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Equivalent Models and Exact Linearization by the Optimal Control of Monod Kinetics Models

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Abstract: *The well-known global biotechnological models are non-linear and non-stationary. In addition the process variables are difficult to measure, the model parameters are time varying, the measurement noise and measurement delay increase the control problems, etc. One possible way to solve some of these problems is to determine the most simple and easy for use equivalent models. The differential geometric approach [DGA] and especially the exact linearization permit an easy application of the optimal control. The approach and its application in the control of the biotechnological process are discussed in the paper. The optimization technique is used for fed-batch and continuos biotechnological processes when the specific growth rate is described by the Monod kinetics.*
Keywords: *Biotechnological process, Exact linearization, Pontryagin maximum principle, Brunovsky normal form.*

Introduction

The control systems are already implemented in modern bioreactors. From biotechnological point of view the straightforward way of improving the economics is to invest in process optimization and control.

The fermentation processes are complex ones and the well-known biotechnological models are non-linear and non-stationary. They are attractive and difficult objects for control, particularly when for the control variable is accepted the dilution rate. Many mathematical models have been proposed but just few have been used successfully because of the peculiarities of the bioprocesses. The conventional linear systems of control and the conventional control methods are used extensively but not in all cases with success [10, 11, 13]. In addition the process variables are difficult to measure and the model parameters are time varying. The measurement noise and the parameters identification delay increase the control problems. The realization of the biotechnological processes for production needs is

impossible without automatic measurement and control. Any real control scheme must take these factors into consideration. Control design methodologies, which take into accounts the robustness properties of the control design, appear highly attractive for control of biotechnological process. Consequently the elaboration and the design of new control systems in the field of biotechnology is an open automation problem.

The mentioned above determines the biotechnological systems and controls like a specific domain of investigations with specific problems and tasks. Very promising in this field is the exact linearization approach that based on the DGA and the GS algorithm [4]. Such approach permits successful utilization of the maximum principle for the determination of the optimal control [1, 2, 3, 4].

Problem statement

The aim of the paper is to demonstrate the possibilities of an integral approach for control determination that include the DGA exact linearization and the Pontryagin maximum principle.

Mathematical models – continuous process

The continuous biotechnological process is a continuously operated bioreactor with one substrate in the feed. The bacterial biomass consumes the substrate to produce more biomass, and the biomass is harvested as the desired end product. The state variables are the biomass (bacterial cell mass) and the substrate concentrations in the bioreactor as a function of the time. The modelling approach in [11, 12, 13, 14] is analysed as a feasible base for control design. In this model Stephanopoulos and San introduced a state variable (colour noise) to aid the convergence of the specific growth rate in the model. After linearization the linear model was not controllable, that is why Wang and all proposed a modification of the dynamic model for the specific growth rate in which are included the maximum growth rate, the Mihaelis-Menten constant and a white noise process. The so defined model is:

$$\begin{aligned} \dot{X} &= \mu X - DX \\ \dot{S} &= -\frac{1}{y}\mu X + (S_0 - S)D \\ \dot{\mu} &= m(\mu_m \frac{S}{K_s + S} - \mu) + v \end{aligned} \tag{1}$$

Where:

-X is the biomass concentration in the bioreactor,

-S is the substrate concentration,

-μ is the specific growth rate,

-K_s is a saturation coefficient (the Mihaelis-Menten constant),

-v is a white noise process,

-S_0 is the substrate concentration in the feed,

-m is a constant determining the dynamic of the growth rate,

-D is the dilution rate,

-μ_m (T, pH) is the maximum growth rate (as a function of the temperature and the acidity of the bioreactor medium pH),

-y biomass yield with respect to substrate.

This model with the third equation is an extension of the well-known Mono model.

The system set point is given by the next expression:

$$\mu_{30} = D_e$$
$$\mu_{30} = \mu_m \frac{S_e}{K_s + S_e} \qquad (2)$$
$$\frac{X_{10}}{y} = S_0 - S_e$$

where

-X_{10} is the biomass concentration in the set point,

- $S_e \equiv (x_{20})$ is the substrate concentration in the set point,

-μ_{30} is the specific growth rate in the set point,

-D_e is the dilution rate in the set point.

