Adaptive control strategies for a class of nonlinear propagation bioprocesses

Emil Petre*[1]*, Dan Popescu** and **Dan Selisteanu

Stratégia adaptívneho riadenia pre triedu nelineárneho rozvoja bioprocesov

This paper presents the control problem of a class of propagation bioprocesses that are carried out in fixed bed reactors. Since the dynamics of these processes are described by partial differential equations, in order to obtain useful models for control purposes, a possible method consists of approximation of their infinitely order associated models by finite order models. A class of nonlinear adaptive controllers are then designed based on these finite order models, which consist of a set of ordinary differential equations obtained here by orthogonal collocation method. Computer simulations conducted in the case of a fixed bed reactor are included to illustrate the performances of the proposed adaptive controllers.

***Key words**: Nonlinear systems, fixed bed bioreactors, distributed parameter systems, orthogonal collocation, adaptive control.*

Introduction

Due to their advantages, over the last decades, the control of industrial bioprocesses has been an important practical problem attracting wide attention. The main motivation in applying control methods to such living systems is to improve operational stability and production efficiency. The operation in Stirred Tank Reactors (STR) has been and it is still a widely used technology in fermentation processes. But, other new technologies such as fixed bed, fluidized bed or air lift reactors, are considered for bioprocesses operation. These reactors present several advantages over the "classical" STR's. For instance, the fixed bed and fluidized bed reactors are characterized by higher production performance, i.e. larger production capacity and higher productivity (Bouaziz, Dochain, 1993). From mathematical point of view, the dynamics of these processes are characterized by partial differential equations and therefore classified as distributed parameter systems (Bastin, Dochain, 1990; Bouaziz, Dochain, 1993; Christofides, 2001; Dochain et al.,1992). It is clear that the distributed parameter feature of the system makes the control problem even more difficult (Bouaziz, Dochain, 1993; Christofides, 2001; Dochain et al.,1992; Slotine, Li, 1991).

In this paper the control problem of a class of propagation bioprocesses involving n components and m reactions that are carried out in fixed bed bioreactors without dispersion is presented. Since the dynamics of these processes are described by partial differential equations, for control purposes it is necessary to approximate these infinitely order models by finite order models. These approximate models are in fact a set of ordinary differential equations obtained here by orthogonal collocation method. More exactly, infinitely dimension of the initial parameter distributed model will be reduced by approximating the partial derivative equation of each reaction component by a finite number, equal to $p+1$, of ordinary differential equations at $p+1$ discrete spatial positions along the bioreactor. These points are chosen as zeros of some orthogonal polynomials. Note that the reduced order method of a fixed bed reactor model via orthogonal collocation has been presented in (Dochain et al., 1992; Petre, 2002; Petre et al., 2007).

Using the obtained results in (Petre et al., 2007), to control these propagation bioprocesses, in this paper a class of nonlinear adaptive controllers are designed based on their finite order models. The nonlinear controller design is based on the input-output linearizing technique. The information required about the process are the measurements of the state variables and its relative degree. It must be noted that if for the analyzed process there are no accessible state variables, these will be estimated by using an appropriate state observer. Computer simulations conducted in the case of a fixed bed reactor are included to illustrate the performances of the presented adaptive control strategies.

The rest of the paper is organized as follows. Section 2 introduces the distributed parameter dynamical model of fixed bed reactors. Its reduction to an ordinary differential equation system is shortly presented in Section 3. The adaptive control strategies of propagation bioreactors are developed in Section 4, the performances of the designed adaptive controllers being presented in Section 5. Concluding remarks finish the paper.

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(Recenzovaná a revidovaná verzia dodaná 28. 11. 2007)

Dynamical model of fixed bed bioreactors

Consider a fixed bed bioreactor that is a reactor where the biomass is immobilized on fixed carriers, operating in plug flow conditions, i.e. without dispersion as shown in Fig. 1 (Petre et al., 2007).

Assume that in bioreactor take place two reactions: (i) an autocatalytic growth reaction with one limiting substrate S and one biomass population X with the reaction rate $\varphi = \mu X$, where μ is the specific growth rate; (ii) a death reaction of microorganisms $X \to X_d$, where X_d is the non-active biomass. If we assume that X_d leaves the bioreactor, then the *distributed parameter dynamical model* of this fixed bed bioprocess is given by (Petre, 2002; Petre *et al.*, 2007):

$$\frac{\partial X}{\partial t} = \mu X - k_d X; \quad \frac{\partial S}{\partial t} = -\frac{F}{A}\cdot\frac{\partial S}{\partial z} - k_1 \mu X; \quad \frac{\partial X_d}{\partial t} = -\frac{F}{A}\cdot\frac{\partial X_d}{\partial z} + k_d X, \tag{1}$$

