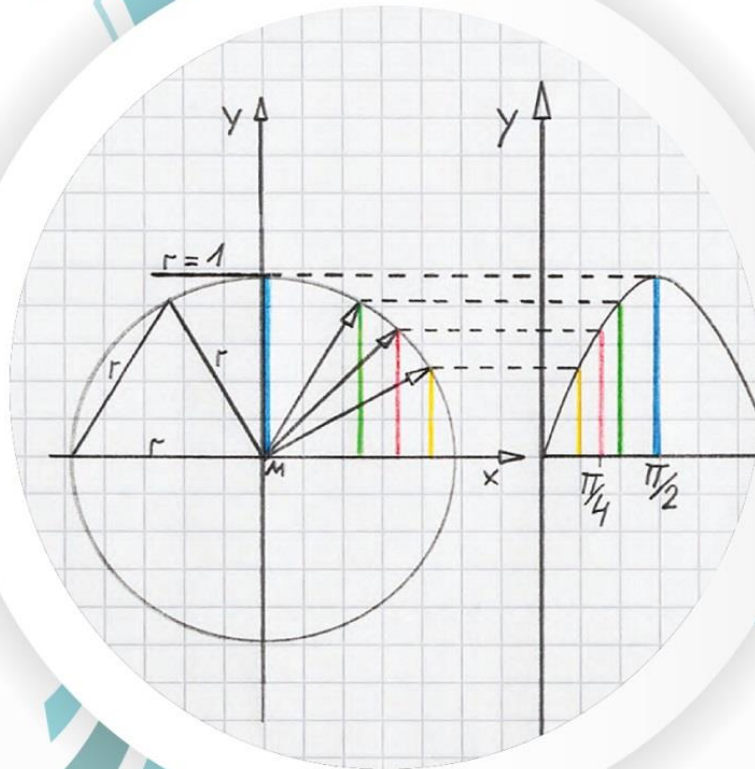


INTERNATIONAL JOURNAL OF

ENGINEERING MATHEMATICS: THEORY AND APPLICATION



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CONTACT

Professor of Computational Engineering Mathematics and
Numerical Analysis
Faculty of Engineering
Zagazig University
Zagazig
P. O. 44519
Egypt
<http://iejemta.com/>
Email: sgamil@zu.edu.eg



Modeling the formation of an electrocardiosignal in the VisSim environment

V.G.Maxsudov, E.Ya.Ermetov, A.Z.Sobirjonov, J.T.Abdurazzoqov, I.B.Zuparov
Tashkent Medical Academy, Department of “Biomedical Engineering, Informatics and Biophysics”.

Abstract In this article, the model, modeling, modeling of medical biological processes, modeling of the formation of an electrocardiosignal in the VisSim environment, modeling knowledge about the person himself and the world around him, studying models of medical biological objects, objects and events in real life are alive and alive. non-physical systems, engineering structures, various processes - physical, chemical, biological objects, identification of their properties, improvement, models of rationalization of construction methods, modeling of electrical processes in the myocardium, TMB membrane potential form, ATMB membrane potential form, structure of the heart and generation of electrocardiosignal The scheme of making is discussed.

Keywords: model, modeling, electrocardiosignal in the VisSim environment, engineering constructions, modeling of electrical processes in the myocardium, TMB membrane potential shape, shape of the ATMB membrane potential, heart structure and electrocardiosignal generation.

Modeling is an integral part of a person’s knowledge of “himself” and the world around him. Modeling is the study of objects of knowledge on their models; construction and study of models of real-life objects and phenomena (living and non-living systems, engineering structures, various processes - physical, chemical, biological, etc.) and constructed objects (to determine, refine their characteristics, rationalize construction methods).

Modeling is the process of replacing the object of study with some of its model and conducting research on the model in order to obtain the necessary information about the object. A model is a physical or abstract image of a simulated object, convenient for research and allowing to adequately display the properties and characteristics of the object that are of interest to the researcher. Models in biology are used to model biological structures, functions and processes at different levels of organization of the living: molecular, subcellular, cellular, organ-systemic, organismic and population-biogenetic. It is also possible to model various biological phenomena, as well as the living conditions of individuals, populations, and



ecosystems. In biology, three types of models are mainly used: biological, physico-chemical, and mathematical (logical-mathematical).

