variables, where k is a fudge constant dependent on the topology of the problem. For simplicity we can assume k = 1. As we can have up to 136 add-multipliers per FPGA, we estimate the computation time of one step calculation of our discrete model to be about:

$$T(1\ \text{step}) = 2n^2 * 0.3 * 10^{-6} / (20 * 136 * m)\ \text{seconds}$$

Where n is the order of the physiological model and m is the number of FPGA devices used in parallel on the hardware acceleration board.

This estimate assumes no special use of the sparse nature of the matrices A, B, C and D. For example a 3D tissue model involving around 1000 cells represented by an electric circuit with about 10000 reactive components would have a computational time of about 0.022/m seconds for one time step of a simulation. Let's assume a heart tissue simulation of 220 beats/minute with the need of using up to the 7th harmonic of the heart beat frequency. This leads to a maximum computational time of about

$$T_{max}(\ 1\ \text{step}\ ) = 1 / ((220 / 60) * 7 * 2)\ \text{sec} = 0.0195\ \text{sec}.$$

We can estimate that a board with 1 FPGA should be able to handle this simulation in real-time. The sparse nature of the problem would lead to a substantial saving in the number of multiplications allowing us to increase the number of cells by about 10 times. As a comparison, it would take about 1.5 hours to simulate 60 seconds of the same model of in a modern 1 GHz Pentium-based workstation.

As an illustration of the capabilities of our simulation platform, we use a detailed model of the coronary bed circulation (Figure 12) [19] in an average human adult. Each ventricle is modeled by a time dependent capacitive current source (Figure 7). Our simulation results (Figures 8-11 and 13-16) agreed with other published models [19], where pressure and flow are measured respectively in mmHg and ml/sec. Time scale is 1 sec in all figures. We assumed a heart rate of 72 beats/min.

We are currently working on developing hardware mappings of our physiological models that take into account the sparse nature of the problem, i.e. a cell has about 6 neighbors in a typical 3D tissue model, leading to clusters of coefficients in the A matrix for example.

V. Conclusion

This presentation discussed the mathematical and computing frameworks to allow real time simulation of biological systems for use by manufacturers of medical devices. The test environment built to evaluate this approach consists of an AMD Athlon XP 2400+ microcomputer and a Digilent Inc. XUP Virtex-II Pro Development System FPGA Card with a 2VP30-7-FF896 Virtex II Pro FPGA. The proposed simulator results were obtained with Mentor Graphics Modelsim 5.6c VHDL simulator and the Xilinx ISE v6.3i Development Environment.

The deterministic nonlinear case was outlined. It is expected that large-scale/ high detail computational simulations of cells, tissues and organs of the human body will speed up the development of new medical devices and treatment protocols. We are currently working on demonstrating how such hardware-based simulation algorithms can be successfully deployed by using this approach for a more detailed model of the lung-heart system at cell, tissue and organ levels of abstraction.

Acknowledgment

J. C. G. Pimentel thanks Xilinx Inc. for its support providing the FPGA prototype board and the development tools used for the simulation and experimental results.

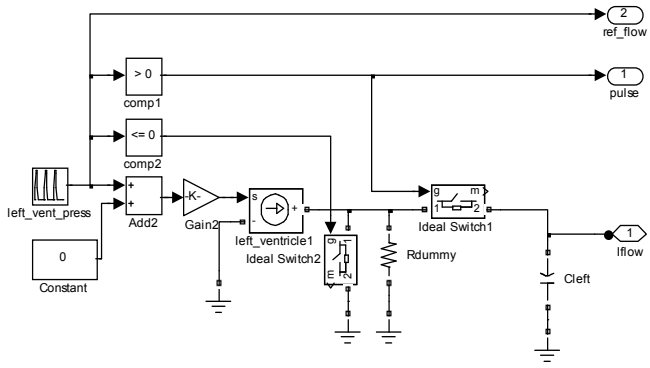

Fig. 7 – Modeling of a nonlinear capacitive blood flow source.

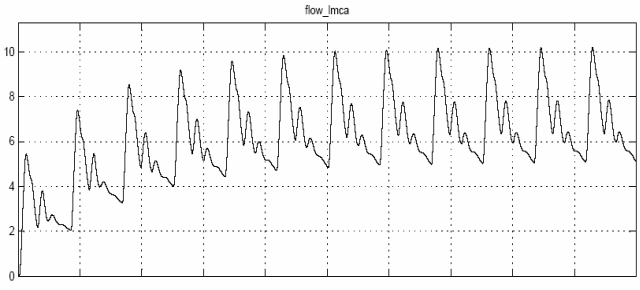

Figure 8 – Blood flow (ml/sec) in coronary branch lmca.

