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Specific Growth Rate and Sliding Mode Stabilization of Fed-Batch Processes

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I. INTRODUCTION

Biotechnological processes are relatively difficult objects for control. Their features have been discussed repeatedly. Among the most-widely used control models for Biotechnological Processes are the so called unstructured models, based on mass balance. In these models the biomass is accepted as homogeneous, without internal dynamic. Most widely used are models based on the description of the kinetic via the well known equation of Monod or some of its modifications (Neeleman, 2002; Galvanauskas, 1998; Staniskis, 1992 Pirt, 1975;).

One of the most important characteristics of biotechnological processes, which make the control design more difficult, is the change of cell population state. A serious obstacle is the existence of noise of non Gaussian type. This type of noise appears in the measurement process as well as in the process of the determination of the structure parameters of the model. But may be the most serious obstacle is provoked by the differences in the rate of changes of the elements of the state space vector of the control system. Combined with the strong nonlinearity of the control system of the Monod type this feature of the control system leads to numerical instability or to unsatisfactory performance of the control algorithms (Neeleman, 2002; Tzonkov, 2006; Roeva, 2007).

The use of the classical methods of the linear control theory is embarrassed, mainly due to the fact that the noise in the system is not of Gaussian or colored type. The changes of the values of the structural parameters of the Monod kinetics models also lead to bad estimates when using Kalman filtering (Diop, 2009). Another serious flaw is that using classical linearization and control solutions via the feeding rate, the linear system is not observable (Wang, 1987). In addition, the Monod kinetics models are characterized by another feature of the optimal control solutions. The dynamic optimization based on the Pontryagin maximum leads to singular optimal control problems (Alekseev, 1979; Krotov, 1973). The above problems have led to development of extended dynamical models in which the dynamic of the changes of the growth rate of the BTP is described by separate equation on the general differential equation. Such extended observable models based on Monod kinetics are the Monod-Wang and Wang-Yerusalimsky models used in the paper (Pavlov, 2008).

These characteristics of biotechnological processes and models have led to search for solutions via approaches and methods related to a wide range of contemporary mathematical areas (DeLisa, 2001; Levisauskas, 2003; Roeva, 2007; Bamieh, 2007; Montseny, 2008; Diop, 2009). Such areas are adaptive systems, nonlinear systems, theory of variable structure systems and their main direction sliding mode control (SMC) (Emelyanov, 1993; Selişteanu, 2007; Mohseni, 2009). In the last decade up to date methods and approaches in the areas of functional analysis, differential geometry and its modern applications in the areas of nonlinear control systems as reduction, equivalent diffeomorphic transformation to equivalent systems and optimal control have been used (Neeleman, 2002; Pavlov, 2001; Mahadevan, 2001; Bamieh, 2007; Montseny, 2008).

In the paper is proposed a new control solution based on a contemporary differential geometric approach for exact linearization of non-linear Monod type models. In our control solution are used observable model based on Monod kinetics, namely the Monod-Wang and Wang-Yerusalimsky kinetic models. Based on

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these models a control design for optimal control and stabilization of the specific growth rate of fed-batch biotechnological processes is presented. The control is written based on information of the growth rate (Neeleman, 2002).

II. Monod and Monod-Wang Biotechnological Models

Most widely used are models based on the description of the kinetic via the well known equation of Monod or some of its modifications. The rates of cell growth, sugar consumption, concentration in a yeast fed-batch growth are commonly described as follows:

$$\begin{aligned}\dot{X} &= \mu_m \frac{S}{K_S + S} X - \frac{F}{V} X \\ \dot{S} &= -k\mu_m \frac{S}{K_S + S} X + \frac{F}{V}(S_0 - S) \\ \dot{V} &= F\end{aligned} \qquad (1)$$

This differential equation is often part of more general and complex dynamic models. Here X is the concentration of the biomass, S is the substrate concentration, V is the volume of the bioreactor. The maximal growth rate is denoted by μ_m and K_S is the coefficient of Michaelis-Menten. With k we denote a constant typical for the corresponding process. The feeding rate is denoted by F. If the process is continuous (F/V) is substituted by the control D, the dilution rate of the biotechnological process (BTP). The third equation is dropped off. Often used models are described in table 1 (Staniskis, 1992; Zelic, 2004; Galvanauskas, 1998; Tzonkov, 2006).