Biological models reproduce certain conditions or diseases that occur in animals or humans in laboratory animals. This makes it possible to study in the experiment the mechanisms of the occurrence of a given condition or disease, its course and outcome, and to influence its course. The cycle of proposed practical exercises is devoted to the basics of modeling various biological processes and systems.

Practical exercises are aimed at deepening and consolidating theoretical knowledge in the main sections of the discipline “Modeling of biological processes and systems”, to gain practical skills in solving modeling problems in biophysics and medicine.

Practical classes contain 5 works and cover the most important questions on the main sections of the theoretical course, in particular: “Fundamentals of mathematical modeling”, “Modeling based on differential equations”, “Simulation modeling”, “Basic models of mathematical biophysics”.

When performing work, a PC and specialized software environments MathCAD, VisSim and NeuroPro are used. It is assumed that students are previously familiar with the basic concepts of computer mathematics (discipline “Informatics”).

Objective. The study of conceptual models in the form of block diagrams; study of the principle of multiple models on the example of modeling the electrical parameters of the cardiovascular system in the VisSim environment.

Theoretical part. A model is a chosen way of describing an object, process or phenomenon, reflecting factors that are significant from the point of view of the problem being solved. Modeling is based on the theory of similarity, which states that absolute similarity can only take place when one object is replaced by another exactly the same. When modeling, absolute similarity does not take place and they strive to ensure that the model reflects the studied side of the object's functioning well enough. One of the key principles of modeling is the principle of multiple models - the created model should reflect, first of all, those properties of a real system (or phenomenon) that affect the selected performance indicator. Accordingly, when using any particular model, only some aspects of reality are known. For a more complete study of it, a number of models are needed that allow reflecting the process under consideration from different angles and with varying degrees of detail. For example, to study the activity of the cardiovascular system, it is possible to create both a model for the formation of electrical potentials of the myocardium and a model for the movement of blood through the vessels /1/.



Software. The software package VisSim (Visual Simulator) from Visual Solutions Inc (USA) is used as a tool for performing this practical lesson. VisSim is an interactive visual shell for developing continuous, discrete, multi-frequency and hybrid system models and modeling the dynamics of these systems. VisSim, the system model is built in the form of a block diagram in the usual way. The main tools are functional blocks and links between them. Each block performs a specific function. The function can be as simple as “sin” or as complex as a 10th order transfer function. VisSim contains more than 100 linear and non-linear blocks, allowing you to simulate arbitrarily complex systems. But if suddenly, for some reason, the provided set of tools turns out to be insufficient, then VisSim provides a simple extension mechanism through custom blocks. All blocks are available through the “Blocks” menu. Most blocks have user-settable parameters that properly define their conversion functions. You can define or change parameter values using the dialog boxes of the same name (“Properties”). Quick access to the “Properties” dialog boxes for most blocks is possible by simply pointing the block with the right mouse button. Connecting blocks with wires tells VisSim in what sequence and to which block to send signals for processing during model simulation. Signals are just data (model coordinate values). The input signals (x_n) include those that arrive at the inputs of the blocks; output signals (y_n) are present at their outputs.

Most VisSim blocks can add or remove pins. If a conductor is connected to it at the time of deleting the pin, it will also be removed from the block diagram. An important element of the models is a device that allows you to monitor the processes occurring in the model - the Plot block (graph, oscilloscope). By default, it has a time axis, however, by activating the XY Plot command, the X axis can be connected to one of the oscilloscope inputs. This command is available when you specify the Plot block and press the “right” mouse button, after which the block properties window appears. After activating the XY Plot command, you need to specify to which input the X signal will be connected (by default, to the first from the top). The color of the oscilloscope inputs indicates what color the graph itself will be displayed. 10 As a signal source, you can use a generator of sinusoidal signals sinusoid, for which in the properties of the block you can specify the delay relative to the beginning of the simulation process, the amplitude of the signal, the frequency. The signal source can also be the import block, in which the signal is specified as an external file in the .dat, .mat, .m, .wav formats. The peculiarity of using this block in the student version of VisSim is the need to connect it using a unity gain block. The signal receiver can be the export block, when using which it is necessary to specify in the block properties the name and extension of the file into which the data is being written. The



summingJunction is used to sum the signals. The default number of inputs is 2, however, using the usual mechanism for increasing the number of inputs, their number can be increased.

The corresponding timeDelay block is used to obtain the signal delay. The delay time in seconds is determined by the block const (constant) connected to the second (non-signal) input.