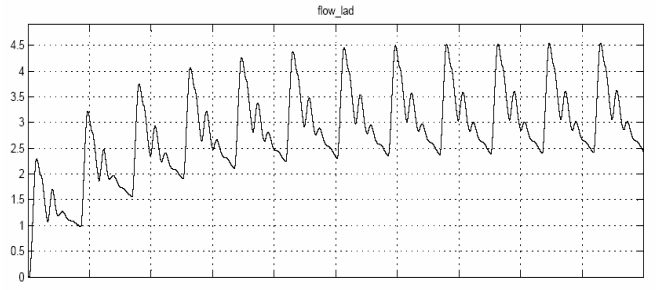

Figure 9 – Blood flow (ml/sec) in coronary branch lad.

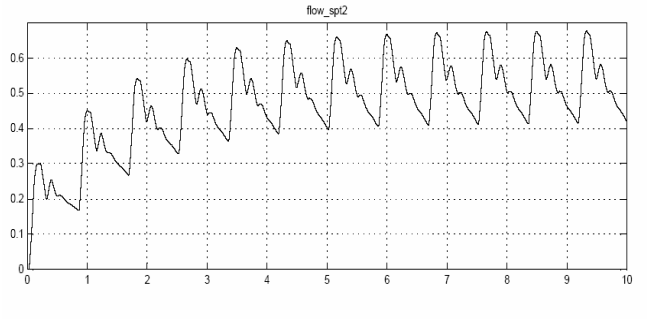

Figure 10 – Blood flow (ml/sec) in coronary branch spt2.

Figure 11 – Pressure (mmHg) in left ventricle.

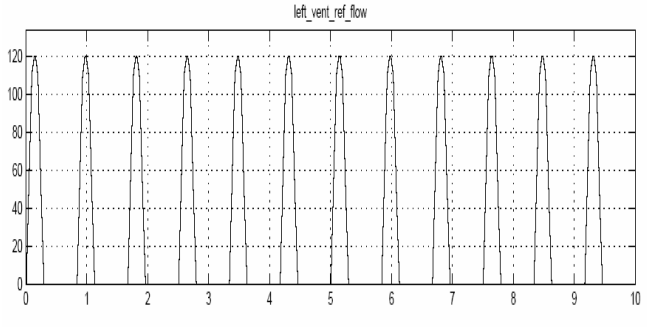

Figure 12 – Blood flow (ml/sec) in left ventricle.