Table 1

Model	μ
1	$\mu_{\max} \frac{S}{(k_s + S)}$
2	$\mu_{\max} \frac{S}{(k_s + S)} \frac{k_i}{(k_i + A)}$
3	$\mu_{\max} \frac{S}{(k_s + S + S^2/k_i)}$

The first model is the well known Monod type model (Roeva, 2004, 2007), the second is the Yerusalimsky model (Galvanauskas, 1998) and the third model includes inhibition term in the denominator. The non-observability of the Monod model has led to the development of the widened dynamical models, in which the dynamics of the specific growth rate of the BTP is described via separate equation in the system of differential equations. The dynamics of the growth rate μ in the Monod-Wang model is modeled as a first order lag process with rate constant m, in response to the deviation in the growth rate. This model called also the model of Monod-Wang determines a linear observable system in the classical linearization (Wang, 1987; Pavlov, 2007).

$$\begin{aligned}\dot{X} &= \mu X - \frac{F}{x_4} X \\ \dot{S} &= -k\mu X + \frac{F}{V}(S_0 - S) \\ \dot{\mu} &= m(\mu_m \frac{S}{K_S + S} - \mu) \\ \dot{V} &= F\end{aligned} \qquad (2)$$

This model concerns a fed-batch biotechnological process. Obviously model (1) is a singular form of model (2). The comparison of both models is shown in Figures (1, 2, 3):

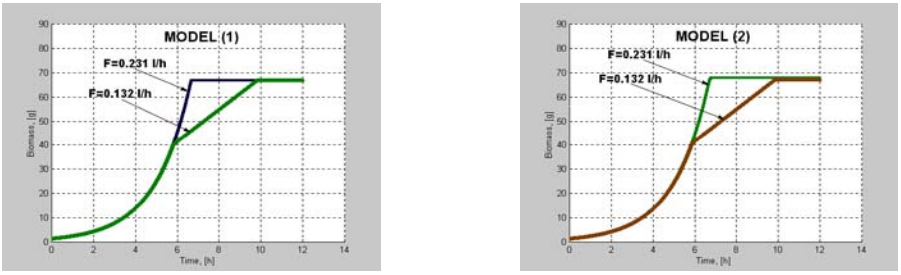

Figure1 : Growth of the biomass using Monod model (1) and Wang-Monod model (2).

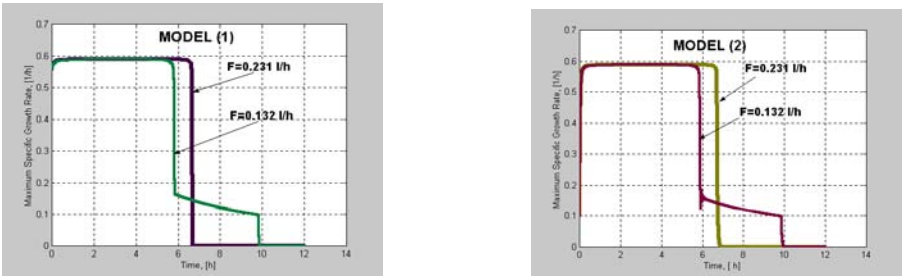

Figure2 : Specific growth rate using Monod model (1) and Wang-Monod model (2).

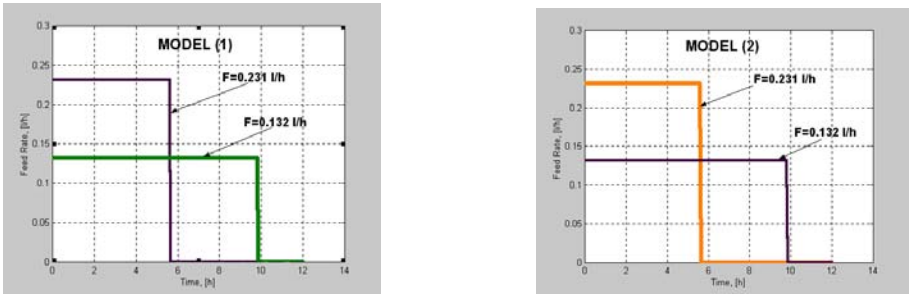

Figure 3 : Feeding rate using Monod model (1) and Wang-Monod model (2).

One general description of the fed-batch biotechnological process looks like (Pavlov, 2007).

$$\begin{aligned}
\dot{X} &= \mu X - \frac{F}{V} X, \\
\dot{S} &= -k\mu X + (So - S)\frac{F}{V}, \\
\dot{\mu} &= m(\mu_m \frac{S}{(K_S + S)} - \mu), \\
\dot{V} &= F, \\
\dot{A} &= = k_3 \mu X - \frac{F}{V} A.
\end{aligned} \tag{3}$$

Here X denotes the concentration of biomass, [g/l]; S – the concentration of substrate (glucose), [g/l]; V - bioreactor volume, [l]; F – substrate feed rate, [h^{-1}]; S_0 – substrate concentration in the feed, [g/l]; μ_{max} - maximum specific growth rate, [h^{-1}]; K_S – saturation constant, [g/l]; k and k_3 – yield coefficients, [g/g], m – rate coefficient [-];. The dynamics of μ in the Monod-Wang model is modeled as a first order lag process with rate constant m, in response to the deviation in μ. The last equation describes the production of acetate (A). This equation is dynamically equivalent to the first one after the implementation of a simple transformation ($X = (1/k_3)\ A$). That is why we replace A with X in Yerusalimsky model. The best description is given by the so called model of Wang-Yerusalimsky:

$$\begin{aligned}
\dot{X} &= \mu X - \frac{F}{V} X, \\
\dot{S} &= -k\mu X + (So - S)\frac{F}{V}, \\
\dot{\mu} &= m(\mu_m \frac{S}{(K_S + S)} \frac{k_i}{(k_i + X)} - \mu), \\
\dot{V} &= F, \\
\dot{A} &= = k_3 \mu X - \frac{F}{V} A.
\end{aligned} \tag{4}$$