where F_{in} is the influent flow rate, A is the constant bioreactor cross section, k_1 is the yield coefficient and k_d is the death coefficient. The limit and initial conditions are defined as $S(t, z=0) = S_{in}(t)$, $X_d(t, z=0) = 0$, $X(0, z) = X_0(z)$, where $S_{in}(t)$ is the influent substrate concentration and $X_0(z)$ is the initial immobilized biomass. If we define the state vector $\xi = [X\ S\ X_d]^T$ with the partitions $\xi_1 = X$, $\xi_2 = [S\ X_d]^T$ and denote by $\tilde{r} = [\tilde{r}_1\ \tilde{r}_2]^T = [\mu X\ k_d X]^T$ the reaction rate vector, then the model (1) can be rewritten as:

$$\frac{\partial \xi_1}{\partial t} = \tilde{K}_1\, \tilde{r}(\xi_1, \xi_2); \quad \frac{\partial \xi_2}{\partial t} = -\frac{F_{in}}{A}\cdot\frac{\partial \xi_2}{\partial z} + \tilde{K}_2\, \tilde{r}(\xi_1, \xi_2), \tag{2}$$

with the limit and the initial conditions $\xi_2(t, z=0) = \xi_{2,in}(t) = [S_{in}\ 0]^T$, $\xi_1(0, z) = \xi_{10}(z)$ and where

$$\tilde{K}_1 = [1\ -1], \quad \tilde{K}_2 = \begin{bmatrix} -k_1 & 0 \\ 0 & 1 \end{bmatrix}. \tag{3}$$

In the case of a fixed bed bioreactor in which m biochemical reactions with n reactants take place, among which n_1 are microorganisms fixed on some supports and which remain within the reactor, and n_2 other components flow through the reactor, the distributed parameter dynamical model will be described also by equations (2) with $\tilde{K}_1$ and $\tilde{K}_2$ having appropriately structures and the limit and initial conditions $\xi_2(t, z=0) = \xi_{2,in}(t)$, $\xi_1(0, z) = \xi_{10}(z)$, where $\xi_1 \in \Re^{n_1}$ is the biomass concentration vector, $\xi_2 \in \Re^{n_2}$ is the other component concentration vector, $\xi_{2,in} \in \Re^{n_2}$ is the influent component concentration vector, $\tilde{r}(\xi_1, \xi_2) \in \Re^m$ is the reaction rate vector, $\tilde{K}_1 \in \Re^{n_1 \times m}$ and $\tilde{K}_2 \in \Re^{n_2 \times m}$ are the yield coefficient matrices.

Approximation of the dynamical model via orthogonal collocation

Since the model (2) is infinitely dimensional, in this section we present the reduced order model obtained by approximating the initial model by a set of ordinary differential equations using the orthogonal collocation method (Petre et al., 2007).

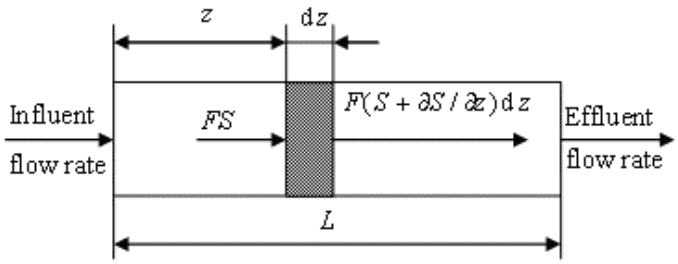

Fig. 1. A schematic view of a fixed bed bioreactor.

This method consists of expanding each variable $\xi_k(t, z)$ in (2) as a finite sum of products of some time functions and space functions:

$$\xi_k(t,z) \cong \sum_{i=0}^{p+1} \beta_i(z) \cdot \xi_{k,i}(t), \quad k = 1, 2 \tag{4}$$

where $\xi_{k,i}(t) = \xi_k(t, z = z_i)$, $i = 0,1,\ldots, p+1$ are the values of $\xi_k(t,z)$ at p internal collocation points along the bioreactor determined by *collocation method*, and the basis functions $\beta_i(z)$ that are chosen as orthogonal functions, e.g. Lagrange polynomials (see Petre, 2002; Petre *et al.*, 2007). The points $z = z_0$ and $z = z_{p+1}$ correspond to the input ($z = 0$) and the output ($z = L$) of the reactor, respectively.