The system operation conditions were fixed by the following set of values: μ_m=0.5 h^{-1}, K_s=0.05 $g.l^{-1}$, m=3, S_e=0.2625 $g.l^{-1}$, S_0=9 $g.l^{-1}$, y=0.5 $g.g^{-1}$, D_e=0.42 h^{-1}.

The noise was taken 0%. The performance of the system without control is shown in Fig. 1.

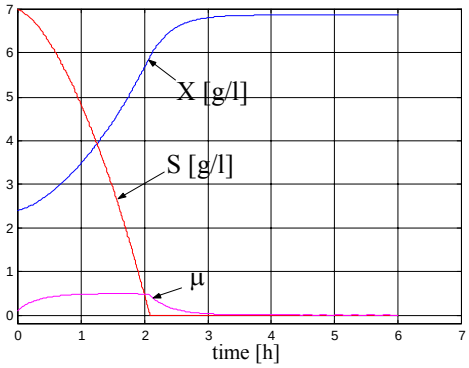

Fig.1 Model (1) - without control

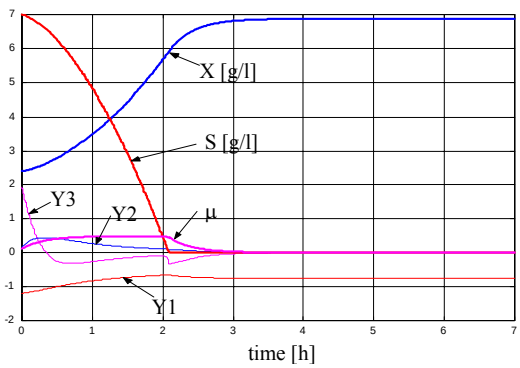

Fig.2 Models (1) and (8) – without control

A complication is that the diffeomorphism defining the equivalent nonlinear transformation from the nonlinear system (1) to the Brunovsky normal linear form is non-regular in the equilibrium point [2, 8]. In the limits the two models (the nonlinear model and the Brunovsky model) converge to the equilibrium points. From computing point of view in the limits arise rounding problems. We escape in parts this problem, taking in account that some evaluations of the state vector coordinates around the set point are influenced faintly. This fact forces a new model determination, in which the third differential equation has a polynomial form (3) where c=0.42, m_1=0.0286, m_2=0.713 [7, 11, 13].

The next two vectors determine the affine space of the new nonlinear system. The vectors $\mathbf{f_0}$ and $\mathbf{f_1}$ determine the appropriate linear space:

$$\mathbf{f}_0 = \begin{pmatrix} \mu X \\ -\frac{1}{y}\mu X \\ m(c - m_1 X - m_3 \mu) \end{pmatrix} \quad \mathbf{f}_1 = \begin{pmatrix} -X \\ S_0 - S \\ 0 \end{pmatrix} \tag{3}$$

Where c, m_1 and m_3 are constants that determined the evaluation of the model around the set point ($d\mathbf{z}/dt=\mathbf{f_0}+\mathbf{f_1}.U$, where U =D is the control input and $\mathbf{z}=(X,S,\mu)$.

Mathematical models – fed batch process

The well-known non-linear model [5, 6, 11, 13] describes the fed batch process:

$$\begin{aligned} \dot{X} &= \mu X - \frac{F}{Vo} X \\ \dot{S} &= -k\mu X + \frac{F}{Vo}(S_0 - S) \\ \dot{\mu} &= m(\mu_m \frac{S}{K_S + S} - \mu) \\ \dot{Vo} &= F \end{aligned} \tag{1*}$$

Where F is the substrate-floating rate and Vo is the volume of the bioreactor. In the paper the DGA is used for the model (3) and model (1*). The DGA demonstrated in the paper is completely applicable for the model (1) too. The inputs of these models are the dilution rate and the substrate-floating rate.

Brunovsky normal form and exact linearization - continuos process

There are difficulties with the linear systems. In some case of the classical linearization the correspondence between the biotechnological process and it linear model is lost. The reason is in the strong non-linearity of the models (1, 1*). In addition the optimization methods like Pontryagin maximum principle are difficult for direct use [3]. Here is proposed a DGA for exact linearization that is a consequence from a non-linear diffeomorphic transformation.

