

## MODELLING OF RESOURCES ACCUMULATION AND THEIR OPERATIONAL CONTROL IN BIOTECHNOLOGICAL, BIOMEDICAL AND WEB INFORMATION SYSTEMS

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**Abstract:** The aim of this work is to build a structure of a mathematical model for resource accumulation and their operational control in biotechnological, biomedical and Web information systems for the in-depth studies of their common properties. For the first time ever a concept of the models for the mentioned processes is proposed as a system of differential equations. The equations describe the dynamics of state variables, of a substrate and of a product of the processes being analysed. Each partial implementation of the conceptual model includes a nonlinear part represented by Monod function. This raises the problem of developing a generalized method for identifying the nonlinear models of the mentioned type, which will be resolved in future publications.

**Key words:** system of nonlinear differential equations, state variable, substrate, system's product, Monod function.

### 1. Introduction

Mathematical modelling is one of the main tools used both for gnoseological purposes and for the problems concerning the management of important processes in the systems under investigation [1]. Today, the processes in physicotchnical objects have been studied more completely than in their biotechnological, medical and Web counterparts. The processes in three latter objects resemble the processes characteristic for the functioning of living organisms. One of the most important processes is that of operational control of the system's resources at extreme or close to extreme loads. Another important class of the processes is rather slow accumulation of resources, which are to ensure operation of the system, increase its capacity, or lead to the formation of useful by-products. Models of such processes make it possible to evaluate and improve the operational effectiveness of the systems mentioned above.

There are two basic approaches to modelling: deductive and inductive. The deductive approach is used in modelling the systems whose elements are subject to simple and clear laws. When there is not enough information on the system under study, the inductive

approach is applied to select a model of optimal complexity based on experimental data [2]. To simulate dynamic and rather complex processes, the approach called "black box" is used. It is focused on the input and output characteristics of the processes without specifying mechanisms of their implementation.

Adequacy of developed models of a system is mainly determined by the level of solving the problem of structural and parametric identification. For dynamic systems, the main structural identification method consists in selection of a class of model structures and solving the problems of parametric identification for each model of the class based on the minimization of a certain criterion of quality [2]. In such a way the inductive approach to structural identification of the systems is implemented. However, the question of selecting the basic functions and components for hypothetical structures able to adequately represent the modelled object remains open.

Works devoted to the problem under investigation propose only few basic functions for hypothetical structures. It is worth to mention Gabor polynomials, trigonometric polynomials, Volterra and Wiener functional series, Hammerstein and Wiener-Hammerstein models that are utilized for development of general nonlinear models of signal processing [3].

Our research results [4, 7, 10, 12] provide the possibility to generalize the features that are immanent for a wide class of biotechnological, biomedical, and Web information systems and come with basic modeling functions that do not belong to the listed ones. The purpose of our work is justification of general mathematical model structure for the mentioned systems with the view of profound investigation of their common features.

### 2. A model of glucose concentration in the blood of diabetics

Diabetes is an incurable disease occupying the third place on the list of dangerous and widespread diseases. At best, a diabetic can stabilize the sugar level in his/her blood, avoiding its excessive concentration. To maintain

this state, the person who suffers from diabetes must balance his/her food consumption according to the insulin dose injected.

For diabetes, the most important characteristics are the concentration of glucose  $G(t)$  and insulin  $i(t)$  (a hormone which mediates glucose uptake) in patient's blood. It is known that insulin is produced when glucose exceeds the baseline  $G_b$ , and decomposes when its own baseline  $i_b$  is exceeded. This dependence is quite accurately described by a linear differential equation. The consumption of food containing carbohydrates  $G_m(t)$  leads to an increase in the concentration of glucose.

The concentration of glucose starts to decrease when it exceeds its baseline, but the most significant decrease in the concentration occurs under the action of insulin. In most models, the intensity of glucose reduction depends on the concentration of insulin only [5]. However, in [6], the author proposed a more realistic model, which takes into account the dependence of intensity on both critical concentrations. Such an interaction is described by the Michaelis-Menten dependence that is formally equivalent to Monod function. It is important to note that in case of a diabetic patient some insulin is introduced into the body with an injection  $N(t)$  [7].

Monod function depends on a function and a parameter and looks like  $M_1(B(t), m) = \frac{B(t)}{m + B(t)}$ , where

$B(t)$  is a certain function and  $m$  is a certain parameter.

Monitoring the dynamics of glycemia in individual patients revealed that most of its fluctuations caused by food consumption cannot be explained by the total amount of the carbohydrates consumed. The reason for this discrepancy was the carbohydrates classification: instant, fast and slow.

Therefore, we accordingly differentiate the variables representing the amount of glucose intake from foods:  $G_{m,1}(t)$  is the amount of glucose in instant carbohydrates,  $G_{m,2}(t)$  is the amount of glucose in fast carbohydrates;  $G_{m,3}(t)$  is the amount of glucose in slow carbohydrates. Besides, it is necessary to take into account the temporal distribution of the action of the carbohydrates consumed and the insulin injected.

The problem of time distribution of the consumed glucose and the injected insulin arises from the fact that these factors do not act immediately. The distribution of these factors can be synthesized based on the distributions of glucose and insulin levels after a single glucose injection. The analysis of the results of experiments showed a similarity of the distribution profiles to the fractional-rational functions representing the distribution of Fisher's statistical criterion, so the

time-dependence of the amount of glucose consumed with  $i$ -th type ( $i=1, 2, 3$ ) of carbohydrate is represented as follows:

$$G_{m,i}^F(t, t) = G_{m,i}^t g_{m,i}(t, t), \quad (1)$$

$$g_{m,i}(t, t) = A_i \Theta(t - t) (t - t)^{a_i} (t - t)^{-k_i}, \quad (2)$$

where  $G_{m,i}^t$  is the amount of consumed carbohydrates of  $i$ -th type at the timepoint  $t$ ,  $\Theta(\cdot)$  represents the Heaviside function,  $A_i$ ,  $a_i$ ,  $k_i$  are the parameters estimated on the basis of the analysis of experimental observations using the method of least squares.