Using (4), the partial derivative of ξ_2 appearing in (2) with respect to z can be written as:

$$\frac{\partial \xi_2}{\partial z} = \sum_{i=0}^{p+1} b_{ji} \cdot \xi_{2,i}(t), \text{ with } b_{ji} = \left.\frac{\mathrm{d}\beta_i(z)}{\mathrm{d}z}\right|_{z=z_j}, i = 0,1,\ldots, p+1, j = 1,\ldots, p+1. \tag{5}$$

By introducing (4) and (5) into (2), each partial derivative equation is transformed into p+1 differential equations at the p interior collocation points and at the output of the reactor. Thus it is obtained the following $n(p+1)$ order system of one order ordinary differential equations:

$$\dot{x}_1 = K_1\, r(x_1, x_2); \quad \dot{x}_2 = -(F_{in}/A)B\, x_2 + F_R + K_2\, r(x_1, x_2), \tag{6}$$

where:

$$x_k = \begin{bmatrix} \xi_{k,1} \\ \xi_{k,2} \\ \vdots \\ \xi_{k,p+1} \end{bmatrix}, K_k = \begin{bmatrix} \widetilde{K}_k & 0 & \cdots & 0 \\ 0 & \widetilde{K}_k & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & \widetilde{K}_k \end{bmatrix}; r(x_1, x_2) = \begin{bmatrix} \widetilde{r}(\xi_{1,1}, \xi_{2,1}) \\ \widetilde{r}(\xi_{1,2}, \xi_{2,2}) \\ \vdots \\ \widetilde{r}(\xi_{1,p+1}, \xi_{2,p+1}) \end{bmatrix}, k = 1,2$$

with

$$x_k \in \Re^{n_k \times (p+1)}, \quad K_k \in \Re^{n_k (p+1) \times m(p+1)}, \quad r \in \Re^{m \times (p+1)};$$

$$B = [B_{ji}], i, j = 1, 2, \ldots, p+1, \text{ with } B_{ji} = diag\{b_{ji}\}, B_{ji} \in \Re^{n_2 \times n_2};$$

$$F_R = \frac{F_{in}}{A} \cdot [\widetilde{b}_1\ \widetilde{b}_2 \cdots \widetilde{b}_{p+1}]^T \cdot \xi_{2.in}(t), \widetilde{b}_j = diag\{-b_{j0}\}, j = 1, \ldots, p+1, \widetilde{b}_j \in \Re^{n_2 \times n_2}.$$

Using the above methodology, for four internal collocation points, i.e. $p = 4$, the reduced order model that approximates the exactly infinitely dimensional model (1) will be described by a system of ordinary differential equations of the form (6) where:

$$x_1 = [X_1\ X_2\ X_3\ X_4\ X_5]^T, \quad x_2 = [S_1\ X_{d1}\ S_2\ X_{d2} \cdots S_5\ X_{d5}]^T, \tag{7}$$

$$r(x_1, x_2) = [\mu_1 X_1\ k_d X_1\ \mu_2 X_2\ k_d X_2 \cdots \mu_5 X_5\ k_d X_5]^T, \tag{8}$$

with $X_i = X(z = z_i)$, $S_i = S(z = z_i)$, $X_{di} = X_d(z = z_i)$, $\mu_i = \mu(X_i, S_i, X_{di})$, $i = 1,\ldots,5$,

$$K_1 = \begin{bmatrix} 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 \end{bmatrix}, \quad K_2 = \begin{bmatrix} -k_1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & -k_1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ \cdots & \cdots & \cdots & \cdots & \cdots & \cdots & \cdots & \cdots & \cdots & \cdots \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -k_1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix},$$

$$B = \begin{bmatrix} B_{11} & B_{12} & B_{13} & B_{14} & B_{15} \\ B_{21} & B_{22} & B_{23} & B_{24} & B_{25} \\ \cdots & \cdots & \cdots & \cdots & \cdots \\ B_{51} & B_{52} & B_{53} & B_{54} & B_{55} \end{bmatrix}, \quad \text{with } B_{ji} = \begin{bmatrix} b_{ji} & 0 \\ 0 & b_{ji} \end{bmatrix}, i, j = 1,2,\ldots,5,$$

$$F_R = -\frac{F_{in}}{A}\cdot\begin{bmatrix} b_{10} & 0 & \cdots & b_{50} & 0 \\ 0 & b_{10} & \cdots & 0 & b_{50} \end{bmatrix}^T \cdot \begin{bmatrix} S_{in} \\ X_{d,in} \end{bmatrix} = -\frac{F_{in}}{A}\cdot [\, b_{10} \;\; 0 \;\cdots\; b_{50} \;\; 0\,]^T \cdot S_{in},$$

where b_{ji}, $i = 0,1,\ldots,5$, $j = 1,\ldots,5$ are given by (5) and $S_{in} = S_0$, $X_{d,in} = X_{d0} = 0$, $X_0 = 0$.

Adaptive control of propagation bioprocesses

In this section, the control problem of a class of propagation bioprocesses that are carried out in fixed bed reactors is presented. The nonlinear adaptive controllers are designed based on the finite order model (6) obtained from exactly model (2) by using the orthogonal collocation method. It can be see that the model (6) may by rewritten as (Bastin & Dochain, 1990; Petre, 2002):

$$\dot{\zeta}(t) = K\, r(\zeta) - D\zeta + F \tag{9}$$

where $\zeta = [x_1^T \;\; x_2^T]^T$ is the state vector, $K = [K_1^T \;\; K_2^T]^T$ is the yield coefficient matrix, $r(\zeta) = r(x_1, x_2)$ is the reaction rate vector, $D = [0 \;\; -(F_{in}/A)B^T]^T$ is the dilution matrix and $F = [0 \;\; F_R^T]^T$ is the influent flow rate vector.