Gain block - the coefficient with a decimal fraction is specified through a dot, and not through a comma.

The transfer function block (transferFunction) transforms the input signal according to the transfer function, which can be determined by enumerating the coefficients of the numerator and denominator polynomials:

$$W(p) = \frac{B_m(p)}{A_n(p)}$$

The following settings are set:

| |
|--|
| <p>Coeff. Gain In this line you need to set the gain of the transfer function. The real value of the gain may differ from the entered value if the ratio of the polynomial coefficients in the numerator and denominator that affect it is not equal to one (for LPF these are free terms in polynomials, for HPF these are the coefficients at s-operators to the greatest extent). Default value 1</p> |
| <p>Numerator (Numerator) In this line it is necessary to list the coefficients of the polynomial 11 of the numerator of the PF, starting with the coefficient at the highest degree. The rightmost value determines the free term of the polynomial. Separated by a space. The order of the numerator polynomial cannot be greater than the order of the denominator polynomial</p> |
| <p>Denominator In this line it is necessary to list the coefficients of the PF denominator polynomial (characteristic polynomial). The rightmost value determines the free term of the polynomial. The transfer function of the nth order must have: n root-poles, or n + 1 coefficient</p> |

Example: you need to create a block with PF

$$W(p) = \frac{12}{0,8p^3 + 1,5p + 1}$$

Numerator: 12

Denominator: 0.8 0 1.5 1

На вход подается сигнал $x(t)$ Blocks –Signal Producer, на выходе – $y(t)$.

Electrical processes in the myocardium. Cardiac muscle is heterogeneous in cellular composition /4/. There are typical contractile myocardial fibers (TMF) and atypical myocardial fibers (ATMF). Significant differences were revealed between them, both in structure and in functions and bioelectrogenesis. For TMV, which form



the bulk of the heart muscle and carry out its contractile activity, membrane potentials are typical, which are shown in Fig. 1 with a contractile activity of the heart of 75 beats per minute. In the membrane potentials of TMB, a stable level of the resting potential is clearly visible, approximately equal to -90 mV. Excitation of TMB is manifested in the appearance of an ascending branch of the action potential, while the potential from -90 mV increases to $10..20$ mV relative to the intercellular medium. The potential rise occurs in 20 ms. Unlike other muscle fibers and axons, the myocardial fiber has little inversion potential. However, the most characteristic features are inherent in the repolarization of the heart muscle. Membrane potentials that are recorded for ATMB look different (Fig. 2). They do not have a stable level of polarization, that is, there is no rest potential. The electrical activity of ATMB is a continuous oscillation of the membrane potential. Upon reaching -60 mV, a slow depolarization spontaneously begins to develop. Then, at a level of about -40 mV, this process accelerates, which corresponds to the appearance of an action potential in the ATMV, with its characteristic inversion. Depolarization is replaced by repolarization, at the end of which slow depolarization begins again, therefore, ATMB is characterized by non-stop dynamics of membrane potentials, which underlies the rhythmic activity of the heart. ATMB tissue is concentrated in the form of islets in various parts of the heart. With this arrangement, ATMV is combined into a single system. Features of the conduction of excitation through the myocardium are associated with the method of interconnecting its individual fibers, between which insertion discs were found, which are duplicates of membranes in which there are gap junctions. These contacts provide an electrical connection between adjacent fibers. Since an electrical impulse (action potential) generated in one of the fibers can be propagated to neighboring fibers through electrical rather than chemical transmission, the heart has the property of an individual cell. It must be emphasized that the electrical connection exists not only between the TMV of the heart, but also between the ATMV. Therefore, the excitation that has automatically arisen in ATMB easily passes to TMB and, thus, spreads throughout the heart.

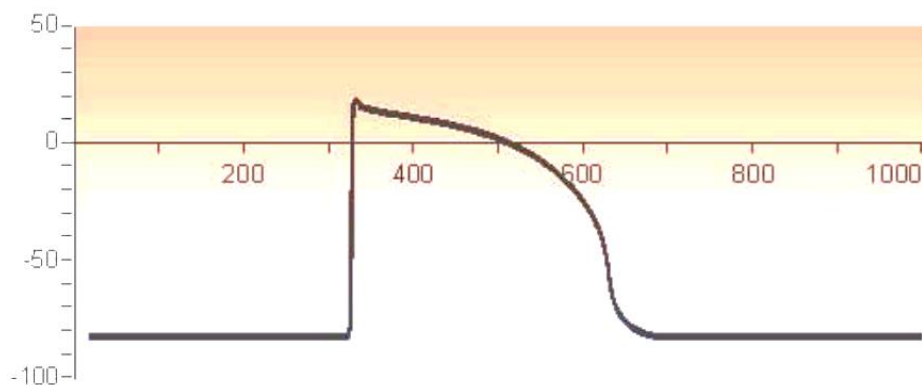


Fig. 1 – TMB membrane potential shape.