In living conditions, to organize a series of experiments on measuring the concentration of insulin in the blood is rather difficult. Therefore, special experiments were organized to determine the distribution of insulin from injections. They were based on the monitoring of dynamics of glucose in the blood when feeding of slow or instant carbohydrates had been completed before the action of insulin. Insulin is proportional to surplus glucose; that is why its dynamics is proportional to the dynamics of glucose in the blood when it is not distorted by food. Thus, for time distribution of injected insulin we apply the following relationship

$$N^F(t, t) = N^t \cdot n(t, t), \quad (3)$$

$$n(t, t) = A_N \Theta(t - t) (t - t)^{a_N} (t - t)^{-k_N}, \quad (4)$$

where  $N^t$  is the amount of insulin injected at the timepoint  $t$ ,  $\Theta(\cdot)$  represents the Heaviside function, parameters  $A_N$ ,  $a_N$ ,  $k_N$  have been obtained on the basis of analysis of experimental observations using the method of least squares.

Fig. 1 shows the time distribution of insulin received from injections.

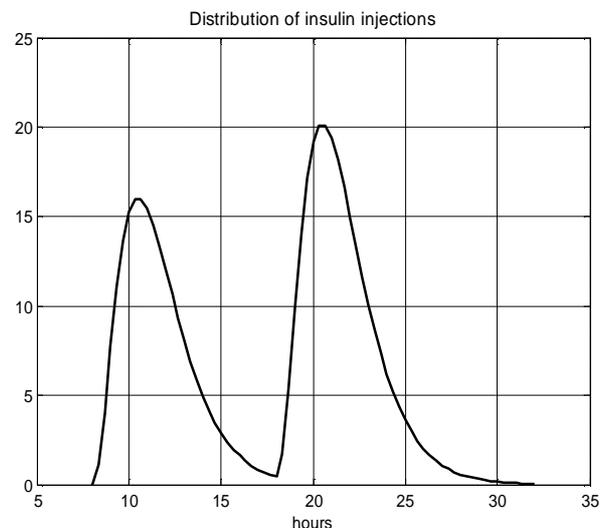


Fig. 1. Insulin distribution over time.

Given those observations, we obtain such model of the glucose distribution in the blood [12]:

$$\frac{d}{dt}G(t) = \sum_{k=1}^{K_m} (p_1 G_{m,1}^{t_{1,k}} g(t_{1,k}, t) + p_2 G_{m,2}^{t_{1,k}} g(t_{1,k}, t) + p_3 G_{m,3}^{t_{1,k}} g(t_{1,k}, t)) - p_4 (G(t) - G_b) - \quad (5)$$

$$- p_5 \sum_{k=1}^{K_N} N^{t_{2,k}} n(t_{2,k}) M_1(G(t), p_6) - p_7 i(t) M_1(G(t), p_6)$$

$$\frac{di(t)}{dt} = p_8 (G(t) - G_b)^+ - p_9 (i(t) - i_b), \quad (6)$$

$$G(t_0) = G_0, \quad i(t_0) = i_0, \quad (7)$$

where  $(G(t) - G_b)^+ = \begin{cases} G(t) - G_b, & \text{if } (G(t) - G_b) > 0 \\ 0, & \text{if } (G(t) - G_b) \leq 0 \end{cases} \quad (8)$

$K_m$  is number of events of carbohydrates consumption;  $K_N$  is number of insulin injections;  $p_j$ , ( $j = \overline{1,9}$ ) are the model parameters;  $M_1(\cdot, \cdot)$  is Monod function;  $t_0$  is the startpoint of observation;  $G_0$  is the glucose amount in the blood at the startpoint;  $i_0$  is the insulin amount in the blood at the startpoint.

Thus, a system of two nonlinear equations has been obtained, and a certain Monod function, which simplifies the presentation of Monod law, has been introduced. This law represents the nonlinear intensity of interactions between the model factors. With the parameter  $p_6$  growing, such intensity is converted into a linear one, similarly to the interaction intensity in the Lotka-Volterra model (Fig. 2).

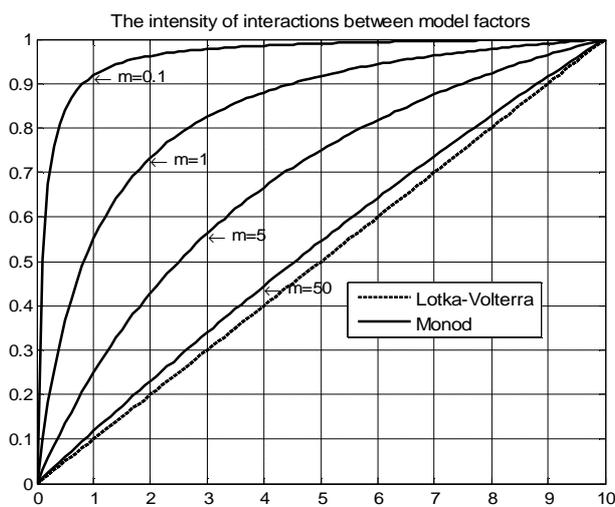


Fig. 2. Intensity of interactions between the parameters of Monod and Lotka-Volterra models.

This model represents the concentration of glucose in the blood within one day with good accuracy (4% maximum relative error of identification (Fig. 2) and 8% relative error of forecasting).