Problem statement

For the bioreactors described by the model (6) the control objective is to regulate the concentration of a single component at the bioreactor output, under the following conditions:

(i). The control input is the influent flow rate F.

(ii). The controlled variable is measured not only at the bioreactor output, but also at every internal collocation point and at the reactor input (only in the case of external substrate).

(iii). The yield coefficients are positive constants (some of them beeig unknown).

(iv). $m_1 \le m$ reaction rates are unknown.

For simplicity, we will denote by y the concentration of the controlled component, by y_i the value of y at every internal collocation point $z = z_i$, $i = 1,\ldots,p$ i.e. $y_i(t) = y(t, z = z_i)$ and by y_{p+1} the value of the controlled component at the bioreactor output $y_{p+1}(t) = y(t, z = z_{p+1})$. Using these notations, y_{p+1} may by expressed as a linear combination of state variables x_1 and x_2 as:

$$y_{p+1} = c^T \begin{bmatrix} x_1 \\ x_2 \end{bmatrix} \tag{10}$$

where $c^T = [c_1^T \;\; c_2^T]$ is a vector with appropriately dimension that selects the controlled variable.

Using (6), the dynamics of y_{p+1} in (10) is given by:

$$\dot{y}_{p+1}(t) = c_1^T K_1 r(\cdot) - (F_{in}/A)\cdot c_2^T B x_2 + c_2^T F_R + c_2^T K_2 r(\cdot) \tag{11}$$

Consider that for the bioprocess described by the model (1), the controlled variable is the substrate concentration at the bioreactor output, that is $y_{p+1} = S_5$. Since the state vector ζ is now given by

$$\zeta = [x_1^T \;\; x_2^T]^T = [X_1 \; X_2 \ldots X_5 \,|\, S_1 \; X_{d1} \ldots S_4 \; X_{d4} \; S_5 \; X_{d5}]^T,$$

then the entries of the vector c in (10) will be: $c^T = [0\;0\ldots0\,|\,0\;0\ldots0\;0\;1\;0]$ with $c_1^T = [0\;0\;0\;0\;0]$, $c_2^T = [0\;0\,|\,0\;0\,|\,0\;0\,|\,0\;0\,|\,1\;0]$ or $c_2^T = [c_{21}\; c_{22}\; c_{23}\; c_{24}\; c_{25}]$.

The dynamics of the concentration S_5 is given by:

$$\dot{S}_5 = -(F_{in}/A)\cdot\sum_{i=1}^{5} b_{5i} S_i - (F_{in}/A)\cdot b_{50} S_0 - k_1 \mu_5(X_5, S_5) X_5 \tag{12}$$

Using (12), the dynamics of y_{p+1} in (11) can be written as:

$$\dot{y}_{p+1}(t) = -\frac{F_{in}}{A} c_2^T B x_2 - \frac{F_{in}}{A}\tilde{c}_2^T \tilde{b}_{p+1}\xi_{2,in} + \tilde{c}_2^T \tilde{K}_2 \tilde{r}(\xi_{1,p+1}; \xi_{2,p+1}) \tag{13}$$

where:

$$\tilde{c}_2^T = c_{25} = [1\;0], \quad \xi_{2,in} = [S_{in} \;\; X_{d,in}]^T = [S_{in} \;\; 0]^T. \tag{14}$$

It is easy to verify that the term Bx_2 in (13) is a linear combination only of variables y_i at the internal collocation points $z_i, i=1,\ldots,p.$ The term $\zeta_{2,in}$ contains the influent concentrations at the input of the bioreactor. With the condition (iv), the last term in (13) can be rewritten as (Dochain *et al.*,1992):

$$\begin{aligned}&\tilde{c}_2^T \tilde{K}_2 \tilde{r}(\xi_{1,p+1}, \xi_{2,p+2}) = K_{21}\tilde{r}_1 + K_{22}\tilde{r}_2^T \\ &= K_{21}\tilde{r}_1 + [\theta_2\ \theta_3 \ldots \theta_{m-m_1+1}][\tilde{r}_{21}\ \tilde{r}_{22} \ldots \tilde{r}_{m-m_1}]^T = \theta^T \Phi\end{aligned} \tag{15}$$

where $\tilde{r}_1$ and $\tilde{r}_2$ contain the unknown and known reaction rates respectively and θ and Φ are given by:

$$\theta^T = [K_{21}\tilde{r}_1\ \theta_2\ \theta_3 \ldots \theta_{m-m_1+1}], \quad \Phi^T = [1\ \tilde{r}_{21}\ \tilde{r}_{22} \ldots \tilde{r}_{m-m_1}]. \tag{16}$$

As a conclusion, θ contains all the unknown parameters and Φ contains the known reaction rates. Then, the dynamics of output y_{p+1} takes the form:

$$\dot{y}_{p+1}(t) = -(F_{in}/A)c_2^T Bx_2 - (F_{in}/A)\tilde{c}_2^T \tilde{b}_{p+1}\xi_{2,in} + \theta^T \Phi \tag{17}$$

Exactly linearizing controller

As it was mentioned above, the control objective is to regulate the concentration of variable y_{p+1} at the output of the bioreactor at a desired value y_{p+1}^* by acting on the feeding substrate flow rate F_{in}.