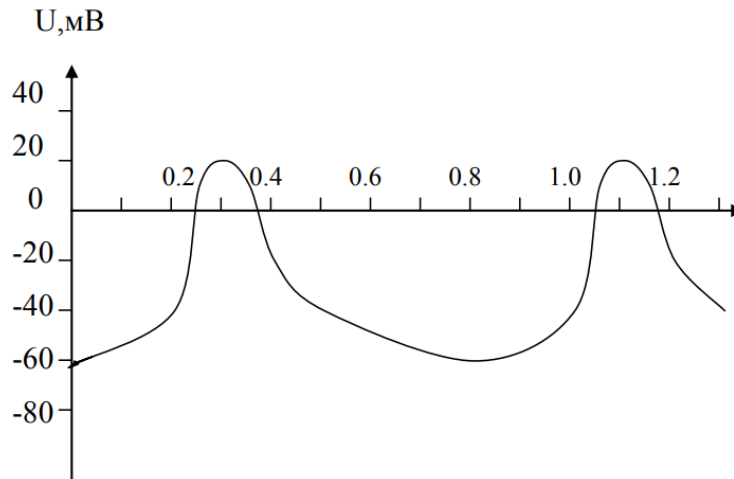


Fig. 2 - The form of the membrane potential ATMB

A clear subordination was established between the tissue islands of ATMB. The leading one is located in the right atrium between the venous sinus and the sinoauricular node (Fig. 3). When this node is automatically excited, and this is a normal state in a healthy person during life, then other parts of the ATMB perform only the function of conducting excitation. At the same time, their own automatism is suppressed, so the sinoauricular node is called the pacemaker. Due to the fact that it is not one ATMB fiber, but a group of approximately 5000 fibers, the heart has a high reliability in maintaining a stable period of spontaneous oscillations. From the ATMV of the sinoauricular node, excitation is transmitted to the TMV of the atria and carried through them at a speed of about 1 m/s. Already after 40 ms from the appearance of the action potential in the pacemaker, all sections of the atrium are in an excited state. Excitation spreads through the atria in a wide front, which is ensured by the presence of gap junctions not only between the ends of individual myocardial fibers, but also between their lateral surfaces. Excitation going to the atrium along different paths simultaneously reaches the second section of the ATMV - the antorioventricular node.

The atria are separated from the ventricles by fibrous tissue, which is unable to conduct excitations. However, in this barrier there is a narrow gap in which the antroventricular node is located, which conducts excitations from the atria to the ventricles. There is no other way for excitation in the myocardium of the ventricles. Slowing down the conduction of excitation from the atria to the ventricles provides an extremely important pause between the contractions of the atria and ventricles, which is extremely important for the normal functioning of the heart - an antroventricular delay, which is necessary so that all the blood accumulated by the atria in diastole completely passes into the ventricles before they begin to contract.

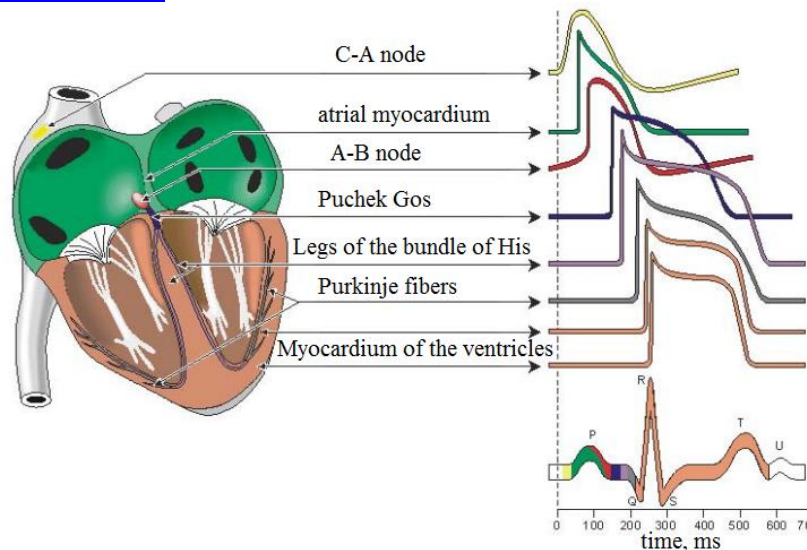


Fig.3-The structure of the heart and the scheme for generating an electrocardiosignal.