In the formula X is the concentration of biomass, [g/l]; S–the concentration of substrate (glucose), [g/l]; V-bioreactor volume, [l]; F–substrate feed rate (control input), [h^{-1}]; S_0–substrate concentration in the feed, [g/l]; μ_{max}-maximum specific growth rate, [h^{-1}]; K_S–saturation constant, [g/l]; k, k_3–constants, [g/g]; m–coefficient [-]; E–the concentration of ethanol, [g/l]; A–the concentration of acetate [g/l]. The system parameters are as follows: μ_m=0.59 [h^{-1}], K_S=0.045 [g/l], m=3 [–], S_0=100 [g/l], k=1/$Y_{S/X}$,, k=2 [–], k_3=1/$Y_{A/X}$, k_3=53 [–], k_i=50 [–], F_{max}= 0.19 [h^{-1}], V_{max}=1.5 [ ] . These data desribed an *E. Coli* process (Cockshott, 1999) and are chosen close to data in table 2 (Roeva, 2004, 2007):

Table 2

Parameter	Model 1	Model 2	Model 3
μ_{max} , [h^{-1}]	0,55	0,52	0,54
k_S , [gl^{-1}]	0,039	0,027	0,029
k_i , [gl^{-1}]	51,3	53,6	50,8
$Y_{S/X}$, [gg^{-1}]	0,501	0,498	0,497
$Y_{A/X}$, [gg^{-1}]	0,015	0,015	0,015

The last equation describes the production of acetate (A). This equation is dynamically equivalent to the first one after the implementation of a simple transformation ($X = (1/k_3)A$). The initial values of the state variables are: $X(0)=0.99$; $S(0)=0.01$; $\mu(0)=0.1$; $A(0) = 0,03$; $V(0)=0.5$.

The following mathematical condition ($k_E \to \infty$) determines the Wang-Monod model as a restricted form of the Wang-Yerusalimsky model (4). The Monod model is a singular form of Wang-Monod model obtained by omission of the third equation. That is why the Wang-Yerusalimsky model is a more general model form.

Interesting moment is that these models are dynamically equivalent to the following Brunovsky normal form (Pavlov, 2001, 2004, 2007):

$$\begin{aligned} \dot{Y}_1 &= Y_2 \\ \dot{Y}_2 &= Y_3 \\ \dot{Y}_3 &= W \end{aligned} \qquad (5)$$

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 (Montseny, 2008; Bamieh, 2007; Elkin, 1999; Gardner, 1992). 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 Pontryagin maximum principle (Alekseev, 1979; Krotov, 1973; Hsu, 1972). Different diffeomorfic transformations of the Monod, Wang and Yerusalimsky models are analyzed in details in the following papers (Pavlov, 2001, 2004, 2007, 2008). The Brunovsky form is a linear model and permits easy optimal control solutions with application of the Pontryagin's maximum principle.

The complexity of the biotechnological systems and their singularities make them difficult objects for control. They are difficult to control also because of the fact that it is difficult to determine their optimal technological parameters. These parameters can depend on very complicated technological, ecological or economical market factors. Their taking into account in one mathematical model directly is impossible for the time being. Because of this reason often in practice expert estimates are used. From outside the estimates are expressed only by the qualitative preferences of the Biotechnologist. The preferences themselves are in rank scale and bring the internal indetermination, the uncertainty of the qualitative expression, which is a general characteristic of human thinking. Because of this reason here the mathematical models from the Utility theory and stochastic programming can be used (Kivinen, 2004; Fishburn, 1970; Keeney, 1993; Aizerman, 1970).

Thus the incomplete information usually is compensated with the participation of imprecise human estimations. Our experience is that the human estimation of the process parameters of a cultivation process contains uncertainty at the rate of [10, 30] %. Here is used a mathematical approach for elimination of the uncertainty in the DM's preferences based both on the Utility theory and on the Stochastic programming (Pavlov, 2010, 2011). The algorithmic approach permits exact mathematical evaluation of the optimal specific growth rate of the fed-batch cultivation process according to the DM point of view even though the expert thinking is qualitative and pierced by uncertainty. The assessed utility criteria are shown on the following figure 4:

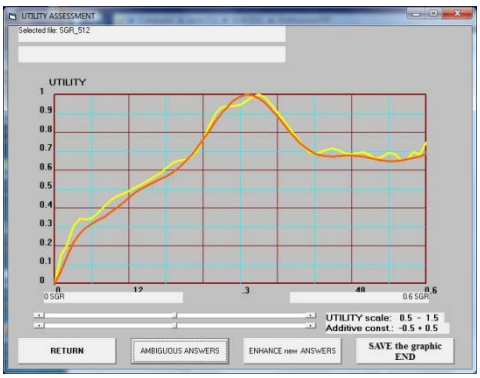

Figure 4 : Expert utility versus Growth rate

Thus we achieve totally analytical mathematical description of the complex system "Technologist-biotechnological process "(Pavlov, 2010, 2011).