Consider the continuous process described by the non-linear model (1). The system operation conditions are fixed by the following set of values: μ_m=0.5 h^{-1}, K_s=0.05 $g.l^{-1}$, m=3, S_e=0.2625 $g.l^{-1}$, S_0=9 $g.l^{-1}$, y=0.5 $g.g^{-1}$, D_e=0.42 h^{-1}, we determined the basis of the appropriate affine space:

$$\mathbf{f}_0 = \begin{pmatrix} \mu X \\ -\frac{1}{y}\mu X \\ m(\mu_m \frac{S}{K_S + S} - \mu x_3) \end{pmatrix} \quad \mathbf{f}_1 = \begin{pmatrix} -X \\ S_0 - S \\ 0 \end{pmatrix}$$

The control input is the dilution rate D. Taking in account the common integral of the field $\mathbf{f_1}$ the model (1) is transformed with the next diffeomorphic transformation:

$$\begin{aligned} x_1 &= X \\ x_2 &= \frac{X}{S - S_0} \quad ,(\text{Transforma tion} \quad \mathbf{K}), \\ x_3 &= \mu \end{aligned}$$

where $\mathbf{z}=(X,S,\mu)$ is the state vector of model (1). The affine model has the next basis:

$$\mathbf{f}_0 = \begin{pmatrix} x_3 x_1 \\ x_3 x_2 + \frac{1}{y} x_3 x_2^2 \\ m(\mu_m \frac{z_2}{K_S + z_2} - x_3) \end{pmatrix} \quad \mathbf{f}_1 = \begin{pmatrix} -x_1 \\ 0 \\ 0 \end{pmatrix} \qquad (4)$$

In what follows in this paragraph the vector $\mathbf{z}=(X, S, \mu)$ is the state vector of the model (1) and the vector $\mathbf{x}=(x_1, x_2, x_3)$ is the state vector of the model (4). The t-differential forms corresponding to the model (4) defined by $\mathbf{f_0}$ and $\mathbf{f_1}$ are the next [2]:

$$w1 = \mathrm{d}x_2 - (x_3x_2 + \frac{1}{y}x_3x_2^2)\mathrm{d}t,$$
$$w2 = \mathrm{d}x_3 - m(\mu_m \frac{x_1 + S_0x_2}{(K_S + S_0)x_2 + x_1} - x_3)\mathrm{d}t, \quad (5)$$
$$\mathrm{d}w2 \wedge w1 \wedge w2 = m\,\mu_m \frac{K_S x_2}{(x_2(K_S + S_0) + x_1)^2}\mathrm{d}x_1 \wedge \mathrm{d}t \wedge \mathrm{d}x_2 \wedge \mathrm{d}x_3 \neq 0$$

According the denotations and the notions in [2] the dual co-distribution (dual vector space) range is:

$$\mathbf{K}_0 \supset \mathbf{K}_1 \supset \mathbf{K}_2 \quad (6)$$

The set $K_0=\{w1, w2\}$, $K_1=\{w1\}$ and $K_2=\varnothing$:

$$w \in \mathbf{K}_{i+1} \quad \Leftrightarrow \quad \mathrm{d}w = 0 \bmod \mathbf{K}_i, \quad w \in \mathbf{K}_i \quad (7)$$

Considering the dual range (6) the equivalent system has the next Brunovsky normal form:

$$\dot{y}_1 = y_2$$
$$\dot{y}_2 = y_3 \quad (8)$$
$$\dot{y}_3 = V$$

All regular conditions are fulfilled excepting in the set point (equilibrium). The diffeomorphic transformation from system (4) to system (8) is a consequence from the dual range (6) [2, 8]:

$$w_1 = \mathrm{d}y_1 - x_3(x_2 + \frac{1}{y}x_2^2)\mathrm{d}t$$
$$\overline{\mathrm{d}y_2} = x_3(1 + \frac{2}{y}x_2)\mathrm{d}x_2 + (x_2 + \frac{1}{y}x_2^2)\mathrm{d}x_3$$
$$\mathrm{d}y_2 = \overline{\mathrm{d}y_2} - \left\{x_3^2(x_2 + \frac{3}{y}x_2^2 + \frac{2}{y^2}x_2^3) + m(\mu_m \frac{x_2S_0 + x_1}{x_2(K_S + S_0) + x_1} - x_3)(x_2 + \frac{1}{y}x_2^2)\right\}\mathrm{d}t$$

