

## **SOFTWARE GENERATOR OF THE BIOTECHNOLOGICAL PROCESSES MODELS**

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**Abstract:** The paper deals with the development of a software system (BIOCALC) for the modelling, identification and simulation of the biotechnological processes. BIOCALC is based on the algorithm developed by George Bastin and Daniel Dochain in (Bastin, et al., 1990), starting with the reaction scheme of the process. The BIOCALC software generates the differential equations of the process, identifies the model coefficients and allows the model simulation comparing the results to the experimental data.

**Keywords:** biotechnology, reaction scheme, model identification, numerical simulation

### 1. INTRODUCTION

Biotechnological processes are very complex, strongly nonlinear and, therefore, quite difficult to model. As there are not enough accurate, reliable and not too expensive sensors, it is practically impossible to perform on-line measurements of the state variables of the process. Many researchers applied classic methods to model all kind of biotechnological processes (continuous, discontinuous and fed-batch), such as:

1. mass balance equations
2. reaction schemes
3. zoning of the biotechnological processes evolution.

All these methods lead to analytical models (structural-functional models) which can be used in control techniques.

Taking into consideration the bioprocesses particularities, the modelling of the biotechnological processes can be assisted by computer. It is wellknown the software system CAMBIO (Computer Aided Modelling of BIOprocesses), developed by the Biosystem team from the Automation Laboratory of Grenoble, France. It is the result of a deep analysis on the bioprocesses modelling made by A. Cheruy, R. Montellano and M. Farza (Farza, 1992). The software mentioned above is based on a functional scheme, which is an intermediary stage between a verbal description and a set of mathematical equations. The user must specify the type of the process variables (substrate, biomass, enzyme, activating or inhibiting agent, reactant or final product) and the reaction links between variables. CAMBIO generates the differential equations of the process model. The present paper deals with a similar software system, namely BIOCALC. It is based on the modelling algorithm presented in (Bastin, et al., 1990) and has as the main

objective to generate the set of differential equations of the process' model. BIOCALC also allows to identify and to simulate the model of the bioprocess, compared to the experimental data.

## 2. THE ALGORITHM FOR THE OBTAINING THE MODEL OF A BIOPROCESS

Once the reaction scheme of a biotechnological process is given, the derivation of a dynamical model is made fully systematic by applying the following rules (Bastin, et al., 1990):

R1) The reaction scheme of the process involves  $N$  components  $\xi_i$  ( $i=1, \dots, N$ ) and  $M$  reactions ( $j=1, \dots, M$ ). The reaction rates are denoted  $\varphi_j$  ( $j=1, \dots, M$ ).

R2) The dynamics of the concentration of each component  $\xi_i$  are written as follows:

$$\frac{d\xi_i}{dt} = \sum_{j \sim i} (\pm) k_{ij} \varphi_j - D\xi_i - Q_i + F_i \quad (1)$$

R3) The notation  $j \sim i$  means that the summation is taken on the reactions with index  $j$  which involve the component with index  $i$ .

R4)  $k_{ij}$  are strictly positive constant yield coefficients, without dimension (i. e. units of mass / mass). They have a "-" sign when  $\xi_i$  is a reactant (i. e. it appears on the left-hand side of the reaction scheme) and a "+" sign when  $\xi_i$  is a product of the reaction (i. e. it appears on the right hand side).

R5)  $Q_i$  is the rate of mass outflow of the component  $\xi_i$  from the reactor in the gaseous form.

R6)  $F_i$  is the mass feed rate in the reactor of the component  $\xi_i$  if it is an external substrate. Otherwise,  $F_i=0$ .

## 3. SOFTWARE IMPLEMENTATION OF THE BIOCALC SYSTEM

This section deals with the main characteristics of the BIOCALC system. For the prototype implementation it has been chosen the software environment Matlab, 5.3.0 version. The application contains a package of files of *m*-type and *mat*-type. The graphic interfaces were performed with *Graphical User Interface Tools* from Matlab. When the application is running there is not the possibility to fill the working memory by opening new windows. This advantage was obtained by an algorithm that suppresses the inactive windows using the windows of *modal*-type.