III. Optimal Control and Stabilization of the Growth Rate

The presentation of the control design follows the presentations in papers (Pavlov, 2004, 2007, 2008). We use the general model (Technologist-biotechnological process). We preserve the notation $U(.)$ for the DM utility function (Pavlov, 2010; Fishburn, 1970; Keeney, 1993). The control design of the fed-batch process is based on the next subsidiary optimal control problem:

Max($U(\mu(T_{int}))$), *where the variable* μ *is the specific growth rate,* ($\mu \in [0, \mu_{max}]$, $D \in [0, D_{max}]$). *Here* $U(\mu)$ *is an aggregation objective function (the utility function – fig.4)* and D is the control input (the dilution rate):

$$\max(U(\mu)),\ \mu\in[0,\mu_{\max}],\ t\in[0,T_{\text{int}}],\ D\in[0,D_{\max}]$$

$$\begin{aligned}\dot{X} &= \mu X - DX\\ \dot{S} &= -k\mu X + (So - S)D\\ \dot{\mu} &= m(\mu_m \frac{S}{(K_S + S)} - \mu)\end{aligned} \tag{6}$$

When T_{int} is sufficiently small the optimization is in fact "time minimization". The differential equation in (6) describes *a continuous fermentation process*. The model permits exact linearization to the next Brunovsky normal form (Goursat, as regard to the differential forms) (Gardner, 1992; Elkin, 1999; Pavlov 2001):

$$\begin{aligned}\dot{Y}_1 &= Y_2,\\ \dot{Y}_2 &= Y_3,\\ \dot{Y}_3 &= W.\end{aligned} \tag{7}$$

The Brunovsky normal form of Wang-Yerusalimsky model (4) is the same (Pavlov, 2008). Here W denotes the control input. The new state vector (Y_1, Y_2, Y_3) is:

$$\begin{aligned}Y_1 &= u_1,\\ Y_2 &= u_3(u_1 - ku_1^2),\\ Y_3 &= u_3^2(u_1 - 3ku_1^2 + 2k^2u_1^3) + m(\mu_m \frac{u_2}{(K_S + u_2)} - u_3)(u_1 - ku_1^2),\end{aligned} \tag{8}$$

$$\begin{bmatrix} u_1(X,S,\mu)\\ u_2(X,S,\mu)\\ u_3(X,S,\mu)\end{bmatrix} = \begin{bmatrix} \frac{X}{S_o - S}\\ S\\ \mu\end{bmatrix}.$$

The derivative of the function Y_3 determines the interconnection between W-model (7) and D-model (6). The control design is a design based on the Brunovsky normal form and application of the Pontrjagin's maximum principle step by step for sufficiently small time periods T. The optimal control law has the analytical form (Pavlov, 2007):

$$D_{opt} = sign\left(\left(\sum_{i=1}^{6} ic_i\mu^{(i-1)}\right)(T-t)\left[\frac{(T-t)\mu(1-2kY_1)}{2} - 1\right]\right)D_{\max}, \tag{9}$$

$$where: sign(r) = 1, r > 0,\ sign(r) = 0, r \le 0.$$

The optimal control law of Wang-Yerusalimsky model (4) has the same form (Pavlov, 2008).This type of control may be used only for cumulative criteria for which the Bellman principle is valid in the optimal control (Hsu, 1972). For example, such are the amount of biomass at the end of the process and the time-minimization optimal control. The sum is the derivative of the utility function $U(\mu)$.The time interval T can be the step of discretization of the differential equation solver.

It is clear that the "time-minimization" control is determined from the *sign* of the utility derivative. Thus, the control input is D=$D_{\max}$ or D=0. The solution is a *"time-minimization"* control (if the time period T is sufficiently small) (Pavlov, 2004). The control brings the system back to the set point for minimal time in any case of specific growth rate deviations. The demonstration is shown in (Pavlov, 2007).

The previous solution permits easy determination of the control stabilization *of the fed-batch process*. The control law is based on the solution of the next optimization problem:

Max($U(\mu(T_{int}))$), *where the variable* μ *is the specific growth rate,* ($\mu\in[0,\ \mu_{max}]$, $F\in[0,\ F_{max}]$). *Here* $U(\mu)$ *is the utility function in figure (3)* and F is the control input (the substrate feed rate):

$$\max(U(\mu(T_{\text{int}}))),\ \mu\in[0,\mu_{\max}],\ t\in[0,T_{\text{int}}],\ F\in[0,F_{\max}]$$

$$\begin{aligned}\dot{X} &= \mu X - \frac{F}{V}X\\ \dot{S} &= -k\mu X + (So - S)\frac{F}{V}\\ \dot{\mu} &= m(\mu_m \frac{S}{(K_S + S)} - \mu)\\ \dot{V} &= F\end{aligned} \tag{10}$$

The control law *of the fed-batch process* has the same form (9) because $D(t)$ is replaced with $F(t)/V(t)$ in the fed-batch model. Thus, the feeding rate $F(t)$ takes $F(t)$=$F_{\max}$ or $F(t)$=0, depending on $D(t)$ which takes D=$D_{\max}$ or D=0.