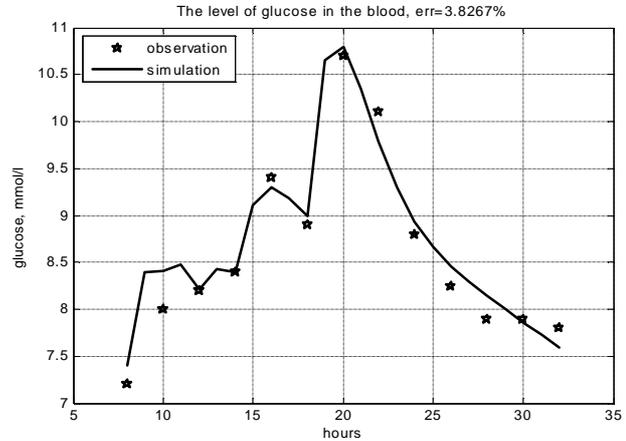


Fig. 3. Identification of the model of time distribution of glucose in the blood.

### 3. A model of rehabilitation processes in cardiology

Cardiovascular diseases are the main factor leading to the losses and disability of population in most countries. The main features of the cardiovascular system are the heart rate and systolic blood pressure. At final stages of rehabilitation, it is very important to observe a body response to submaximal physical activity.

The values of state variables change proportionally to significant changes in the system load. Therefore, it is natural to assume that changes in the patient's condition are determined by a derivative of the function of patient's effort power.

It has been accepted a hypothesis that the transition to state variables stabilization is proportional to some degrees of their deviation. To simulate a smooth transition from a linear disturbance due to physical activity to the stable state, we have used an expression of difference between unit value and Monod function depending on the delta-expansion of the function of patient's effort power.

The expansion is introduced to model a residual effect of the submaximal efforts of a patient. The power of patient's effort  $W(t)$  can be measured using veloergometry. The duration of heart rate and pressure stabilization period after the patient's physical exercise indicates an acceptable level of such activity. Thus, we obtain the following model of characteristics of a cardiovascular system being subjected to submaximal physical activity.

$$\begin{aligned}\frac{dh(t)}{dt} &= p_1 \frac{dW(t)}{dt} - p_2 [1 - M_1(W_d(t), m)] h(t)^{p_3}, \\ \frac{dp(t)}{dt} &= p_4 \frac{dW(t)}{dt} - p_5 [1 - M_1(W_d(t), m)] p(t)^{p_6}.\end{aligned}\quad (9)$$

$$h(t_0) = h_0, \quad p(t_0) = p_0 \quad (10)$$

$$W_d(t) = \begin{cases} W(t) & t < t_r, \\ W(t_r) & t_r \leq t < t_r + d, \\ W(t_r) \frac{t - t_r - 2d}{t - t_r} & t_r + d \leq t \leq t_r + 2d, \\ 0 & t > t_r + 2d, \end{cases} \quad (11)$$

where  $h(t)$  is the heart rate,  $p(t)$  represents the blood pressure,  $dW(t)/dt$  denotes the first derivative of the function of patient's effort power,  $W_d(t)$  is  $d$ -expansion of the power function,  $t_r$  stands for the timepoint of the activity termination;  $M_1(\cdot, \cdot)$  is Monod function;  $p_j$ , ( $j = \overline{1,6}$ ) are the model parameters;  $t_0$  is the startpoint of observation;  $h_0$  is heart rate at the startpoint;  $p_0$  is blood pressure at the startpoint.

The identification of the model has proved its adequacy. Fig.4. presents an example of the power of submaximal exercises. Fig. 5 and 6 present the results of the identification of the heart rate and blood pressure model for a patient subjected to submaximal exercises.

The model of the features of the cardiovascular system at the initial stage of rehabilitation is a bit more complex. At this stage, due to the exhaustion of the cardiac muscle, submaximal activities are out of the question.

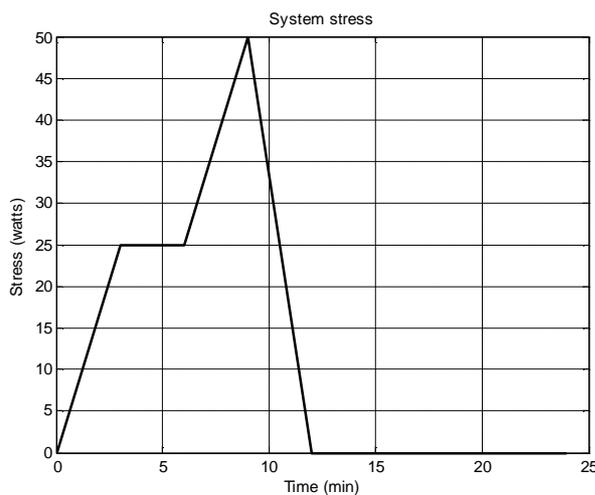


Fig. 4. Example of the power of submaximal exercises.

It is very important to monitor the body's response to increasing the durations of nonintensive physical activities up to the full adaptation. In forming the

models, the cardiac muscle exhaustion leads to the fact that all terms on the right side of the differential equations become nonlinear and are represented by Monod functions as given in the equations (12)–(15).