The first window (the welcome window) is presented in figure 1 and contains the three main options: *modelling*, *identification* and *simulation*.

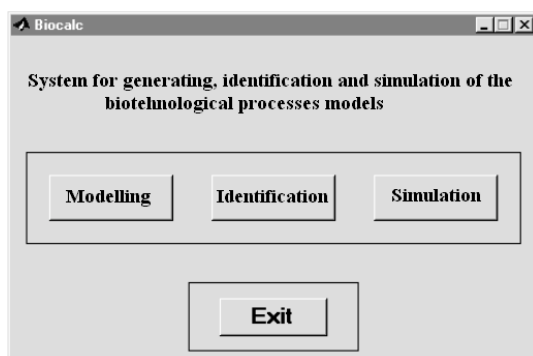


Fig. 1. The wellcome window

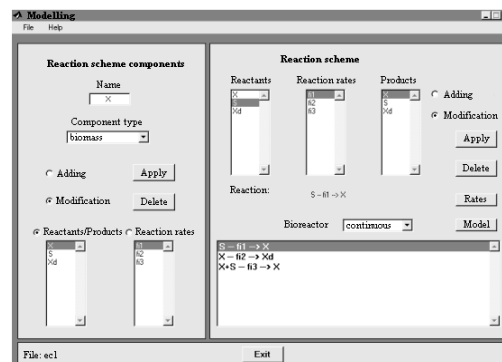


Fig. 2. The reaction scheme window

The *modelling* option allows obtaining the bioprocess model, the option *identification* calculates the coefficients of the model compared to the experimental data and the option *simulation* simulates the model and the experimental data. Once the modelling option was selected, a new window with two sectors does appear on the screen (figure 2). In the left sector the process variables (reactants, reaction products and reaction rates) are introduced. In the right sector, the program builds the reaction scheme. The reactants and the reaction products are shown to the left side and to the right side respectively of the reaction rates list. The reaction is build selecting element by element the reactants from the first list, the reaction rate from the second list and the reaction products from the third list, according to the algorithm presented in section 3 of the paper. Every reaction is save in a file and shown in the window under the three lists with process variables. The window from figure 2 also allows selecting the bioreactor type (continuous or discontinuous). For the generating of the reaction scheme is necessary to define the reaction rate form (the *pushbutton* Rate in the window from figure 2). This will generate a new window (figure 3) with some possibilities to select the form of the reaction rate.

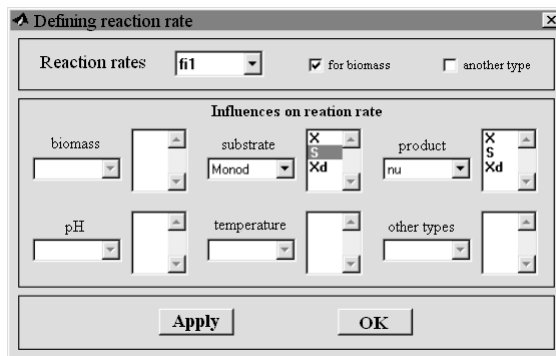


Fig. 3. The selection of the reaction rate

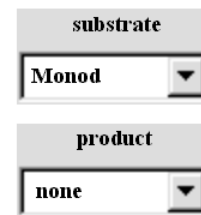


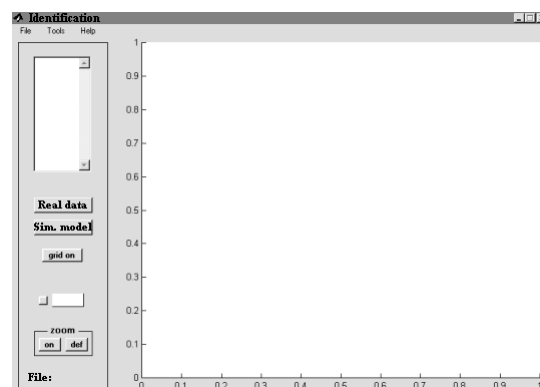
Fig. 4. The selection of the specific reaction rate type

As one can see in figure 3, the software can model all the phases of a biotechnological process (the biomass developing, the decay phase, etc). BIOCALC allows to the user to express the reaction rate as function of biomass, substrate, product, pH, temperature and other variables. The user must select the specific reaction rate  $\mu$  as it can be seen in figure 4.

