

Equivalent Models and Sliding Mode Stabilization of Cultivation Processes

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Summary: In the paper a control design and stabilization of cultivation processes is presented. The control is based on an enlarged Wang-Monod-Yerusalimsky kinetic model and their restricted Monod-Wang and Monod forms.

Keywords: Fed-batch, Yerusalimsky model, Monod kinetic, Equivalent models, Brunovsky normal form, Sliding mode control

1. INTRODUCTION

This article deals with an investigation of Monod-Wang kinetic models. The mathematical investigation is based on both the differential geometry and the sliding mode control [7, 13]. This approach permits new control solutions for stabilization of continuous and fed-batch cultivation processes.

Complicated structure and non-linearity of the compartment characterize the cultivation processes. A possible way out of these difficulties is the functional state modeling approach [10, 11]. After this approach the cultivation process is decomposed into operation regimes. Simpler mathematical models in these regimes dynamically describe the process performances [5, 10, 11]. The control problems are decomposed into subproblems that could be described and solved separately in more limited process state conditions.

This paper presents a control design for stabilization of cultivation processes described by Monod kinetic. The control design is based on both the equivalent transformations to Brunovsky normal form of an enlarged Monod-Wang-Yerusalimsky model, and a chattering optimal control and sliding mode (SM) control solutions.

The simpler Monod and Monod-Wang models used in the operational regimes are restricted forms of Monod-Wang-

Yerusalimsky model. This is why the Monod-Wang-Yerusalimsky kinetic model could be accepted as a common model in the different regimes [5, 8].

The objective of this paper is to present comfortable tools and mathematical methodology that permits control stabilization of biotechnological processes with synchronized utilization of different mathematical approaches.

2. DESCRIPTION OF MONOD-WANG-YERUSALIMSKY MODEL

Unstructured biotechnological models take cell mass as a uniform quality without internal dynamic. The reaction rates depend only on the macroscopic conditions in the liquid phase of the bioreactor. Mathematical unstructured models of fed-batch process can be written, based on mass balance equation [9, 11, 12, 14]. Below, we investigate an enlarged form of the Yerusalimsky kinetic model (Monod-Wang-Yerusalimsky model [5, 8, 15]):

$$\begin{aligned}\dot{X} &= \mu X - \frac{F}{V} X, \\ \dot{S} &= -k \mu X + (S_0 - S) \frac{F}{V}, \\ \dot{\mu} &= m \left(\mu_m \frac{S}{(K_S + S)} \frac{k_E}{(k_E + X)} - \mu \right), \\ \dot{V} &= F, \\ \dot{E} &= k_2 \mu E - \frac{F}{V} E, \\ \dot{A} &= k_3 \mu X - \frac{F}{V} A,\end{aligned}\tag{1}$$

where X is the concentration of biomass, [g·l⁻¹]; S – the concentration of substrate (glucose), [g·l⁻¹]; V – bioreactor volume, [l]; F – substrate feed rate, [h⁻¹]; S_0 – substrate concentration in the feed, [g·l⁻¹]; μ_{max} – maximum specific growth rate, [h⁻¹]; K_S – saturation constant, [g·l⁻¹]; k , k_2 , k_3 and k_E – constant, [g·g⁻¹]; m – coefficient [-]; E – the concentration of ethanol, [g·l⁻¹]; A – the concentration of acetate [g·l⁻¹].

The parameters are as follows: $\mu_m = 0.59$ [h^{-1}], $K_S = 0.045$ [$\text{g}\cdot\text{l}^{-1}$], $m = 3$ [-], $S_0=100$ [$\text{g}\cdot\text{l}^{-1}$], $k=2$ [-], $k_2=3.79$ [-], $k_3=1/71$ [-], $k_E=50$ [-], $F_{max}=0.19$ [h^{-1}], $V_{max} = 1.5$ [l]. The dynamics of μ is modeled as a first order lag process with rate constant m , in response to the deviation in μ . The 5th equation describes the production of ethanol (E). The last equation describes the production of acetate (A). The first and the last equations become dynamically equivalent to a simple transformation ($X=(1/k_3)A$). The new non-linear kinetic model is:

$$\begin{aligned}\dot{X} &= \mu X - \frac{F}{V} X, \\ \dot{S} &= -k\mu X + (S_0 - S) \frac{F}{V}, \\ \dot{\mu} &= m \left(\mu_m \frac{S}{(K_S + S)} \frac{k_E}{(k_E + X)} - \mu \right), \\ \dot{V} &= F, \\ \dot{E} &= k_2 \mu E - \frac{F}{V} E.\end{aligned}\tag{2}$$

The initial values of the state variables are: $X_i(0)=0.99$; $S_i(0)=0.01$; $\mu_i(0)=0.1$; $E_i(0)=0.1$; $V_i(0)=0.5$. The parameters are taken from different sources [10, 11].