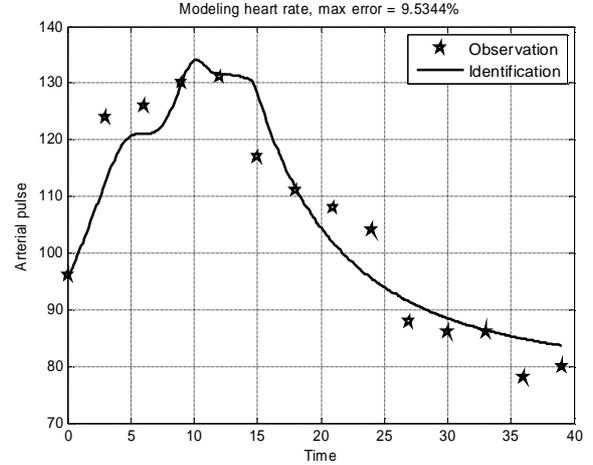


Fig. 5. Identified model of a heart rate under submaximal exercises (maximum relative error is of 5.4 %).

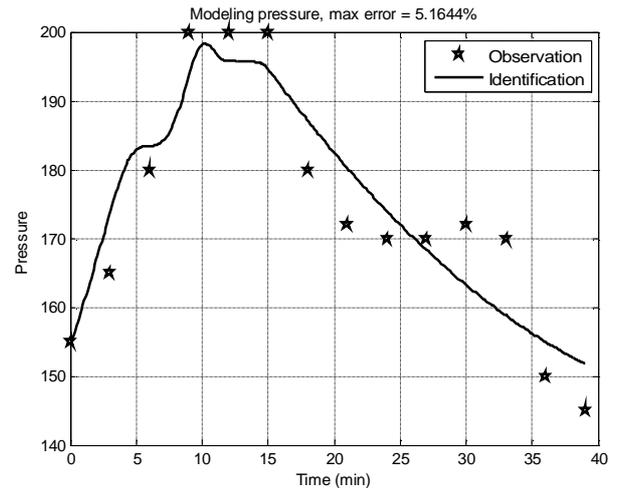


Fig. 6. Identified model of a heart rate under submaximal exercises (maximum relative error is of 5.2 %).

$$\frac{dh(t)}{dt} = p_1 M_1(r(t), m) - p_2 [1 - M_1(r(t), m)] h^{p_3}(t), \quad (12)$$

$$\frac{dp(t)}{dt} = p_4 M_1(r(t), m) - p_5 [1 - M_1(r(t), m)] p^{p_6}(t), \quad (13)$$

$$r(t) = \begin{cases} S(t), & t < t_r, \\ 0, & t \geq t_r, \end{cases} \quad (14)$$

$$h(t_0) = h_0, \quad p(t_0) = p_0, \quad (15)$$

where  $r(t)$  is the exhaustion;  $m$  is the model parameter;  $S(t)$  is the covered distance causing the exhaustion;  $M_1(\cdot, \cdot)$  is Monod function;  $p_j$ , ( $j = \overline{1,6}$ ) are the model

parameters;  $t_0$  is the startpoint of observation;  $h_0$  is heart rate at the startpoint;  $p_0$  is blood pressure at the startpoint.

The proposed model has been identified with satisfactory accuracy; its maximum relative error is of 3.9 % (Fig. 7, 8).

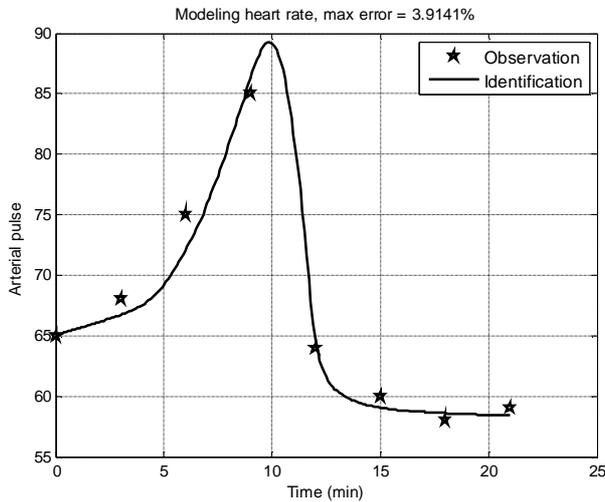


Fig. 7. Identified model of a heart rate under prolonged nonintensive exercises (maximum relative error is of 3.9 %).

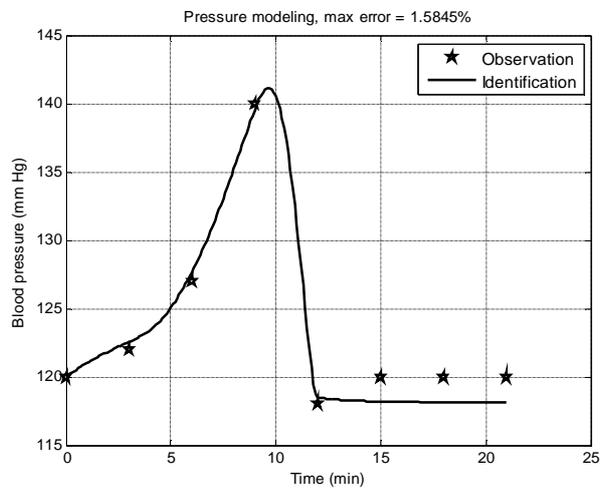


Fig. 8. Identified model of a blood pressure under prolonged nonintensive exercises (maximum relative error is of 1.6 %).

#### 4. A model of fermentation processes in biotechnological systems

Technological processes for restoration of power and natural resources as well as engineering procedures in food and pharmaceutical industries play an essential part in the development of productive forces of society. They are periodically or continuously involved in the chemical-technological systems (CTS).

A substrate, microorganisms and, sometimes, additional initiating substances are injected into a chemical-technological system. As a result of reactions, both basic (target) products and by-products are obtained [8].