We conclude that the control law (9) bring the system to the optimal point (optimal growth rate) with a" time minimization" control, starting from any deviation point of the specific growth rate (Fig. 5).

Thus, we design the next control law:

1. At the interval [0, t_1] the control is "time-minimization" control (9), where $\mu(t_1)=(\mathbf{x_{30}-\varepsilon})$, $\varepsilon>0$, $x_{30}=max(U(\mu))$. D is replaced with $F=\gamma F_{max}$, $1\geq\gamma>0$, when $D=D_{max}$. The choice of γ depends on the step of the equation solver and is not a part of the optimization (here $\gamma=0.123$);
2. At the interval $[t_1, t_2]$ the control is $F=0$ ($\mu(t_1)=(\mathbf{x_{30}-\varepsilon})$, $\mu(t_2)=\mathbf{x_{30}}$ - to be escaped an overregulation);
3. After this moment the control is the control (9) with $F=\gamma F_{max}$, when $D=D_{max}$ (chattering control with $1\geq\gamma>0$).

The deviation of the fed-batch process with this control is shown on figures (5, 6).

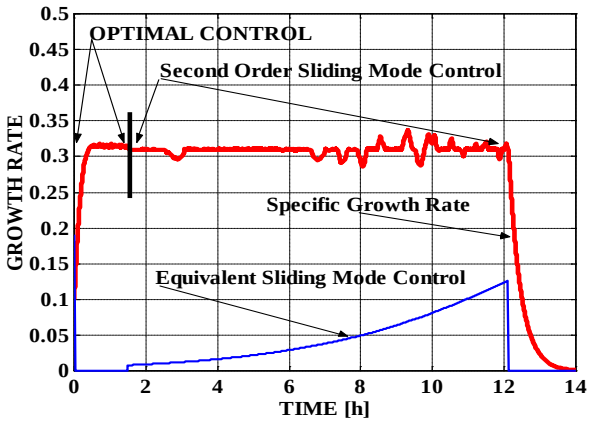

Fig. 5 : Stabilization of the fed-batch process

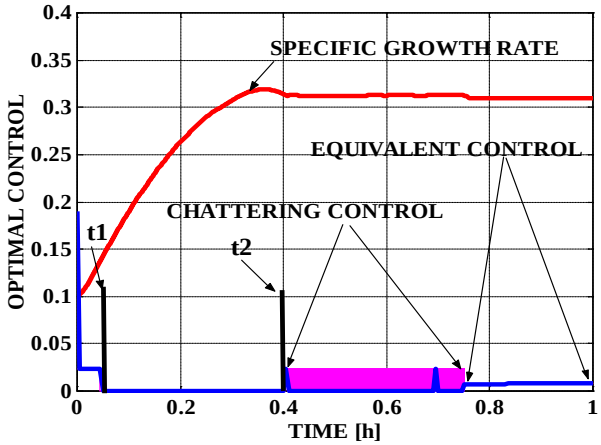

Fig. 6 : Optimal profile

After the stabilization of the system in equivalent sliding mode control position the system can be maintained around the optimal parameters with sliding mode control (Fig.5, 6). Possible solution in sliding mode is alternation of μ_m (as a function of the temperature and the acidity in the bioreactor) or alternation of F (Pirt, 1975; Pavlov, 2007). The iterative utility function design and the iterative corrections in the DM preferences permit adjustment of the control law and of the optimal control final results in agreement with the changes in the opinion of biotechnologist. The procedure could be interprets as learning procedure in the two opposite directions, in direction to biotechnologist or in direction to the final optimal solution.

IV. Mathematical Problems Arising From the Sliding Mode Control

Control solution results are shown in control systems based on the solutions of variable structure systems (Selişteanu, 2007; Mohseni, 2009). Here a different problem arises. Good control via sliding mode control is possible when the system is led to the initial position in a point from the area of the "equivalent control solution" (Pavlov, 2007, 2008). This is a specific task for fed-batch control via information about the growth rate of the biomass.

A common manifestation in sliding mode control is some overregulations of the biotechnological process. Such overregulations are shown in figures (7 and 8). In case of start in sliding mode in system conditions different from the area of "equivalent sliding mode control" then the process arrives in some over regulations (Utkin, 1981).