Therefor the nonlinear transformation has the form [2]:

$$y_1 = x_2$$
$$y_2 = x_3(x_2 + \frac{1}{y}x_2^2)$$
$$y_3 = x_3^2(x_2 + \frac{3}{y}x_2^2 + \frac{2}{y^2}x_2^3) + m(\mu_m \frac{x_2S_0 + x_1}{x_2(K_S + S_0) + x_1} - x_3)(x_2 + \frac{1}{y}x_2^2)$$

The comparison of the model (1) and the model (8) evaluations is shown in Fig. 2. There are computer-rounding problems with model (8) because of the fact that the set point is non-regular. A new model (3) of polynomial form has been proposed (c=0.42, m_1=0.0286, m_2=0.713). The affine representation of this model is [7, 8]:

$$\mathbf{f}_0 = \begin{pmatrix} \mu X \\ -\frac{1}{y}\mu X \\ m(c - m_1 X - m_3 \mu) \end{pmatrix} \quad \mathbf{f}_1 = \begin{pmatrix} -X \\ S_0 - \frac{X + x_2 S_0}{x_2} \\ 0 \end{pmatrix}$$

It overcomes in parts the computer-rounding problems. The equivalent non-linear transformation from the model (3) to the Brunovsky normal form (8) is:

$$\begin{aligned} y_1 &= x_2 \\ y_2 &= x_3(x_2 + \frac{1}{y}x_2^2) \\ y_3 &= x_3^2(x_2 + \frac{3}{y}x_2^2 + \frac{2}{y^2}x_2^3) + m(c - m_1 x_1 - m_3 x_3)(x_2 + \frac{1}{y}x_2^2) \end{aligned} \tag{9}$$

The control V of the Brunovsky model is linked with the control U=D of the model (1, 3) with the formulae:

$$\begin{aligned} V &= -mm_1(x_2 + \frac{1}{y}x_2^2)(x_3 x_1 - x_1 U) + \\ &+ \left\{ x_3^2(1 + \frac{6}{y}x_2 + \frac{6}{y^2}x_2^2) + m(c - m_1 x_1 - m_3 x_3)(1 + \frac{2}{y}x_2) \right\} \\ &x_3(x_2 + \frac{1}{y}x_2^2) + \left\{ 2x_3(x_2 + \frac{3}{y}x_2^2 + \frac{2}{y^2}x_2^3) - mm_3(x_2 + \frac{1}{y}x_2^2) \right\} \\ &(c - m_1 x_1 - m_3 x_3)m \end{aligned} \tag{10}$$

The control input U of the model (1) is in fact the dilution rate D. Evaluations of the model (8) are calculated with the diffeomorphism described by (9):

Model (1) == (Transformation K)===> Model (4)==(Transformation 9)===> Model (8)

Direct application of the Brunovsky model is the analytical determination of the optimal control in order to reach the set point for minimal time. The Hamilton function has the form:

$$H = T_1 y_2 + T_2 y_3 + T_3 V$$

$$T_1 = C_1$$

$$T_2 = -C_1 t + C_2$$

$$T_3 = \frac{C_1 t^2}{2} - C_2 t + C_3$$

We suppose $t \in [t_0, t_1]$ and like optimization criterion is chosen min $F(x(t_1))=[x_1(t_1)-x_1^0]^2$, where $x_1^0=4.37$, where x_1 is the first variable in the model (3). The formulae $x_1(y_1, y_2, y_3)$ has the next huge form:

$$x_1 = \frac{1}{m_1}\left[y_3 - \frac{y_2^2}{(y_1 + \frac{1}{y} y_1^2)^2}(y_1 + \frac{3}{y} y_1^2 + \frac{2}{y^2} y_1^3) \right] \frac{1}{m(y_1 + \frac{1}{y} y_1^2)} - \frac{c}{m_1} + \frac{y_2}{(y_1 + \frac{1}{y} y_1^2)} \frac{m_3}{m_1}$$