The main process parameters are temperature, pressure and alkalinity of the medium, the temperature tending to be a control parameter. The processes taking place in a continuous mode are economically more efficient than in a periodic one, but a number of important processes can take place only in the latter. These, in particular, are the production of alcohol and dairy foods, pharmaceuticals such as vitamins, antibiotics, and hormones. Therefore, the study of chemical-technological systems in a periodic regime is of particular interest. The objective of their mathematical modeling is studying the dynamics of concentration of the substances mentioned.

In the simplest case, CTS is supposed to have only one state variable - monotonically decreasing substrate concentration  $S(t)$ . In this case, the dynamics of the process is described by a single differential equation proposed by Leonor Michaelis and Maud Leonora Menten for modelling the processes of chemical synthesis [8]:

$$\frac{dS(t)}{dt} = -A_1 \cdot M_1(S(t), A_2), \quad (16)$$

with the initial condition

$$S(t_0) = S_0, \quad (17)$$

where  $A_1$  is the maximum reaction rate,  $A_2$  denotes the Michaelis constant,  $S(t)$  represents the state variable of substrate concentration,  $M_1(\cdot, \cdot)$  is Monod function;  $t_0$  is the startpoint of observation;  $S_0$  stands for the initial concentration of the substrate in the periodic mode system.

In Monod periodic model, the rates of microorganisms growth  $dX(t)/dt$  and substrate consumption  $dS(t)/dt$  are proportional to their current levels, i.e. to the levels of  $X(t)$  and concentration of the nutrient substrate  $S(t)$ . This results in a system of equations [9]:

$$\begin{cases} \frac{dX(t)}{dt} = (A_1 \cdot M_1(S(t), A_4) - A_2) X(t), \\ \frac{dS(t)}{dt} = -A_3 \cdot M_1(S(t), A_4) X(t), \end{cases} \quad (18)$$

with the initial conditions

$$X(t_0) = X_0, \quad S(t_0) = S_0. \quad (19)$$

where  $X(t)$  is the microorganisms concentration;  $S(t)$  stands for the nutrient substrate concentration;  $M_1(\cdot, \cdot)$  is Monod function;  $A_j$ , ( $j = \overline{1,4}$ ) are the model parameters;  $t_0$  is the startpoint of observation;  $S_0$

represents the initial substrate concentration,  $X_0$  denotes the initial microorganisms concentration in the periodic mode system.

It has been found that the monotonous accumulation of the target product  $P(t)$  slows down the consumption of substrate and the growth of microorganisms. This pattern is called product inhibition and is taken into account in the family of models with feedback. The feedback models are based on the classical Monod system (18), (19), introducing additionally the function of growth inhibition into the equation of state variable  $X(t)$  and supplementing the system with the equation of target product intensity  $P(t)$  [10]. In such case we use generalized Monod function that looks like  $M_2(B_1(t), B_2(t), m) = \frac{B_1(t)}{m + B_2(t)}$ , where  $B_1(t)$ ,  $B_2(t)$  are certain functions and  $m$  is a certain parameter.

The proposed model has been identified with satisfactory accuracy – its maximum relative error is of 2% (Fig. 9).

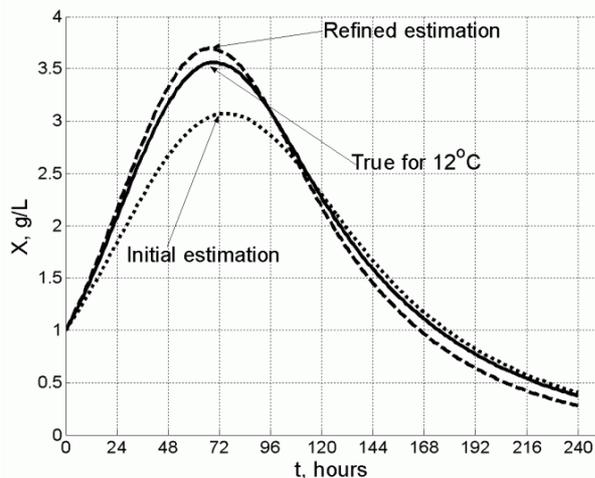


Fig. 9. Identified model of the substrate and microorganisms concentration (max. relative error does not exceed 2%).

### 5. Model of Web site traffic

An important tool for achieving high performance of a Web site is its sufficient traffic. At the same time, low and very low traffic is typical for most Web sites, though funds are spent on their development and support. There is a whole range of services and recommendations aiming at improving the visibility of certain materials in the mentioned systems, commonly called by a term “search engine optimization” or SEO. These recommendations are of empirical and often even of semi-legal nature.

On ethical grounds, and because of intensification of struggle against overoptimization of Web sites by leading search engines, there is an increase in the need

for a scientific approach to the study of the problem of traffic increasing.

Mathematical modelling provides effective and well-grounded recommendations. A significant increase in Web site traffic requires systematic support for updating the content or its advertising in the network. This requires a great deal of time spent by qualified staff. The impact of such actions manifests itself with a significant time delay. Prediction of traffic dynamics after applying some SEO-strategy would make the use of support team efforts more rational.

Web site traffic is a random process, which is difficult to model. It is characterized by the phenomena of seasonality with weekly and annual periods. In order to eliminate the weekly seasonality and reduce the random fluctuations, a daily traffic is replaced by its weekly averaged analogues. When observing a yearly period of seasonality, it is refined using multiplicative seasonal factors. In addition, to eliminate additional random fluctuations, we use multiple smoothing by applying the method of moving average up to obtaining uncorrelated residuals.

The analysis of Web sites traffic and their selected pages traffic processed in the above-mentioned way shows the correspondence between the growth in total traffic and the rise in traffic of certain topical page.