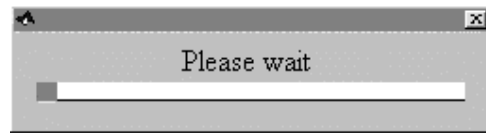
The software also allows selecting a double dependence of the reaction rate, based on the multiplying principle. The reaction scheme can be obtained activating the *pushbutton* OK from the window in figure 2. The reactions generated by BIOCALC are presented in figure 5:



Fig. 5. The reaction scheme

Fig. 6. The window for *identification option*

The option *identification* allows the obtaining of the model coefficients based on experimental data. The experimental data are stored in a file and used by the identification algorithm (figure 6). The window contains a *menubar* divided in three option groups: *File*, *Tools* and *Help* (figure 7).

Fig. 7. The *menubar* windowFig. 8. The *waitbar* window

Very important are the options *Run* (begin the identification process) and *Clear* (delete the curves from the right side of the window). While the identification process is running, a *waitbar* window appears on the screen (figure 8).

The calculus of the model parameters is made by a search procedure (unidimensional search) in the parameters space. The search procedure minimizes the distance between the model curves and experimental data. Before the identification process starts the initial values of the model coefficients must be introduced (figure 9).

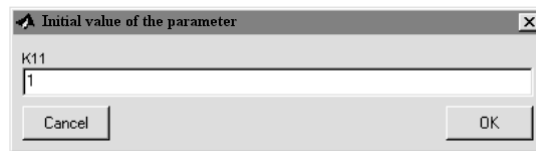


Fig. 9. The initial values of the model coefficients

The *simulation* option calculates the reactants and reaction products concentrations as functions of time  $t$  for an identified set of the model coefficients or another set chosen by the user. The corresponding window is similar to the one used for the *identification* option.

#### 4. CASE STUDY

Let's consider the biotechnological process given by the following reaction scheme:



Based on the algorithm presented in section 3, BIOCALC determines the following model (figure 5):

$$\frac{dX}{dt} = k_{11}\varphi_1 - k_{12}\varphi_2 - DX \quad (5)$$

$$\frac{dS}{dt} = -k_{21}\varphi_1 - k_{23}\varphi_3 - DS + F_2 \quad (6)$$

$$\frac{dX_d}{dt} = k_{32}\varphi_2 - DX_d \quad (7)$$

where

$$\varphi_1 = \mu(S) \cdot X \quad (8)$$

$$\varphi_2 = k_d \cdot X \quad \text{cu} \quad k_d = \text{const.} \quad (9)$$

$$\varphi_3 = k_m \cdot X \text{ cu } k_m = \text{const.} \quad (10)$$

The specific reaction rate is given by the Monod form.

$$\mu(S) = \frac{\mu^* S}{k_M + S} \quad (11)$$

Replacing relations (8) - (11) in the model equations (5) - (7), results

$$\frac{dX}{dt} = k_{11} \frac{\mu^* S}{k_M + S} X - k_{12} k_d - DX \quad (12)$$

$$\frac{dS}{dt} = -k_{21} \frac{\mu^* S}{k_M + S} X - k_{23} k_m - DS + F_2 \quad (13)$$

$$\frac{dX_d}{dt} = k_{32} k_d - DX_d \quad (14)$$

which can be rewritten in the following form:

$$\frac{dX}{dt} = k_X \frac{S}{k_M + S} X - k_{12} k_d - DX \quad (15)$$

$$\frac{dS}{dt} = -k_S \frac{S}{k_M + S} X - k_{23} k_m - DS + F_2 \quad (16)$$

$$\frac{dX_d}{dt} = k_{32} k_d - DX_d \quad (17)$$

with

$$k_X = k_{11} \mu^* \quad (18)$$

$$k_S = k_{21} \mu^* \quad (19)$$

The coefficients that must be identified are:  $k_X$ ,  $k_S$ ,  $k_{12}$ ,  $k_{23}$ ,  $k_{32}$ ,  $k_M$ . For the other parameters, the following values has been considered:  $k_m=0.5$ ;  $k_d=0.5$ ;  $F_2=25$ ;  $D=0.3$ . The initial values of the unknown coefficients are set to 1. The integrating parameters have the following values:

- $t_0=0$  (the initial time for integrating)
- $t_f=10\text{h}$ , (the final time for integrating)
- $tol=10^{-5}$ , (the tolerance)
- $step=0.05$ , (the initial search step = 5% of the initial value of the coefficient)

The initial values of the state variables:  $X_0=1$  [g/l];  $S_0=5$  [g/l];  $X_{d0}=0.1$  [g/l]. The experimental data used for the model identification are presented in fig. 10.

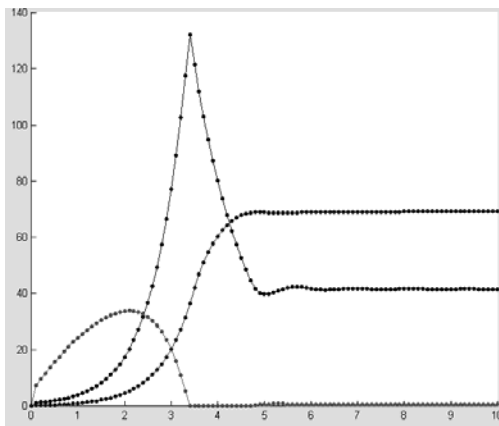


Fig. 10. The set of experimental data

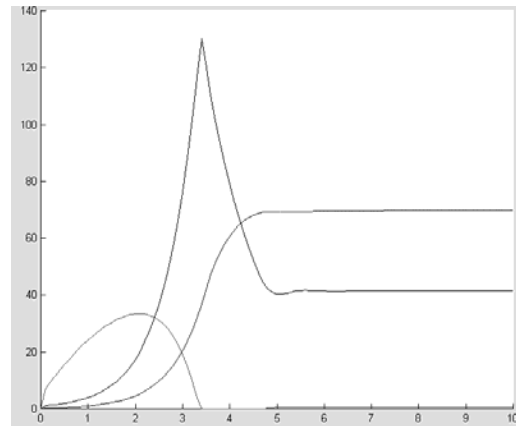


Fig.11. The results of the model simulation with the set of coefficients identified by BIOCALC system

It has been used an extended set of experimental data for the identification procedure, obtained by interpolation. The final values of the unknown coefficients determined by BIOCALC system are the following:

$$k_X=2.47$$

$$k_S=0.3324$$

$$k_{I2}=0.99274$$

$$k_{23}=0.9863$$

$$k_{32}=1.0168$$

$$k_M=1.0006$$

The results of the model simulation with the set of coefficients identified by BIOCALC system are presented in figure 11.

## 5. CONCLUSIONS

The following conclusions can be drawn:

1. BIOCALC system is an automatic generator of the models, which can be implemented on a computer, connected "on-line" to the bioreactor.
2. The functions implemented so far are limited mainly due to the biotechnological processes complexity and the time variations of the parameters. They influence very strong the process evolution. The large number of variants for parametrizing the most important coefficients of the biotechnological processes also influence the process.
3. The next step is to add new variants for parametrizing the specific growth rate as well as to diversify the identification and the integration methods for the model of the biotechnological process.
4. The BIOCALC prototype was implemented using the MATLAB environment due to its abilities to integrate and represent graphics. The final version will be implemented using VISUAL C++.

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