Controller design is made by using the input-output linearizing technique. Remember that the input-output linearizing principle (Isidori, 1995) consists of the calculus of a nonlinear control law such that the behaviour of closed loop system (controller + process) is the same as the behaviour of a linear stable system.

Assume that for the closed loop system we wish to have the following first-order linear stable dynamics:

$$\frac{d}{dt}(y_{p+1}^* - y_{p+1}) + \lambda_1(y_{p+1}^* - y_{p+1}) = 0, \quad \lambda_1 > 0, \tag{18}$$

where y_{p+1}^* is the desired value of y.

Firstly, we consider the ideal case, where maximum prior knowledge concerning the process is available. In particular we suppose that the parameters θ in (17) are known and all the state variables are available for on-line measurements. It can be seen that equation (17) has the relative degree equal to 1 (Isidori, 1995). Then, from (17) and (18), the above closed-loop dynamics will be achieved by implementing the following exactly linearizing nonlinear control law:

$$F_{in} = A\frac{\dot{y}_{p+1}^* + \lambda_1(y_{p+1}^* - y_{p+1}) - \theta^T \Phi}{-\tilde{c}_2^T \tilde{b}_{p+1}\xi_{2,in} - c_2^T B x_2} \tag{19}$$

The control law (19) leads to the following linear error model:

$$\dot{e}(t) = -\lambda_1 e(t), \tag{20}$$

with $e(t) = y_{p+1}^*(t) - y_{p+1}(t)$. It is clear that for $\lambda_1 > 0$, the error model (20) has an asymptotic stable point at $e = 0$. It is well known that because of the reaction rates (the dynamical kinetics are strongly nonlinear and not exactly known), for the bioprocesses (12) the adaptive control techniques result in the best performances (Petre, 2002; 2003).

Adaptive control of propagation bioprocesses

If the parameters denoted by θ in (19) are assumed unknown (see the conditions (iii) and (iv)), these will be replaced by their estimates $\hat{\theta}$. Then the control law (19) becomes the adaptive control law given by:

$$F_{in} = A\frac{\dot{y}_{p+1}^* + \lambda_1(y_{p+1}^* - y_{p+1}) - \hat{\theta}^T \Phi}{-\tilde{c}_2^T \tilde{b}_{p+1}\xi_{2,in} - c_2^T B x_2} \tag{21}$$

The estimates $\hat{\theta}$ can be on-line calculated by using for example a linear regressive parameter estimator (Bastin & Dochain, 1990; Petre, 2002), described here by the following equations:

$$\begin{cases} \dot{\Psi} = -\omega\Psi + \Phi \\ \dot{\Psi}_0 = -\omega\Psi_0 - \omega y_{p+1} - \dfrac{F_{in}}{A}\left(c_2^T Bx_2 + \tilde{c}_2^T \tilde{b}_{p+1}\xi_{2,in}\right) \\ \dot{\hat{\theta}} = \Gamma\Psi(y_{p+1} - \Psi_0 - \Psi^T\hat{\theta}) \\ \dot{\Gamma} = -\Gamma\Psi\Psi^T\Gamma + \lambda\Gamma, \quad \Gamma(0) > 0, 0 < \lambda \le 1 \end{cases} \tag{22}$$

where Ψ and Ψ_0 are the state variables of some linear and stable filters, Φ stands for regressor matrix, Γ is a positive and symmetric gain matrix, and λ, named forgetting coefficient, and $\omega > 0$ are design parameters to control the stability and convergence properties of the estimator (for details see Petre, 2002; Sastry, Bodson, 1989).

Simulation results

The performances of the designed nonlinear adaptive controllers were verified by numerous simulation experiments performed upon the fixed bed bioreactor described by the model (1). The values of bioreactor and process parameters used in simulation are (Petre *et al.*, 2007): L = 1 m, A = 0.02 m^2, k_1 = 0.4, k_d = 0.05 h^{-1}. For the specific growth rate μ we have chosen a Contois model:

$$\mu(S, X) = \mu_{\max}\frac{S}{K_C X + S} \tag{23}$$

with $\mu_{\max}$ = 0.35 h^{-1} and $K_C = 0.4$.