This phenomenon can be explained by the fact that the growth of popularity of some topics either under development or under advertisement contributes to the improvement of visibility of the topic pages in search engines at different retrieval requests. The improvement of visibility contributes to the rise of the traffic of all Web site pages, thereby increasing the total traffic. Construction of this dependence allows the problem of the total traffic simulation to be reduced to the simulation of major topical page traffic and establishing a function describing the correspondence between the local and total traffics. Detecting a major topical page is done in two steps. Firstly, we come with the instant when the total smoothed traffic started its substantial growth; this is the instant when the traffic derivative starts to exceed its certain minimum magnitude

$$dY(t)/dt > D_{\min} \quad (20)$$

The value  $D_{\min}$  is selected for each Web site individually,  $Y(t)$  stands for the total smoothed traffic. Secondly, after fixing the start point of the traffic increase interval, we look after the pages, whose content change essentially supports the total traffic. Among the pages, we choose the one that is characterized by a maximum gain, and define it as a major topical page.

To predict the major local traffic, we have used a typical representation of a growth cycle in the Web site traffic given in [11]. Its similarity to Monod population

models suggests an idea of applying just that very model to local traffic prediction. As a substrate, we use a formal variable, which characterizes the amount of potential audience interested in possible alternations in major (top) topics of a given Web site [12]. Finally, we have obtained a system (17)-(19) of differential equations, which simulates the total Web site traffic  $Y(t)$ :

$$\begin{cases} \frac{dX(t)}{dt} = (a_1 \cdot M_1(A(t), a_4) - a_2) X(t), \\ \frac{dA(t)}{dt} = -a_3 \cdot M_1(A(t), a_4)(X(t) - kX_0)^+, \\ \text{if } dA(t)/dt = 0 \Rightarrow dX(t)dt = 0. \end{cases} \quad (21)$$

$$Y(t) = Y(t_0) + q_1 (X(t) - X_0)^{q_2} e^{-q_3 t}, \quad (22)$$

$$X(t_0) = X_0, \quad A(t_0) = A_0 = X_{\max}, \quad (23)$$

where  $X(t)$  is the local traffic of the major topical page,  $A(t)$  is the amount of remaining potential audience (not observed),  $Y(t)$  is the total Web site traffic,  $M_1(\cdot, \cdot)$  is Monod function;  $a_j$ , ( $j = \overline{1, 4}$ ) are the model parameters;  $q_j$ , ( $j = \overline{1, 3}$ ) are the model parameters;  $t_0$  is the startpoint of observation;  $X_0$  is the local traffic at the startpoint;  $A_0$  is the potential audience at the startpoint;  $X_{\max}$  represents the approximate estimate of the maximum value  $X$ ,  $k$  stands for the approximate level of the total traffic growth.

The peculiarity of this model is the necessity to take into account a human factor. The proposed model has been identified with satisfactory accuracy – its maximum relative error is of 6.2 % (Fig. 10).

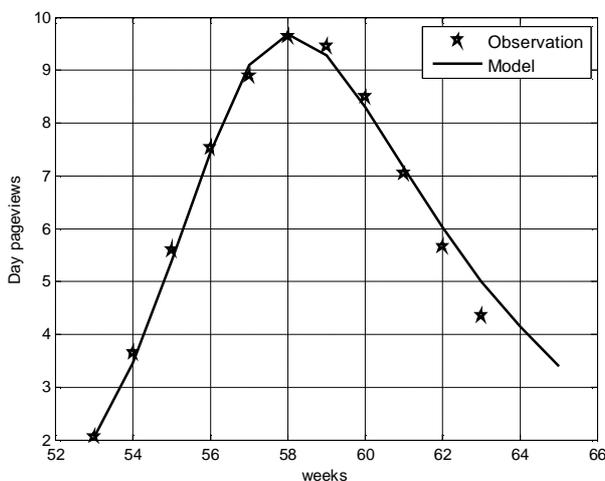


Fig. 10. Identified model of a Web site's local traffic (maximum relative error does not exceed 6.2 %).

## 6. Concept of models of accumulation and operational control of resources in biotechnological, biomedical and Web systems

Having considered the instances of modelling, we move on to forming a model of operational resource control and resource accumulation in biotechnological, biomedical and Web systems.

Since the processes mentioned are accompanied by changes in the system states, the model should include a state variable  $x$ .

System resources are formed by transformation of some substance – substrate  $s$ , so the model of such a process includes this variable. Based on the substrate, another component that is designated as a product  $p$  of the process is formed.

In a system, external actions can influence both the state variable and the substrate concentration. The state variable in the operational resource control systems is directly impacted at loads close to maximum. The increment (gain) in the state variable in this case is proportional to the load change; when the action of the load  $W$  is stopped, the system starts its restoration. As a matter of fact, since the intensity of the load is close to extreme, the system starts its restoration when the action of  $d$ -extended load  $W_d$  stops. In many systems, a substrate is introduced at the beginning of the process activation and works until its full exhaustion. However, in some systems, the substrate comes in through various channels with different intensities  $U_j$  throughout the process. The developed concept also admits that the state variable can be replenished from external sources ( $V$  stands for the replenishment amount of the state variable) and, therefore, its impact on the substrate dynamics can increase.

Thus, the concept includes three differential equations, which describe the dynamics of the state variable  $x$ , the substrate  $s$  and the target product  $p$ . The state variable dynamics is subject to two opposite trends. The first one promotes the growth of state variable value caused by the load increment or by the substrate availability. The response of the state variable can manifest itself in different ways: from a linear response to substrate increase (in the event of modest exceeding of the basic substrate level) up to an interaction between the substrate and the state variable, that can be accompanied by the product inhibition described by Monod law.