Finally the optimal control has the next functional form (11) (max (H)):

$$V = g(\text{sign}\left\{ \left[\frac{C_1}{2}(t - t_1)^2 + A(t_1 - t) + B \right] m m_1 y_1 (y_1 + \frac{1}{y} y_1^2) \right\} U, x_1, x_2, x_3) \qquad (11)$$

The function $g(.)$ in formulae (11) connect the optimal control V with the optimal control U in formulae (10). Taking in account the conditions for optimal control we found that the constants C_1 and C_2 have the forms:

$$C_1 = \frac{-2(x_1 - 4.37)}{m m_1} \left\{ \frac{2 y_2^2}{y(y_1 + \frac{1}{y} y_1^2)} - \frac{2 y_2^2 (1 + \frac{2}{y} y_1)^2}{(y_1 + \frac{1}{y} y_1^2)^3} + \frac{y_3 (1 + \frac{2}{y} y_1)}{(y_1 + \frac{1}{y} y_1^2)^2} + \frac{m_3 y_2 (1 + \frac{2}{y} y_1)}{m_1 (y_1 + \frac{1}{y} y_1^2)} \right\}$$

$$C_2 = \frac{-2(x_1 - 4.37)}{m m_1} \frac{2 y_2 (1 + \frac{2}{y} y_1)}{(y_1 + \frac{1}{y} y_1^2)^2} + \frac{2(x_1 - 4.37) m_3}{m_1} \frac{1}{(y_1 + \frac{1}{y} y_1^2)} + C_1 t_1$$

The constant C_3 presents the similar huge formulae like C_1. The constants A and B were derived from C_1, C_2 and C_3.

$$A = \frac{-2(x_1 - 4.37)}{m m_1} \frac{2 y_2 (1 + \frac{2}{y} y_1)}{(y_1 + \frac{1}{y} y_1^2)^2} + \frac{2(x_1 - 4.37) m_3}{m_1} \frac{1}{(y_1 + \frac{1}{y} y_1^2)} \qquad B = \frac{2(x_1 - 4.37)}{m m_1} \frac{1}{(y_1 + \frac{1}{y} y_1^2)}$$

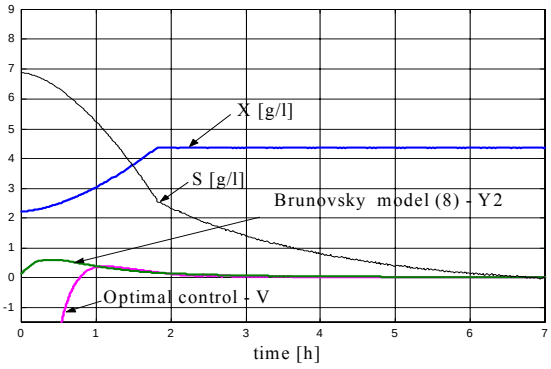

Fig.3 Models (3) and (8) – optimal control

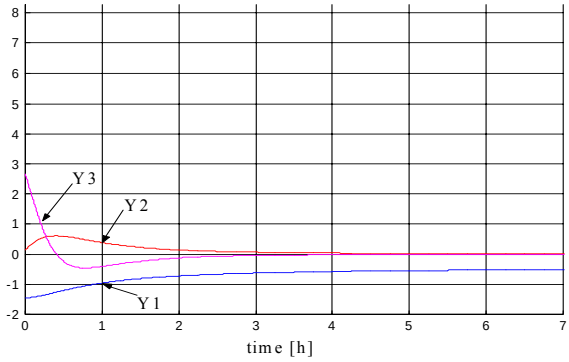

Fig.4 Brunovsky model (8)

The constants C_1, C_2 and C_3 were calculated at the moment t_1. If the optimal control is calculated by iterations from $[t_i, t_{i+1}]$ and these intervals are relatively small, we find the formulae for V. The optimal evaluations of the models (3 and 8) are shown in Fig. 3. The deviations of the Brunovsky model with this control are shown on Fig. 4.

