

# **NETLOGO INTEGRATED DEVELOPMENT ENVIRONMENT FOR MODELING PHYSIOLOGICAL PROCESSES**

## **Victor IAPĂSCURTĂ1,2**

<sup>1</sup> Department of Software Engineering and Automatics, Technical University of Moldova, Chișinău, Moldova *<sup>2</sup>Department of Anesthesia and Intensive Care, N. Testemitanu University of Medicine and Pharmacy, Chișinău, Republic of Moldova* 

\*Corresponding author: Victor Iapăscurtă, [victor.iapascurta@doctorat.utm.md](mailto:victor.iapascurta@doctorat.utm.md)

Tutor/coordinator: **Ion Fiodorov**, PhD, doctor in computer science, Department of Software Engineering and Automatics, Technical University of Moldova, Chișinău, Moldova

*Abstract. NetLogo integrated development environment (IDE) is a powerful tool for modeling various complex systems, including human physiological processes. This software provides a userfriendly interface and a versatile programming language that enables researchers and educators to simulate and study different aspects of human physiology in a virtual environment. One key benefit of using NetLogo IDE to model human physiological processes is its ability to visualize and simulate dynamic systems. The software allows users to create agents representing different human body components, such as cells, organs, and tissues. These agents can interact with each other, exchange information, and respond to external stimuli, mimicking the behavior of natural physiological systems. This paper presents an example of modeling the cardiovascular system using NetLogo IDE to simulate cardiac output, blood flow, heart rate, and blood pressure. By manipulating various parameters, such as vessel diameter, contractility of the myocardium, and others, one can examine the impact of different factors on the overall functioning of the cardiovascular system. This can help in understanding cardiovascular diseases and exploring potential treatment strategies.* 

*Keywords: NetLogo, system dynamics modeling, agent-based models, cardiovascular system model* 

#### **Introduction**

 Advancements in technology and computational power have revolutionized the field of biomedical research, enabling scientists to develop sophisticated software applications that model and simulate human physiological processes. These software tools provide valuable insights into complex physiological systems, aiding in understanding disease mechanisms, drug discovery, and personalized medicine. A number of software applications are widely used for modeling human physiological processes, including PhysiCell [1], Virtual Physiological Human (VPH) toolkit [2], OpenSim [3], and others.

 NetLogo integrated development environment (IDE) [4] is a different software application offering unique advantages compared to PhysiCell, VPH toolkit, and OpenSim. Some key benefits of NetLogo IDE are (a) accessibility and simplicity, which makes it an excellent choice for beginners or those who want to quickly develop and explore simulations without delving into complex coding; (b) educational value; (c) community and model sharing by providing a repository of well-documented and validated models that can be easily adapted for specific research questions; (d) flexibility and interdisciplinary applications by supporting a wide range of modeling paradigms, including agent-based modeling, cellular automata, and network modeling; (e) visualization and experimentation using powerful visualization capabilities that allow users to observe and analyze simulation results in real-time. This feature facilitates the exploration of model behavior, identifying emergent properties, and analyzing complex systems' dynamics.



NetLogo IDE also allows users to conduct experiments by systematically varying model parameters and observing the effects on the system.

It is important to note that while NetLogo IDE offers unique advantages, PhysiCell, VPH toolkit, and OpenSim are specialized software applications focused on modeling human physiological processes with more specific capabilities in their respective domains. The choice of software will finally depend on the user's specific research goals and requirements.

### **Some capabilities and features of NetLogo IDE**

NetLogo IDE provides a unique platform for creating agent-based models. In these models, individual agents represent different components of the human body, such as cells, tissues, or organs. These agents can be programmed with specific behaviors and rules, simulating complex physiological interactions.

NetLogo IDE also supports the integration of external data and models. Researchers can import and incorporate data from experiments or clinical studies into their models. This enables the validation and calibration of the model against real-world data, enhancing its accuracy and relevance. Additionally, mathematical models developed using tools like MATLAB or R can be integrated into NetLogo IDE, allowing for the combination of computational and agent-based modeling approaches.

Furthermore, NetLogo IDE offers a variety of analysis tools to examine the results of the simulations. Researchers can collect and analyze data on agent behavior, system dynamics, or emergent properties. This analysis can involve statistical measures, such as mean values, standard deviations, or correlation coefficients, to quantify and interpret the simulation outcomes.

Another advantage of NetLogo IDE is its extensibility. The software supports the creation of custom extensions, enabling users to incorporate specific functionalities or models tailored to their research needs. This flexibility allows researchers to explore different aspects of human physiology and adapt the software to suit their particular research questions.

Moreover, NetLogo IDE has a thriving community of users and developers who share models, resources, and expertise. This collaborative environment fosters knowledge exchange and encourages the development of new models and techniques. Users can access various pre-existing physiological models, saving time and effort in model development and facilitating interdisciplinary collaborations.

Lastly, NetLogo IDE is not limited to modeling human physiology alone. It can be used to simulate and study various other biological systems, such as ecological systems, population dynamics, or biochemical reactions. This versatility expands the range of research possibilities and allows for interdisciplinary investigations.