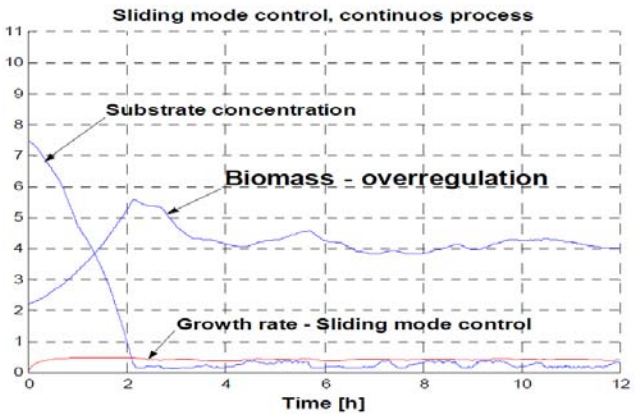

Fig.7 : Continuous process – overregulation of the biomass in SMC

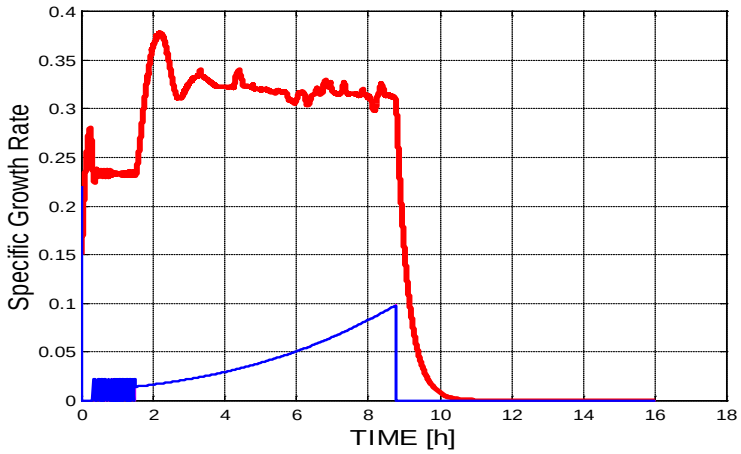

Fig.8 : Fed batch process- overregulation of the growth rate in SMC

These characteristics of biotechnological processes table new mathematical control problems for discussion and resolution. The overregulations in SMC are provoked by the differences in the rate of changes of the elements of the state space vector of the control system. It is needed control solution that fixes the system in "equivalent control" position, staring from any initial positions.

These characteristics of biotechnological processes and models have led to search for solutions via approaches and methods related to a wide range of contemporary mathematical areas. Such areas are differential geometry and its modern applications in the areas of nonlinear control systems as diffeomorphic transformation to equivalent systems. Solutions that fix the system in "equivalent control" position, staring from any initial positions are showed in (Fig. 9, 10).

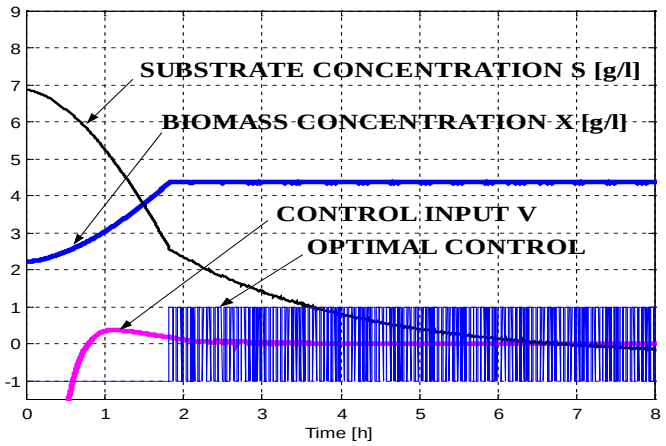

Fig.9 : Continuous process – Optimal feed rate and fixation of the biomass

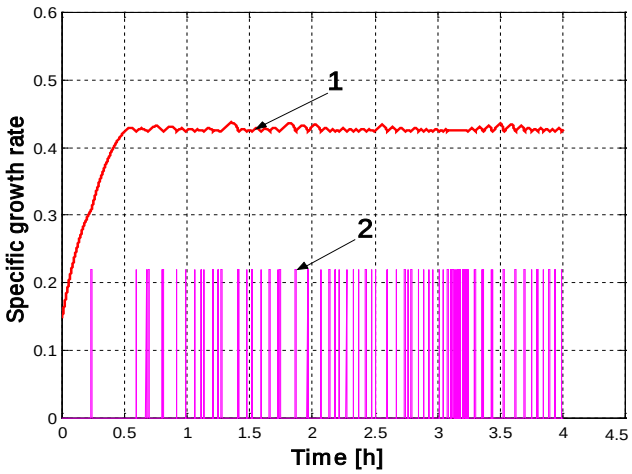

Fig.10 : Fed batch process, Chattering control: growth rate (1); feed rate control (2)

Detailed descriptions of such controls are discussed in (Pavlov, 2007, 2008). In the last decade up to date methods and approaches in the areas of functional analysis, differential geometry and its modern applications in the areas of nonlinear control systems as reduction, equivalent transformation to equivalent systems have been used for surmount the discussed difficulties (Pavlov, 2005; Bamieh, 2007; Montseny, 2008; Diop, 2009).

V. Sliding Mode Control and Stabilization of the Fed-Batch Process

The sliding mode control is a good solution for stabilization under varying conditions (parameters deviations, noises etc.) (Emelyanov, 1993, 1996; Utkin 1987; Selişteanu, 2007). In the paper is demonstrated a sliding mode control for stabilization of the specific growth rate in "the best" growth rate (Pavlov, 2007).