The internal collocation points of the reduced model (6) have been chosen as the zeros of the Jacobi polynomials (see Petre *et al.*, 2007). For $p = 4$, $\alpha = 0$ and $\beta = 4$ the abscises of the four internal collocation points are: z_1 = 0.3121, z_2 = 0.5789, z_3 = 0.8130, z_4 = 0.9627. Of course these values will determine the values of the entries b_{ji} in the matrices B_{ji} and b_j.

The control objective is to regulate the substrate concentration S_5 at the bioreactor output, i.e. $y_{p+1} = S_5$. From (6), (7) and (8) the dynamics of S_5 is obtained as:

$$\dot{S}_5 = -\frac{F_{in}}{A}\sum_{i=1}^{5} b_{5i}S_i - \frac{F_{in}}{A}b_{50}S_0 - k_1\mu_5(X_5, S_5)X_5 \tag{24}$$

The exactly linearizing control law (19) takes the form:

$$F_{in} = A\frac{\dot{S}_5^* + \lambda_1(S_5^* - S_5) + k_1\mu_5(\cdot)X_5}{-b_{50}S_{in} - \sum_{i=1}^{5} b_{5i}S_i}. \tag{25}$$

The behaviour of the closed loop system in the ideal case when all the parameters are known is presented in Fig. 2.

To verify the regulation properties of the controller for the reference variable, a piece-wise constant variation was considered as:

$$S^* = S_5^* = \begin{cases} 0.35\,g/l, & 0 \le t < 80\,s \\ 0.30\,g/l, & 80 \le t < 175\,s \\ 0.25\,g/l, & 175 \le t < 215\,s \\ 0.30\,g/l, & 215 \le t < 250\,s \end{cases} \tag{26}$$

The initial simulation conditions correspond to a process steady state (see Petre *et al.*, 2007). So, for the internal collocation points, the used values are: $X_0(0)$ = 0 mg.l^{-1}, $X_1(0)$ = 44.1051 mg.l^{-1}, $X_2(0)$ = 19.8101 mg.l^{-1}, $X_3(0)$ = 9.8169 mg.l^{-1}, $X_4(0)$ = 6.2634 mg.l^{-1}; $X_5(0)$ = 5.6010 mg.l^{-1}; $S_0(0) = S_{in}(0)$ = 7.5 g.l^{-1}, $S_1(0)$ = 2.9403 g.l^{-1}, $S_2(0)$ = 1.3207 g.l^{-1}, $S_3(0)$ = 0.6545 g. l^{-1}, $S_4(0)$ = 0.4176 g.l^{-1}, $S_5(0)$ = 0.3734 g.l^{-1}.

The value of the gain parameter λ_1 in (25) is $\lambda_1 = 2$. The system evolves in open loop from the time $t = 0$ to time t_1 = 10 s, after which the system is closed by using the control law (25). The influent substrate concentration S_{in} acts as a perturbation given by

$$S_{in}(t) = S_{in0}\cdot(1 + 0.2\cdot\sin(\pi t/25) - 0.05\cdot\cos(\pi t/5)) \tag{27}$$

with $S_{in0} = 7.5$ g/l for $0 \le t < 125$ s and $S_{in0} = 15$ g/l for $t > 125$ s.