### **Using NetLogo to model the human cardiovascular system. Results and discussion**

In this project, the cardiovascular system was primarily modeled using the Netlogo System Dynamics Modeler (SDM) and, to a lesser extent, the IDE's Agent-Based Modeling capabilities.

In the model, the cardiac output (CO) refers to the volume of blood that the heart pumps out in one minute. It is a critical measure that is influenced by various factors, which are routinely monitored in an intensive care unit (ICU). As explained by Ohm's law, the concept of the heart as a pump, which forms the basis for determining cardiac output, is supported by straightforward hydraulic models and the analogous relationship between electrical and fluid dynamics:

$$
I = \frac{U}{R} \tag{1}
$$

The equation (1) states that the current (I) is equal to the voltage (U) divided by the resistance (R). In this context, the current represents the flow rate of a fluid, the voltage represents the fluid pressure, and the resistance represents the resistance of different segments of the circulation. Additionally, the charge (Q) represents the volume, and the capacitance (C) represents compliance. Elastance is the inverse of compliance (1/C). This is illustrated in Fig. 1.





**Figure 1. The hydraulic model supported by the analogy between the electrical domain and fluid dynamics, based on Ohm's law.** 

From a system dynamics point of view, the model comprises three compartments: two passive compartments for the arterial and venous components of the circulation, and an active compartment for the left ventricle. Figure 2 illustrates the utilization of the NetLogo SDM system dynamics approach [4]. It showcases multiple stocks and the flows between them, which are situated in proximity to the hydraulic domain. Ordinary differential equations (ODE) determine the model's behavior, which explains the dynamics and connection between three stocks (volumes of the left ventricle, arterial, and venous segment) and their corresponding flows.



**Figure 2. Representation of the stocks and flows in the model. Stocks (V) symbolize the left ventricle (V\_LV), arterial segment (V\_AO), and venous segment (V\_V).**

The pulsatile flow is determined by a driver function that imitates the heart muscle contractions and a Heaviside step function that replicates the valve mechanism, following the principle of opening in response to pressure and closing in response to flow. The model utilizes the following types of equations:

$$
Q_t = \frac{P_1 - P_2}{R},\tag{2}
$$

$$
\frac{dV}{dx} = Q_{in} - Q_{out},\tag{3}
$$

where *P* denotes pressure, *V* – volume, and *Q* flow. The model's outputs include stroke volume (SV), CO, and ejection fraction (EF) (Fig. 3).



*Technical Scientific Conference of Undergraduate, Master, PhD students, Technical University of Moldova* 



**Figure 3. The model's graphical interface. In the middle are monitors for SV, CO, and EF.** 

In addition, the model produces a pressure-volume loop (PVL) that is specific to a particular scenario or pathological condition. This PVL can be seen in the black window in Figure 3, which shows two examples of a "normal" PVL (in green) and hypertension (in red). The PVL can offer valuable insights for the diagnosis, monitoring, and treatment of a specific patient. The region enclosed by PVL is regarded as a reliable indicator of the amount of oxygen the myocardium requires [5]. This parameter cannot be directly evaluated but can significantly impact the progression of the disease, the final result, and the approach to treatment. The model can effectively demonstrate the impact of various factors, such as preload, afterload, myocardial contractility, and heart rate, on cardiac output. The impact of altering various model parameters can be observed in the resulting pressures and volumes in the plot area [6]. Additionally, these changes can be seen in the PVL and CO of the left ventricle, both in normal and pathology. It is possible to simulate several pathological states by setting model parameters to different values.

#### **Conclusions**

NetLogo IDE offers a comprehensive set of tools and features for modeling human physiological processes. Its agent-based modeling approach, integration of mathematical models, visualization capabilities, and extensibility make it a valuable tool for researchers and educators in the field of physiology. By utilizing this software, scientists can gain insights into the human body's complexities, explore hypotheses, and contribute to advancements in understanding and treating physiological conditions.

#### **References**

- [1] "OpenSim," [Online]. Available: https://simtk.org/projects/opensim/
- [2] "The VPH ToolKit," [Online]. Available: https://www.jstor.org/stable/25704687
- [3] "PhysiCell," [Online]. Available: http://physicell.org/
- [4] U. Wilensky. "NetLogo." Center for Connected Learning and Computer-Based Modeling, Northwestern University, Evanston, IL. Dec 12, 2018, ccl.northwestern.edu/netlogo/index.shtml
- [5] K. R. Walley, "Left Ventricular Function: Time-Varying Elastance and Left Ventricular Aortic Coupling," *Critical Care*, 20(1), 2016 270. doi:10.1186/s13054-016-1439-6.
- [6] V. Iapascurta. "Cardiac\_output-Simple\_Model\_01\_01," NetLogo Modeling Commons. Apr 2018, Available: www.modelingcommons.org/browse/one\_model/5361#model\_tabs browse\_info.