The following mathematical condition ($k_E \rightarrow \infty$) determines the Wang-Monod model as a restricted form of the Wang-Monod-Yerusalimsky model (1). The Monod model is a singular form of Wang-Monod model obtained by omission of the third equation and application of the simple Monod kinetic. That is why the Monod-Wang-Yerusalimsky model is a more general model form. Interesting moment is that all models are dynamically equivalent to the following Brunovsky normal form:

$$\begin{aligned}\dot{Y}_1 &= Y_2 \\ \dot{Y}_2 &= Y_3 \\ \dot{Y}_3 &= W\end{aligned}\tag{3}$$

Here by W is noted the control input. This model is linear. The non-linearity of model (1) is transformed and included in the input function W [3, 6, 7]. The input function W depends from the space

vector of model (1) and that has to be underlined because this is a limitation of the application of the maximum principle.

Different diffeomorphic transformations of the Monod, Wang and Yerusalimsky models are analyzed in details in the following papers [4, 5, 6, 8]. The Brunovsky form is a linear model and permits easy optimal control solutions with application of the Pontryagin's maximum principle [7].

3. MATHEMATICAL PROBLEMS ARISING FROM THE APPLICATIONS OF SLIDING MODE CONTROL

A common manifestation in sliding mode control is some overregulation of the biotechnological process. Such overregulation is shown in Figures 1 and 2:

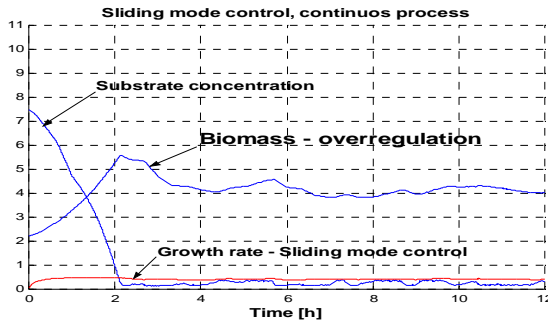


Fig. 1 Continuous process – overregulation of the biomass

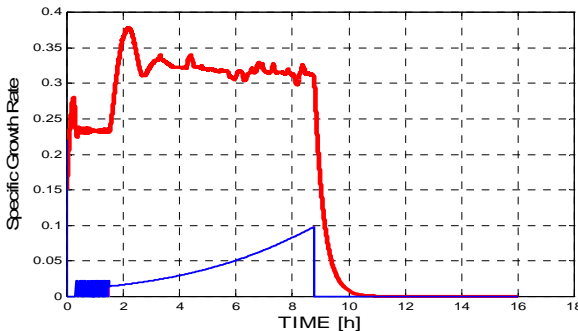


Fig. 2 Fed batch process – overregulation of the growth rate

If the sliding mode starts in system conditions different from the so called “equivalent sliding mode control” conditions then the cultivation process arrives in some over regulation situations.

That is why have to be solved some new control problems for the resolution of these restrictions [4, 5, 8]. It is needed control solutions that fix the system vector state in “equivalent control” position starting from any different initial positions. Such control solutions are showed in figures (3 and 4).

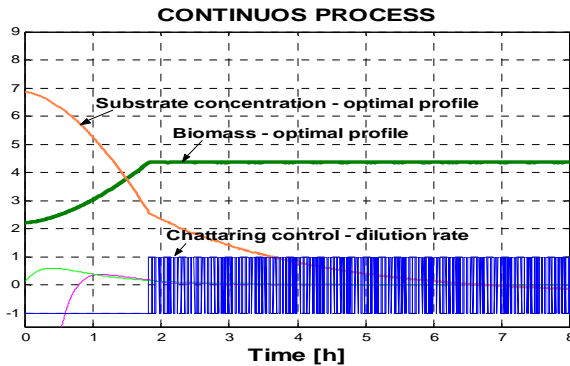


Fig. 3 Continuous process - Fixation of the biomass

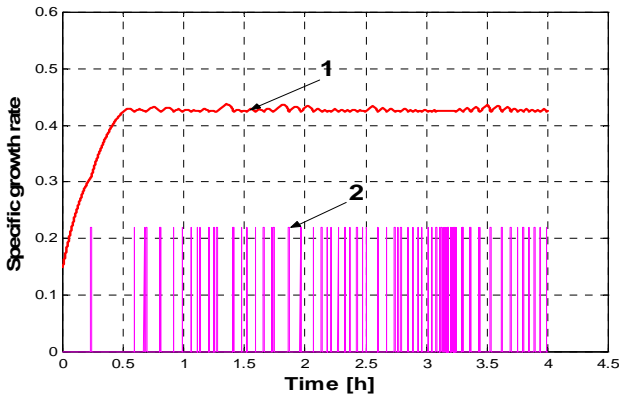


Fig. 4 Fed batch process – Chattering fixation of the growth rate:
1 – growth rate; 2 – control

Detailed descriptions of these control solutions are shown in the following papers [4, 5, 6, 8]. These control solutions are based on mathematical techniques from differential geometry and optimal control theory.