The second trend promotes the reduction of state variable value governed by simple exceeding of some basic level, or, in the case of an operational control system, by a function proportional to the state variable raised to a certain power. In the latter case, it is

necessary to start a decelerating mechanism by means of  $d$ -expanded load  $W_d$ . The start should be very smooth to eliminate incidental fluctuations of the state variable. For the smooth transition from minimum values to the values commensurable with one, we use the difference between the unit value and Monod function of  $d$ -expanded load  $W_d$ ). Consequently, we obtain the following differential equation (24) of the dynamics of the state variable.

$$\begin{aligned} \frac{dx(t)}{dt} = & a_1 \frac{dW(t)}{dt} + a_2(s(t) - s_b)^+ + a_3 M_1(s(t), m_1) + \\ & + a_4 M_2(s(t), p(t), m_2)x(t) - b_1(x(t) - x_b) - \\ & - b_2(1 - M_1(W_d(t), m_3)x(t))^{a_5} \end{aligned} \quad (24)$$

where  $a_j, (j = \overline{1,5})$  are the model parameters;  $b_j, (j = \overline{1,2})$  are the model parameters;  $m_j, (j = \overline{1,3})$  are the model parameters;  $M_1(\cdot, \cdot)$  is Monod function;  $M_2(\cdot, \cdot, \cdot)$  is generalized Monod function.

The trends of growth and decay are also present in the dynamics of the substrate. The trend of substrate reduction is a principal one since operation of the system supposes that the substrate is worked over.

The substrate is assumed to be able to decompose just in the course of its accumulation when its concentration exceeds a basic level. However, a typical substrate conversion is related to its interaction with the state variable that is going on with varying intensity, i.e. according to Monod dependence. Additionally, an increase in the concentration of the state variable by replenishment from external sources is allowed; the increase is described by the function  $V(t)$ . Moreover, an increase in the substrate concentration during the process of its transformation also is admissible. Such an increase can take place through various channels with their corresponding dynamics variations  $U_j(t)$ . As a result, we have the following differential equation of substrate dynamics

$$\begin{aligned} \frac{ds(t)}{dt} = & -c_1(s(t) - s_b) - c_2 M_1(s(t), m_4) - \\ & - kx_b + c_3 V(t) + \sum_{j=1}^J e_j U_j(t) \end{aligned} \quad (25)$$

where  $c_j, (j = \overline{1,3})$  are the model parameters;  $e_j, (j = \overline{1,J})$  are the model parameters;  $m_4$  is a model parameter;  $M_1(\cdot, \cdot)$  is Monod function.

The dynamics of the process target product is closely coordinated with the dynamics of substrate consumption through the following linear relationship

$$\frac{dp(t)}{dt} = -f \frac{ds(t)}{dt}. \quad (26)$$

As we can see, the concept comprises three differential equations that describe the dynamics of the state variable  $X(0) = X_0, ,$  the substrate  $x$  and the target product  $p$ . To develop a specific model based on the general concept, it is convenient to specify the class  $M_K$  and the structure  $M_S$  of Monod model. The class of the model defines a list of its variables, and the structure defines non-zero coefficients of the general concept  $a_j, (j = \overline{1,5}); b_j, (j = \overline{1,2}); m_j, (j = \overline{1,4}); c_j, (j = \overline{1,3}); e_j, (j = \overline{1,J}), k, f$ .

The model of rehabilitation process in cardiology is described by a differential vector equation, each component of which belongs to the class  $M_K(x, 0, 0)$  with the structure  $M_S(a_3, a_5, b_2, m_1)$ , where  $a_3$  corresponds to the  $p_1$  in (12),  $a_5$  corresponds to the  $p_3$  in (12),  $b_2$  corresponds to the  $p_2$  in (12),  $m_1$  corresponds to the  $m$  in (12).

The glucose dynamics model belongs to  $M_K(x, s, 0)$  class with the structure  $M_S(a_2, b_1, c_1, c_2, c_3, m_4, e_1, e_2, e_3)$ , where  $a_2$  corresponds to the  $p_8$  in (6),  $b_1$  corresponds to the  $p_9$  in (6),  $c_1$  corresponds to the  $p_4$  in (5),  $c_2$  corresponds to the  $p_7$  in (5),  $c_3$  corresponds to the  $p_5$  in (5),  $m_4$  corresponds to the  $p_6$  in (5),  $e_1$  corresponds to the  $p_1$  in (5),  $e_2$  corresponds to the  $p_2$  in (5),  $e_3$  corresponds to the  $p_3$  in (5); insulin concentration being the state variable, and the glucose concentration being the substrate.

The model of fermentation process belongs to the class  $M_K(x, s, p)$  with the structure  $M_S(a_3, a_4, m_1, b_1, c_2, f)$ , where  $a_3$  corresponds to the  $A_1$  in (18),  $b_1$  corresponds to the  $A_2$  in (18),  $c_2$  corresponds to the  $A_3$  in (18),  $m_1$  corresponds to the  $A_4$  in (18). The parameters  $a_4$  and  $f$  can be found in the elaborated fermentation process model given in [10].

The model of major Website page traffic belongs to the class  $M_K(x, s)$  with the structure  $M_S(a_3, b_1, c_2, k)$ , where  $a_3$  corresponds to the  $a_1$  in (21),  $b_1$  corresponds to the  $a_2$  in (21),  $c_2$  corresponds to the  $a_3$  in (21),  $k$  corresponds to the  $k$  in (21).

So, the whole set of differential equations (26) - (28) makes up the concept of models of resources accumulation and their operational control in biotechnological, biomedical and Web systems. It

includes the differential equations of state variable, substrate and target product dynamics.