For some types of BTP it is possible to choose the control via the temperature and/or via changing the acidity in the bioreactor (Pirt, 1975). What we mean is indirect influence on the biomass maximum growth rate, which, according to the contemporary researches, is one of the main factors, determining the quality of the cultivation process (Neeleman, 2002). Here the problem about the observability of the control system arises again, because this directly concerns the possibility for satisfactory identification of the state space vector of the control system and more specifically for the determination of the specific growth rate of the BTP. This group of questions is still a topical branch in the theory of the biotechnological control systems (Diop, 2009).

The sliding mode in the paper is realized with Wang-Monod model (3). This more exotic SM control solution is obtained with alternations of the maximum specific growth rate $\mu_m(T, pH)$ through changes of the temperature (t^o) and the acidity of the bioreactor medium (pH)(Pirt, 1975) . This control gives us the possibility to use the temperature (t^o) and the acidity (pH) as input control values. More classical SM solutions with substrate concentration S as control value could be seen in the literature (Selişteanu, 2007; Mohseni, 2009).

The sliding affine subspace is defined by the equation $S(\mu) = (\mu - 0{,}31) = 0$. The general stability conditions are derived from the Liapunov's function $(S(\mu))^2$ (Utkin, 1981). In sliding mode control the substrate concentration S in the bioreactor is constant. The substrate concentration S is constant $Se = 0{,}0498$. The equivalent growth rate control is determined exactly and the SM control is possible (Utkin, 1981):

$$Ue\mu = \frac{(Ks + S)\mu}{S} \tag{11}$$

The feeding rate F(t) is derived from the substrate concentration: $F(t)=(kX(t)\mu(t)V(t)/(So-S_e)$, where $X(.)$ is the quantity of biomass in the bioreactor. Deviations of the system in sliding mode are showed in Fig. (11, 12).

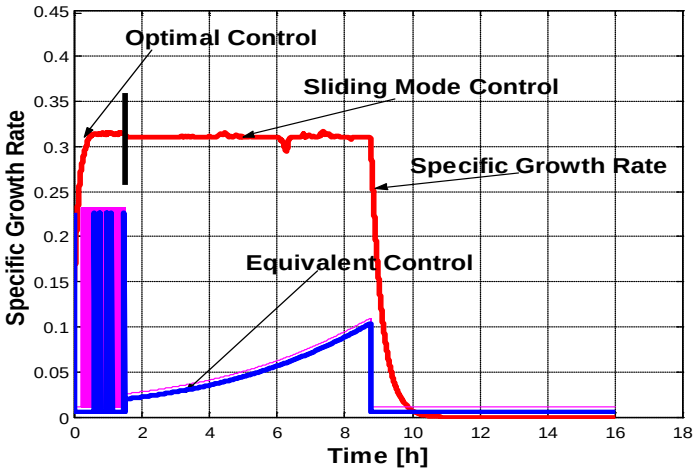

Fig.11 : Specific Growth Rate stabilization in sliding mode

The mathematical model and the corresponding stability conditions determine the SM control law:

$$Control \Rightarrow \Delta\mu_m = -\left[\left|\frac{(Ks + S)\mu}{S} - \mu_m^1\right| + \mu_m^2\right] sign(Sl_1) \tag{12}$$

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

$$\mu_m^1 = 0.31, \mu_{m0} = \frac{(Ks + Se)\times 0.31}{Se}. \tag{13}$$

The value μ_m^2 is a sufficiently small supplementary value. This SM control law eliminates the deviations of the parameters, noises and structure modifications. This solution overcomes successfully some of the difficulties mentioned above.

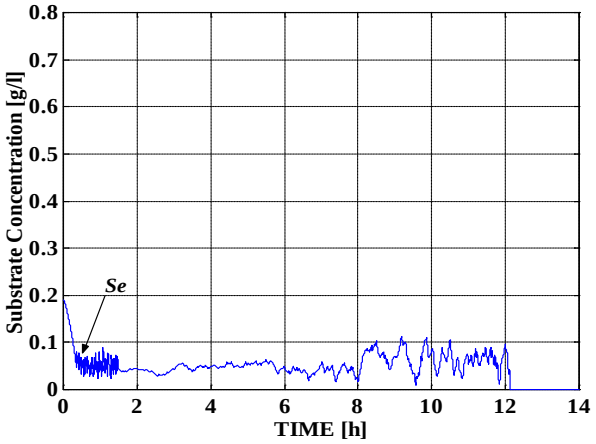

Fig.12 : Substrate concentration S in sliding mode

The Russian scientists Emelyanov, Korovin and Levant evolve high-order sliding mode methods in control systems (Emelyanov, 1993, 1996). We propose in our investigation a second order sliding mode control following Emelyanov and Korovin. The control algorithms of second order are used so that the system deviations become cooler but a little more imprecise. Out of this approach the second order SM manifold becomes:

$$S_1 \cap \dot{S}_1, \text{where } S_1 = (\mu - 0.31) \text{ and } \dot{S}_1 \text{ is the time derivative.} \quad (14)$$