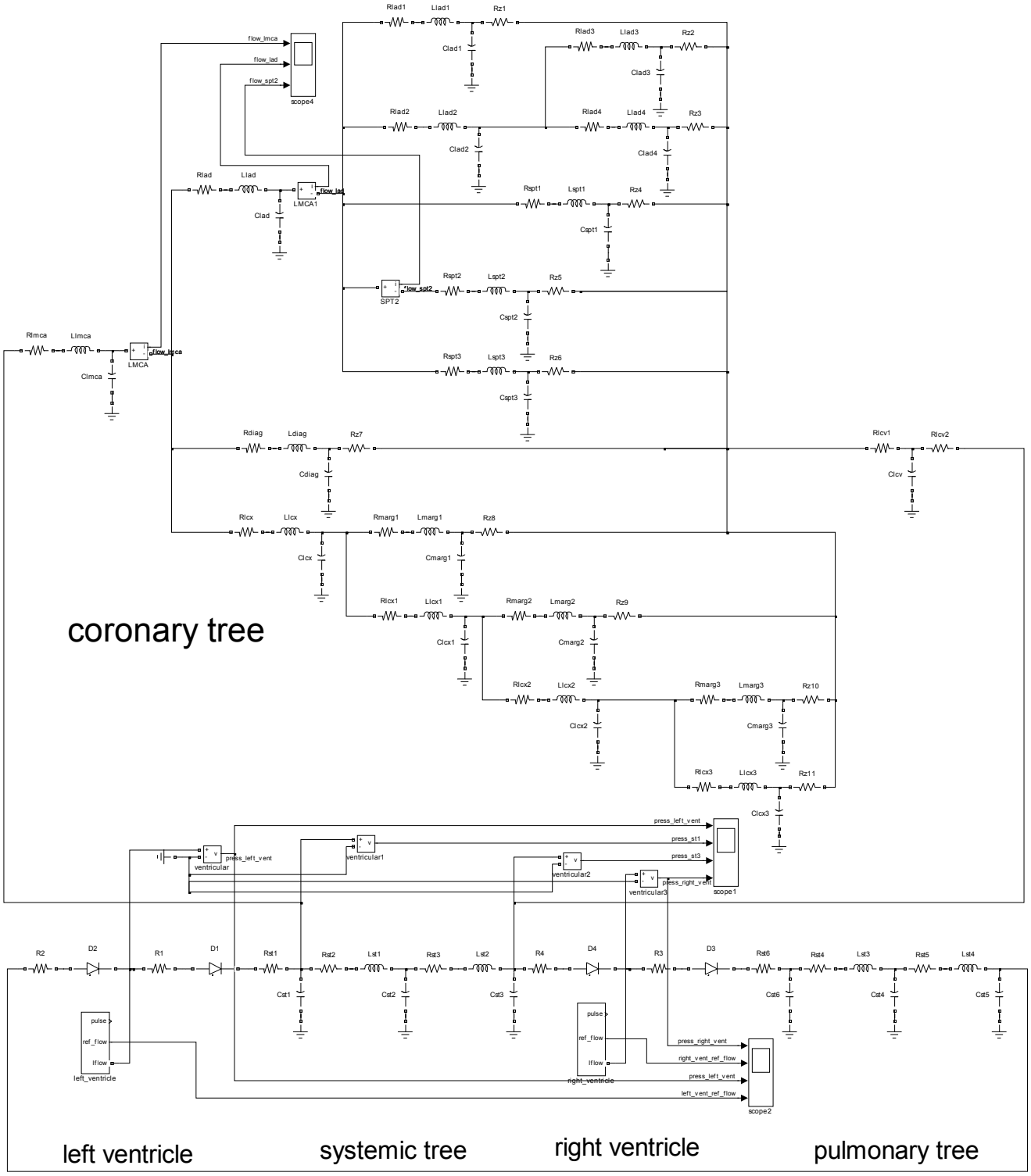

Figure 12 – Detailed model of coronary circulation [19].

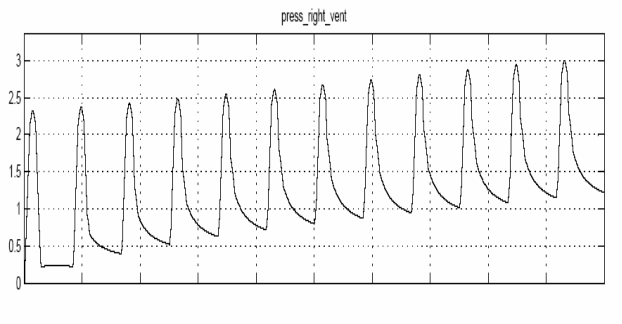

Figure 13 – Pressure in right ventricle (mmHg)

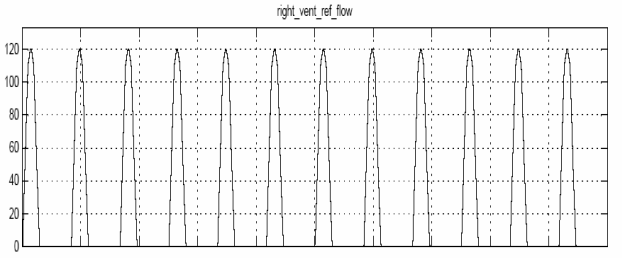

Figure 14 – Blood flow (ml/sec) in right ventricle

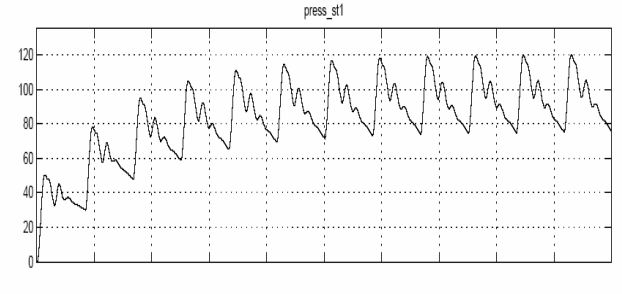

Figure 15 – Pressure (mmHg) in coronary branch st1.

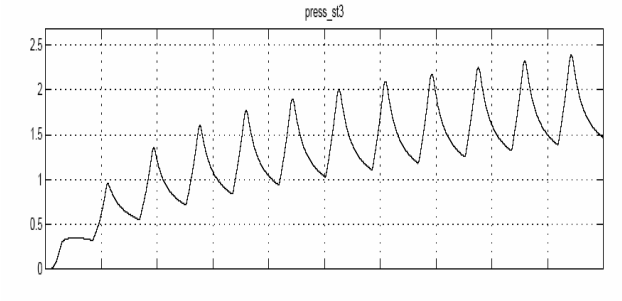

Figure 16 – Pressure (mmHg) in coronary branch st3.

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