4. SLIDING MODE CONTROL

The sliding mode control is a good solution for stabilization under varying conditions (parameters deviations, noises etc.). In the paper is demonstrated a sliding mode control for stabilization of the specific growth rate in “the best” technological conditions [8]. Binary control algorithms of first order are used so that the system moves along the constraint manifold in sliding mode [1, 2, 13]. This sliding mode control is based on the alternations of the maximum specific growth rate $\mu_m(T, pH)$ [8]. The temperature T and the acidity of the bioreactor medium pH could be used for archiving this solution [9].

In this sliding mode solution is used the *Wang-Monod* model. The sliding affine subspace is defined by the following equation $SL(\mu) = (\mu - 0,31) = 0$ ($x_{30} = 0,31$ [h⁻¹]). The general stability conditions are derived from the Liapunov’s function $(SL)^2$ [13]. The performances of the system with this control are shown on the figures (5, 6, 7, 8).

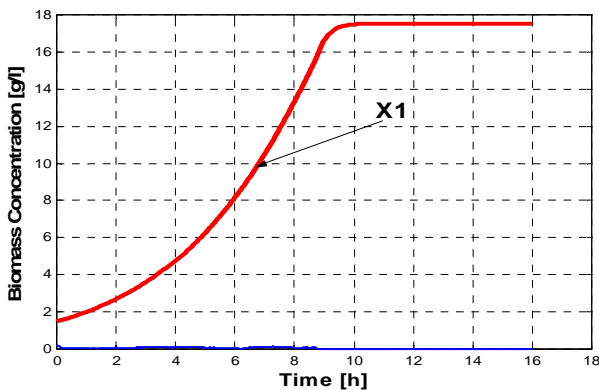


Fig. 5 Biomass concentration X (x_1)

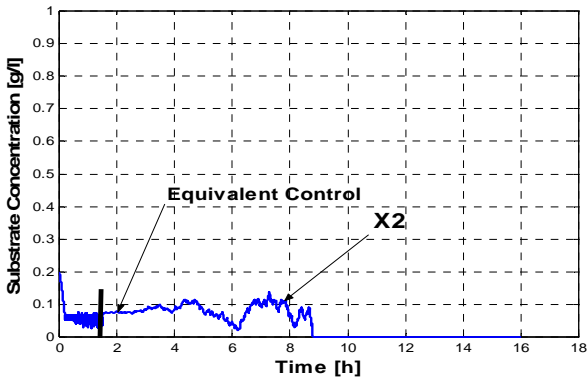


Fig. 6 Substrate concentration $S(x_2)$

The equivalent control has the presentation:

$$U_{eq}\mu = \frac{(K_S + S)\mu}{(S)} \quad (4)$$

In sliding mode control the substrate concentration S in the bio-reactor is constant $x_2 = x_{s0}K_S/(\mu_m - x_{s0}) = 0,31 \cdot 0,045 / 0,28 = 0,0498$.

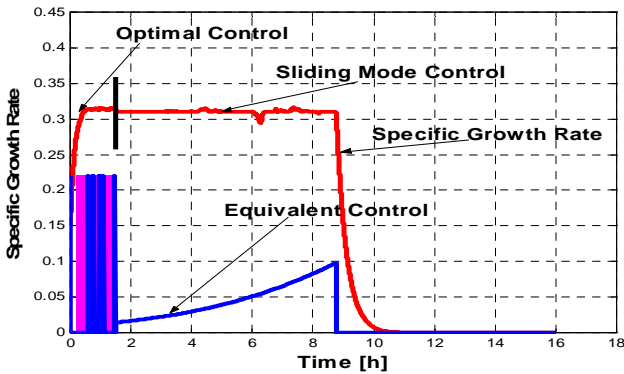


Fig. 7 Specific Growth Rate stabilization

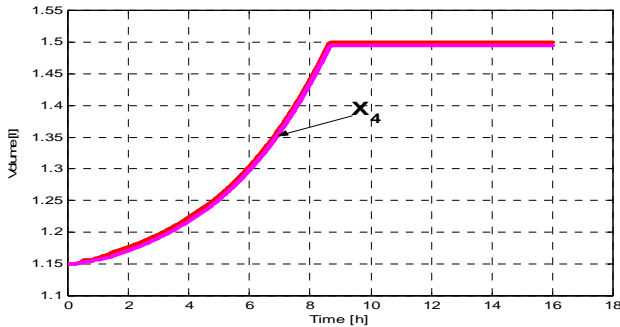


Fig. 8 Volume of the Bioreactor $V(x_4)$

The feeding rate $F(t)$ is derived from the equation of the substrate concentration and has the form

$$F = \frac{kx_{30}XV}{(S_0 - x_2)} \quad (5)$$

The mathematical model and the corresponding stability conditions determined the SM control law [13]:

$$\Delta\mu_m = - \left[\left| \frac{(K_s + S)\mu}{S} - \mu_m^1 \right| + \mu_m^2 \right] \text{sign}(SL) \quad (6)$$