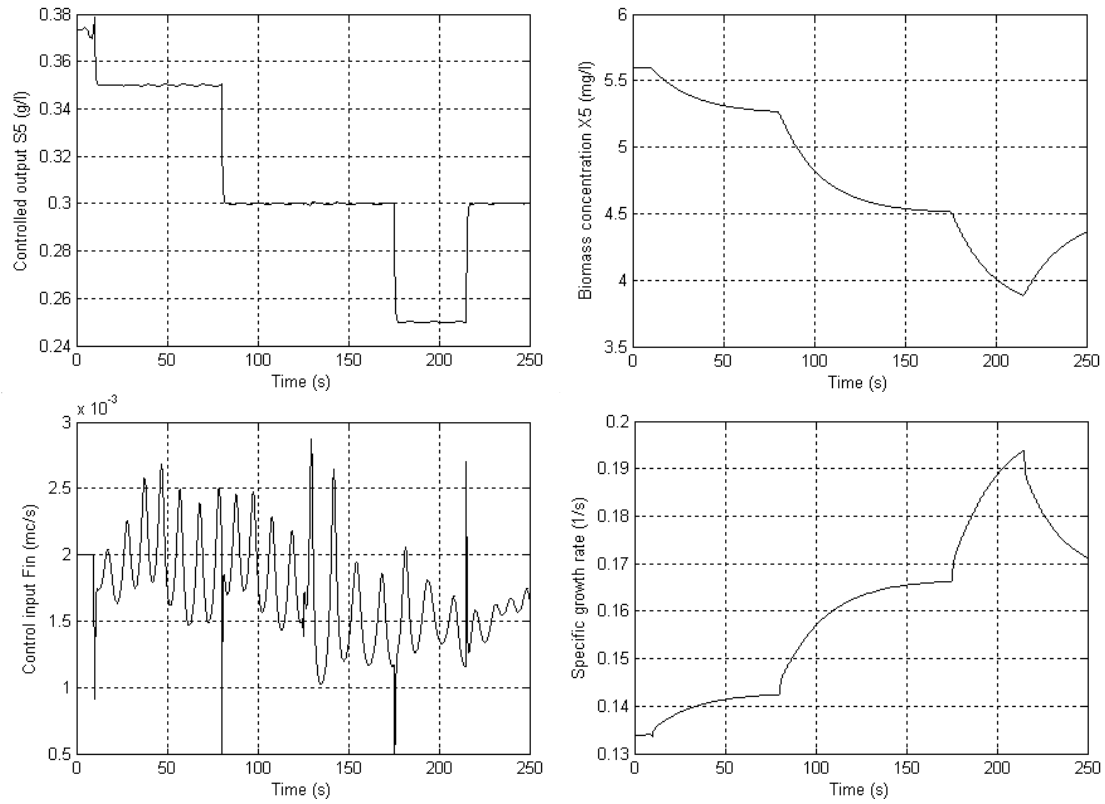

Fig. 2. The behaviour of the closed loop system with the exactly linearizing controller.

From Fig. 2 one can deduce that the controller (25) is efficiently both in regulation of controlled variable and in rejection of the perturbation S_{in}.

Assume now that the death parameter k_d is known, and the yield coefficient k_1 and the specific growth rate μ are unknown. Assume also that $\mu_5(\cdot)$ in (25) can be rewritten as:

$$\mu_5(\cdot) = \rho_5 S_5 \tag{28}$$

where ρ_5 is considered as an unknown positive parameter. It is clear that if $\mu_5(\cdot)$ should be known, then ρ_5 is a function of bioreactor state given by:

$$\rho_5(X_5, S_5) = \mu_{\max} \frac{1}{K_C X_5 + S_5} \tag{29}$$

Assume also that at the bioreactor output the only measured variable is the substrate concentration S_5.

It can be seen that the practical implementation of the control law (25) requires the knowledge of the state X_5, and of the specific reaction rate μ_5.

Since the variable X_5 is not directly measurable, this will be substituted by its estimate $\hat{X}_5$. For the estimation of unmeasured variable X_5, independent of the unknown specific reaction rate $\mu_5(\cdot)$, we use an asymptotic state observer (Petre, 2002), which can be derived as follows. Let us define the auxiliary state *z* as:

$$z = S_5 + k_1 X_5 \tag{30}$$

The dynamic of z deduced from model (6)-(8) is expressed by the following linear stable equation:

$$\dot{\hat{z}} = \frac{F_{in}}{A}\left(-b_{50} S_{in} - \sum_{i=1}^{5} b_{5i} S_i\right) - k_d(\hat{z} - S_5) \tag{31}$$

where $\hat{z}$ stands for the estimate of z.

With the definitions of ρ_5 and z in (28) and (30), respectively, the dynamics of output S_5 takes the form:

$$\dot{S}_5 = \frac{F_{in}}{A}\left(-b_{50}S_{in} - \sum_{i=1}^{5} b_{5i}S_i\right) - \rho_5 S_5(\hat{z} - S_5). \tag{32}$$

Then, the adaptive version of the control law (25) is given by:

$$F_{in} = A\frac{\dot{S}_5^* + \lambda_1(S_5^* - S_5) + \hat{\rho}_5 S_5(\hat{z} - S_5)}{-b_{50}S_{in} - \sum_{i=1}^{5} b_{5i}S_i}, \tag{33}$$

where the estimates $\hat{\rho}_5$ of ρ_5 are on-line calculated by using the regressive parameter estimator (22) where $\theta = \rho_5$ and $\Phi = S_5(\hat{z} - S_5)$, $\hat{z}$ is calculated by using (31) and the estimate of $k_1 X$ is given by:

$$k_1\hat{X}_5 = \hat{z} - S_5 \tag{34}$$

The adaptive algorithm given by (33), (31) and (22) was implemented under the same conditions as in the first case. Note that the values of the controller design parameters used in simulations are: $\lambda_1 = 2.5$, $\lambda = 0.665$, $\omega = 10$, and the initial conditions are: $\hat{\theta}(0) = \hat{\rho}_5(0) = 0.139$, $\Gamma(0) = 0.1$, $\hat{z}(0) = 2.6\text{g.l}^{-1}$.

The simulation results are shown in Fig. 3. As in the first case, the system evolves in open loop starting from $t = 0$ to time $t_1 =$ 10 s, after that the system is closed by using the above adaptive algorithm. The perturbation S_{in} has the same evolution as in the ideal case.