Here is used the so-called "contraction" algorithm [5]. After Emelyanov the second order SM control input in the "contraction" algorithm becomes:

$$Control \Rightarrow \Delta\mu_m = -\left[\frac{(1{,}15K_s + 1{,}15S)1{,}15\mu}{0{,}85S} - \mu_m^1\right| + \mu_m^2\Big] \times$$
$$\times \left(\frac{2}{3}\text{sign}(S_1) + \frac{1}{3}\text{sign}\left(\left(\mu_m \frac{S}{(S+K_s)} - \mu\right)(\mu_m - 0.59)\right)\right) \quad (15)$$

It is known that this algorithm ends for finite time (Emelyanov, 1993, 1996). The input in second order SM is smoother but the control becomes is more imprecise. The performances of the system with this SM control are showed in Fig. (13, 14) (Pavlov, 2007, 2008).

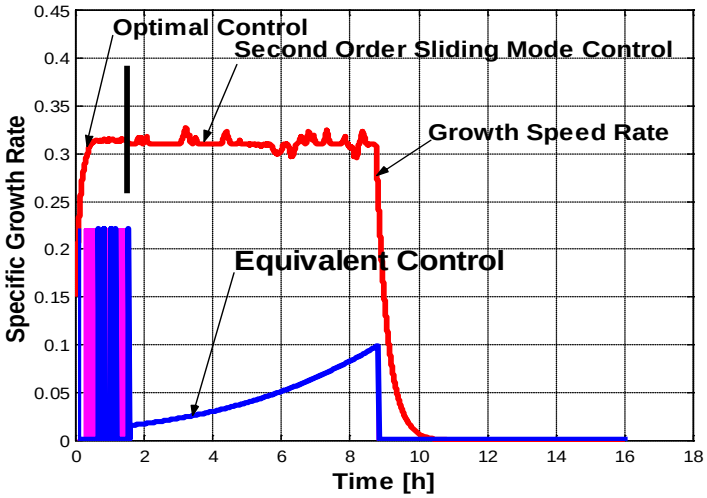

Fig.13 : Second order SM - μ

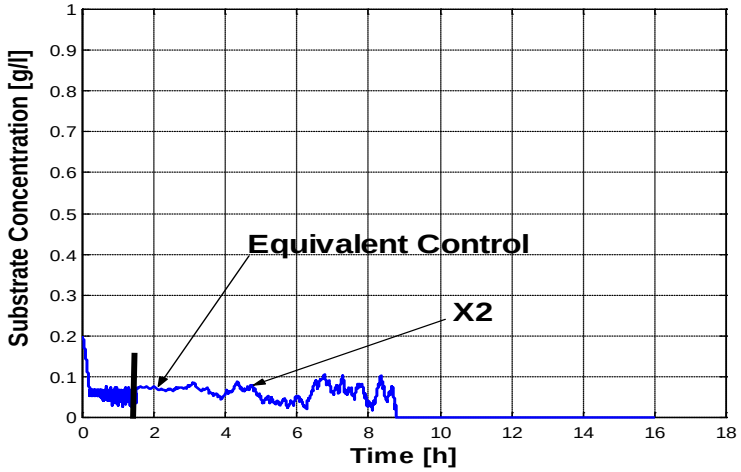

Fig.14 : Second order SM - substrate concentration S - (x_2)

The devolving from the "discontinuity" to "continuity" in sliding mode control not only raise the control quality but permits to solve control problems with smaller quantity of priory information (Emelyanov, 1993, 1996).

By now we have reached a full mathematical description of the complex system "Biotechnologist-fed-batch process". We have overcome the restrictions connected with the observability of the Monod kinetics; we have overcome the obstacles with the singularities of the optimal control via finding and using of the Brunovsky normal form of the differential equation. The system was led to the working point from the "equivalent control in sliding mode" smoothly and stabilized in the optimal specific growth rate position (Pavlov, 2007). The solution and the determination of the optimal profile was

done via synchronized usage of several mathematical approaches for modeling, reduction of nonlinear system, application of the Pontryagin maximum principle.

VI. Conclusion

A methodology for specific growth rate optimal control is developed. This approach aims utilization of control based only on specific growth rate measurement. In the paper are investigated the possibilities of the second order sliding mode. We have overcome the restrictions connected with the observability of the Monod kinetics through Monod-Wang and Wang-Yerusalimsky models; we have overcome the obstacles with the singularities of the optimal control via finding and using of the Brunovsky normal form of the differential equation. The system was led to the working point from the "equivalent control in sliding mode" smoothly and stabilized in the optimal specific growth rate position. This solution permits to win through difficulties arising from the biotechnological peculiarities in order to be obtained good control solutions.

The inclusion of a value model as objective function as part of a dynamical system reached a full mathematical description of the complex system "Biotechnologist-fed-batch process". This is done with the use of the expected utility theory and the stochastic programming. Such a good objective function would allow the user to vary iteratively his value judgments and to correct iteratively the control law in agreement with his value judgments.

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