The temperature (T) and the acidity (pH) assure the alternation of μ_m around the equilibrium ($\mu_m = \mu_{m0} + \Delta\mu_m$), where:

$$\mu_m^1 = x_{30} \text{ and } \mu_{m0} = \frac{(K_s + x_2)x_{30}}{x_2} \quad (7)$$

The value μ_m^2 is a sufficiently small value. It is supposed that $\mu_m(T, pH) \in [0,74, 0,44]$. The control could be determined aiming elimination of 15% parameter and measurement noises:

$$\Delta\mu_m = - \left[\left| \frac{(1,15K_s + 1,15S)1,15\mu}{0,85S} - \mu_m^1 \right| + \mu_m^2 \right] \text{sign}(SL) \quad (8)$$

This SM control law eliminates the deviations of the parameters, noises and structure modifications in the condition that it starts in “equivalent control” position. For this purpose we begin the control

design with a chattering control solution demonstrated in figures 7 and 9 [4, 5, 8].

5. SECOND ORDER SLIDING MODE CONTROL

The Russian scientists Emelyanov, Korovin and Levant evolve high-order sliding mode methods in control systems. The order of the sliding mode algorithm is defined by the proximity of the system state to the constraint manifold [1, 2]. The control algorithms of second order are used so that the system deviations become cooler but a little more imprecise. Such a control is shown on Figures 9 and 10.

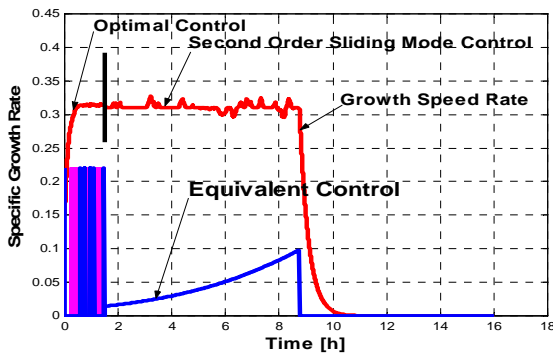


Fig. 9 Second order SM – μ

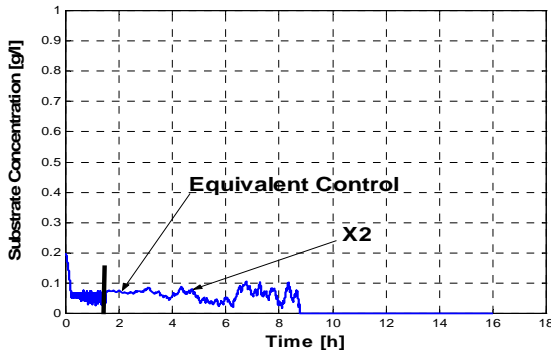


Fig. 10 Second order SM – substrate concentration $S(x_2)$

Out of the Emelyanov's approach the second order SM manifold becomes:

$$SL \cap \dot{SL}, \text{ where } SL = (x_3 - 0.31) \text{ and } \dot{SL} \text{ is the time derivative} \quad (9)$$

We use in this investigation the so called "contraction" algorithm [1, 2]. After Emelyanov the SM control input becomes:

$$\Delta \mu_m = - \left[\left| \frac{(1,15 K_s + 1,15 S) 1,15 \mu - \mu_m^1}{0,85 S} + \mu_m^2 \right| \left(\frac{2}{3} \text{sign}(SL) + \frac{1}{3} \text{sign} \left(\mu_m \frac{S}{(S + K_s)} - x_3 \right) (\mu_m - 0.59) \right) \right] \quad (10)$$

It is known that this algorithm ends for finite time. The solutions are shown on Figures 9 and 10. The control input in SM is smoother but more imprecise.

6. CONCLUSIONS

In the paper is analyzed an enlarged Monod-Wang-Yerusalimsky form of biotechnological model. This form permits a unification of the models in the functional state approach.

The investigation demonstrates the behavior of the fed-batch and continuous processes when the control algorithm is constructed by synchronized utilization of different approaches for control. The synchronized utilization of different control algorithms permits to overcome the difficulties arising from the biotechnological peculiarities in order to obtain more precise control solutions. These control laws is based on the specific growth rate measurement.

The possibilities of the second order SM are investigated and the results are that the control becomes smoother but little more imprecise. The utilization of sliding mode control is acceptable when the system is in a "sliding mode equivalent control" position.

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