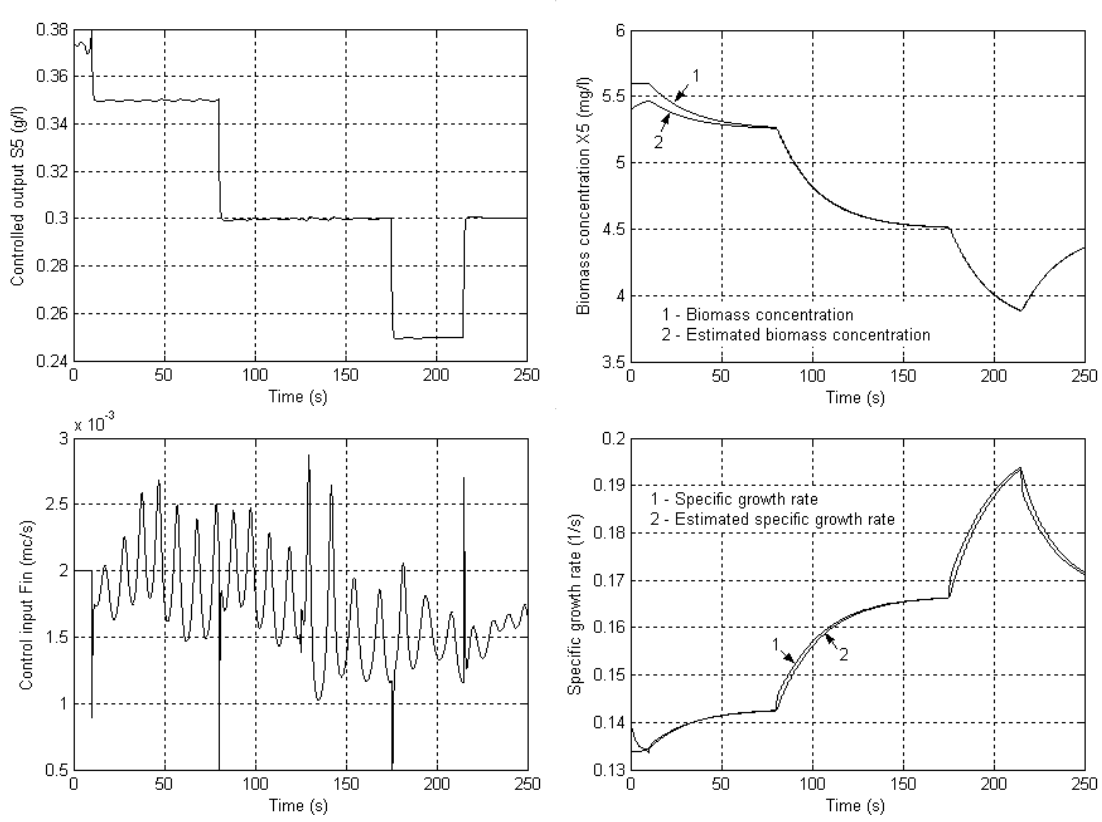

Fig. 3. The behaviour of the closed loop system with the adaptive controller.

From the graphics in Fig. 3 one can deduce that even if the initialization of $\hat{z}$ and $\hat{\rho}_5$ are different from their ideal values (given by $\hat{z}(0) = S_5(0) + k_1 X_5(0)$ and $\hat{\rho}_5(0) = \mu_{\max}/(K_M X_5(0) + S_5(0))$, the adaptive controller is efficiently both in regulation of controlled variable and in rejection of the perturbation S_{in} despite the very high load variations of S_{in}.

One can observe also a good behaviour both of the proposed state observer (31), (34) and parameter estimator (22).

Moreover, it was proved that the adaptive algorithm given by (33), (31) and (22) is robust, that is even though the process model (1) has uncertainty parameters, the behaviour of closed loop system is good. It was verified that if the death coefficient k_d suffers variations by comparison to its nominal value (e.g. $k_d = 0.04 - 0.06\ \text{h}^{-1}$) the obtained results are still good.

Concluding remarks

In this paper it has been presented the design method of nonlinear adaptive controllers for a class of propagation bioreactors based on their finite order models.

The controller design is based on the input-output linearization technique. The obtained algorithm was tested in the controlling problem of substrate concentration for a propagation bioprocess that is carried out in a fixed bed reactor.

The simulation obtained results demonstrated that the designed adaptive algoritms used in the control of propagation bioreactors yield good results closely comparable to those obtained in the case when the process prameters are completely known and/or time invariable.

Moreover, these algorithms prove themselves to be robust as well yielding good results even though the model parameters suffer variations between wide limits. It must be also noted that these algorithms can relatively easily be extended to other types of distributed parameters bioreactors: fluidized bed and air lift reactors.

Acknowledgement: *This work was created in the frame of the CNCSIS research grant No. 29C/2007, Code 621, Theme 13 and the research project CEEX-MENER No. 717/P1/2006, financed by the Education and Research Ministry, Romania.*

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