From the antroventricular node, excitation in a single front enters the antroventricular bundle or bundle of Hiss. There, the speed of excitation increases rapidly and reaches 2-3 m/s. The increase in speed is due to the thickening of the ATMB and the increase in the density of gap junctions in the insert disks. Closer to the apex of the heart, Purkinje fibers depart from the bundle of Giss. These ATMBs come into contact with the TMBs of the ventricles. Purkinje fibers have the largest diameter compared to other myocardial fibers. The speed of their excitation reaches 4-5 m / s. The connection between the Purkinje fibers and TMV of the ventricles is carried out by numerous thin branches of the ATMV. A separate thin fiber acts on the TMW as a point source of current, therefore, from the point of contact between them, depolarization propagates in the form of a spherical wave, while there are no conditions for the propagation of the excitation front. In this regard, in contact of the branches of the Purkinje fibers with ventricular TMB, the transmission of excitation slows down, which ensures the synchronization of excitation of the entire ventricular myocardium.

Excitation from a separate Purkinje fiber passes to one TMV, but since their number is very large, the TMV of the ventricles begins to decrease almost in phase. Excitation along the myocardium of the ventricles moves from the apex to the base of the heart, that is, in the opposite direction relative to the Hiss bundle. The last ones that are excited are those parts of the ventricles that are located near the atria /4/.

The electrical activity of the heart can be modeled as follows. Let's divide the myocardium into segments, each of which has an electrical potential in a certain phase of the cardiocycle. Using the TMW potential model, we organize their delay relative to each other, in accordance with the provisions of the model. In addition,

since the projections of these potentials on the sides of the Eithoven triangle are different, we will take into account this difference using the coefficients by which we will multiply each TMW potential. Choosing the number of TMV segments equal to 14, taking into account the delays and coefficients assigned to each segment, we obtain a table of initial data for ECG modeling.

As a TMW potential, we use a signal given in a table (.dat format file), corresponding to the shape of Fig.4.

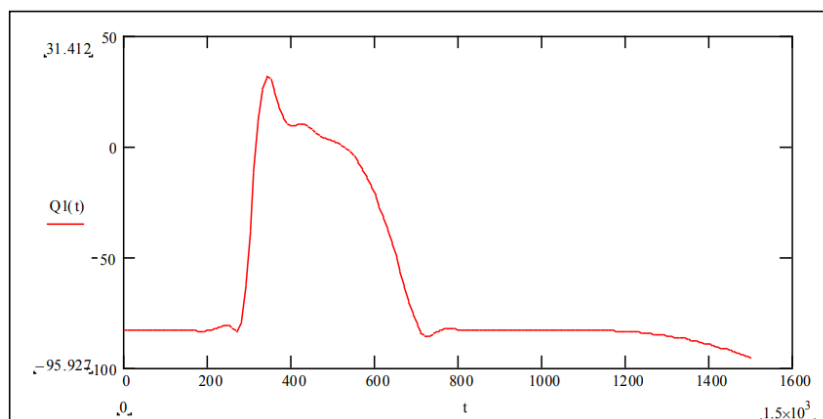


Fig.4 - TMB waveform.

To create a model, you must use the Import block, delay, gain blocks, and an oscilloscope.

In conclusion, we say that the model, modeling, modeling of medical biological processes, modeling of the formation of an electrocardiosignal in the VisSim environment, modeling knowledge about the person himself and the world around him, studying models of medical biological objects, objects and events in real life live and non-living systems, engineering structures, various processes - physical, chemical, biological objects, identification of their properties, improvement, models of rationalization of construction methods, modeling of electrical processes in the myocardium, TMB membrane potential form, ATMB membrane potential form, Heart structure and the scheme of generating electrocardiosignal is considered.

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