The concept is based on the following principles: a substrate (and in some cases a target product) plays the role of limitation factor of a resource accumulation process, and it interacts with a system state variable according to Monod law. In the processes of operational control of resources, the adequate modelling of the system transition from its response to the load to its stabilization is implemented using Monod function with respect to the load applied; the substrate concentration is a limitation factor of the interaction between the substrate and the state variable, and its dynamics is implemented using Monod function. As we can see, Monod function is the key element for modelling the processes of accumulation and operational control of resources in biotechnological, biomedical, and Web information systems.

The equilibrium state of an open system is distorted by onetime or long-term intervention in the system structure through the introduction of disturbing or stabilizing components. Those components interact until one of them is eliminated and significantly affect the state of the system. Therefore, their interaction is described by a nonlinear dependence of varying intensity, i.e. by Monod dependence. Another type of nonlinear reaction of the system of similar kind arises when the linear system with strong stabilization aptitude is loaded to its highest capacity and afterwards the load is removed. In this case, Monod function provides a convenient one-parameter formula for an adequate simulation of the system response with minimal side effects.

## 7. Conclusions

A concept of the models of resource accumulation and their operational control in biotechnological, biomedical, and Web systems has been proposed for the first time. The concept is formed as a system of differential equations describing the dynamics of a state variable, substrate and target product of the analyzed interacting processes.

The structure of the system mentioned is based on the fact that the substrate (with possible participation of the target product of the resource accumulation process) serves as a limitation factor to the process, and it interacts with the state variable of the system according to Monod law. Similarly, in the processes of operational resource control, an adequate simulation of the system transition from the load reaction to the state stabilization is implemented by means of Monod function.

Each partial implementation of the conceptual model includes a nonlinear part represented by Monod function.

This fact complicates the development of an effective method for model identification. In certain cases, it is possible to utilize the identification method based on a formal derivation of first approximation values and their subsequent correction using the Levenberg-Marquardt method. We intend to extend such approach to a general case which will be the subject of further research.

## References

- [1] A. A. Samarskiy and A. P. Mikhailov, *Principles of Mathematical Modeling. Ideas, Methods, Examples*. London, UK and New York, USA: Taylor and Francis, 2002.
- [2] A. G. Ivakhnenko and V. S. Stepashko, *Noise-immunity of modeling*. Kyiv, Ukraine: Naukova dumka, 1985. (Russian).
- [3] M. Salukvadze and B. Shanshiashvili, "Identification of Nonlinear Continuous Dynamic Systems with Closed Cycle", *International Journal of Information Technology & Decision Making*, vol. 12, no. 2, pp. 179–199, 2013.
- [4] O. Vovkodav and R. Pasichnyk, "Mathematical Model of a Cardiovascular System on a Measured Physical Exercise", in *Proc. The Experience of Designing and Application of CAD Systems in Microelectronics (CADSM 2013)*, pp. 378–379, Lviv-Polyana, Ukraine, 2013.
- [5] M. Breton, "Silico preclinical trials: a proof of concept in closed-loop control of type 1 diabetes", in *Proc. 2006 IEEE EMBS Conference*, pp. 5647–5650, New York, USA, 2006.
- [6] C. D. Man, "Meal Simulation Model of the Glucose-Insulin System", *IEEE Transactions on Biomedical Engineering*, vol. 54, no. 10, pp. 1740–1749, 2007.
- [7] Y. Chaikivska and R. Pasichnyk, "Mathematical model of glucose dynamics during food digestion process", in *Proc. XII-th International conference TCSET'2014*, p. 753, Lviv-Slavske, Ukraine, 2014.
- [8] A. Cornish-Bowden, *Fundamentals of enzyme kinetics*. Boston, USA: Butterworth, Inc., 1979.
- [9] C. D. Kinghtes, "Statistical analysis of nonlinear parameter estimation for Monod biodegradation kinetics using bivariate data", *Biotechnology and Bioengineering*, vol. 69, no. 2, pp. 160–170, 2000.
- [10] R. Pasichnyk and Y. Pigovskyy, "Modeling of dynamics of microorganisms systems under uncertainty", in *Proc. IX-th International Conference CADSM'2007*, pp. 115–119, Lviv-Polyana, Ukraine, 2007.
- [11] J. Ratkiewicz, S. Fortunato, and A. Flammini, "Characterizing and Modeling the Dynamics of

Online Popularity”, *Physical Review Letters*, <http://arxiv.org/pdf/1005.2704.pdf>, 2010.

- [12] N. Pasichnyk, M. Dyvak, and R. Pasichnyk, “Mathematical modeling of Website quality characteristics in dynamics”, *Journal of Applied Computer Science*, vol. 22, no. 1, pp. 171–183, Lodz, Poland: Technical University Press, 2014.

**МОДЕЛЮВАННЯ ПРОЦЕСІВ  
НАГРОМАДЖЕННЯ РЕСУРСІВ  
ТА ОПЕРАТИВНОГО УПРАВЛІННЯ  
НИМИ В БІОТЕХНОЛОГІЧНИХ,  
БІОМЕДИЧНИХ  
ТА ВЕБ-ІНФОРМАЦІЙНИХ СИСТЕМАХ**

Роман Пасічник

Метою цієї праці є побудова структури математичної моделі процесів нагромадження ресурсів та оперативного управління ними в біотехнологічних, біомедичних та веб-інформаційних системах для поглибленого вивчення їх спільних властивостей. Вперше запропоновано концепцію

моделей згаданих процесів у вигляді системи диференціальних рівнянь, які описують динаміку змінних стану, субстрату та продукту аналізованих процесів, що взаємодіють. Кожна часткова реалізація концептуальної моделі містить нелінійну частину, представлену функцією Моно. Це породжує проблему побудову узагальненого методу ідентифікації нелінійних моделей згаданого виду, яку планується розв’язати в подальших публікаціях.



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Areas of Research Interests: Modelling of Processes in Complex Systems.