Brunovsky normal form and exact linearization - fed-batch process

The well-known non-linear model [1, 2] describes the fed batch process:

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

Here X is the biomass concentration, S is the substrate concentration, μ is the specific growth rate, Vo is the volume of the bioreactor. The maximum growth rate is noted as μ_m and K_S is a saturation coefficient and k=1/y where y=0.5 [11, 12, 13, 14].

The growth dynamics are modelled by the third equation according Stephanopulos. The control input is F. The basis of the appropriate affine space is [2]:

$$\mathbf{f}_0 = \begin{pmatrix} \mu X \\ -k\mu X \\ m(\mu_m \dfrac{S}{K_S + S} - \mu) \\ 0 \end{pmatrix} \qquad \mathbf{f}_1 = \begin{pmatrix} -\dfrac{X}{Vo} \\ \dfrac{-(S - S_0)}{Vo} \\ 0 \\ 1 \end{pmatrix} \tag{12}$$

The next step is a simplification of the basis of the affine model space. We transform the state vector $\mathbf{x}=(X, S, \mu, V_o)$ of the model (1*) with the use of the common integrals of the field $\mathbf{f_1}$. The transformation is:

$$\begin{pmatrix} u_1 \\ u_2 \\ u_3 \\ u_4 \end{pmatrix} = \Phi(x_1, x_2, x_3, x_4) = \begin{pmatrix} X \\ \dfrac{X}{S - S_0} \\ \mu \\ \log(X) + \log(Vo) \end{pmatrix} \tag{13}$$

The new affine model has the next basis:

$$\mathbf{f}_0 = \begin{pmatrix} \mu X \\ \mu u_2 + k\mu u_2^2 \\ m(\mu_m \dfrac{S}{K_S + S} - \mu) \\ \mu \end{pmatrix} \qquad \mathbf{f}_1 = \begin{pmatrix} -\dfrac{X}{Vo} \\ 0 \\ 0 \\ 0 \end{pmatrix} \tag{14}$$

The new affine model has the form $d\mathbf{u}/dt=\mathbf{f_0}+\mathbf{f_1}F$, were $\mathbf{u}=(u_1, u_2, u_3, u_4)$, $\mathbf{x}=(x_1, x_2, x_3, x_4)=(X, S, \mu, V_o)$. The t-differential forms corresponding to the model (14) affine space defined by f_0 and f_1 are the next:

$$\begin{aligned} w_1 &= du_2 - (\mu u_2 + \frac{1}{y}\mu u_2^2)\,dt\,, \\ w_2 &= du_3 - m(\mu_m \frac{S}{(K_S + S)} - \mu)\,dt\,, \\ w_3 &= du_4 - \mu\,dt \end{aligned} \tag{15}$$

After the denotations and notions in [2] the dual co-distribution (dual vector space) range is:

$$\boldsymbol{K}_0 \supset \boldsymbol{K}_1 \supset \boldsymbol{K}_2 \tag{16}$$

Where the set $\boldsymbol{K_0}=\{w_1, w_2, w_3\}$, $\boldsymbol{K_1}=\{w_1, w_3\}$ and $\boldsymbol{K_2}=\varnothing$. Here is used the theorem 1.23 of [2]:

$$w \in \boldsymbol{K}_{i+1} \quad \Leftrightarrow \quad dw = 0 \bmod \boldsymbol{K}_i, \qquad w \in \boldsymbol{K}_i \tag{17}$$

From the dual range (1) the equivalent diffeomorph model has the form:

$$\begin{aligned} \dot{Y}_1 &= Y_2 \\ \dot{Y}_2 &= Y_3 \\ \dot{Y}_3 &= V \\ \dot{Y}_4 &= \frac{Y_2}{(Y_1 + kY_1^2)} \end{aligned} \tag{18}$$

All regular conditions are fulfilled excepting in the points where the denominator of the differential form dw_2 is zero. The diffeomorphism from the model (14) to the model (18) is a consequence from the dual range [2, 5, 6]:

$$\begin{aligned} w_1 &= dy_1 - u_3(u_2 + \frac{1}{y}u_2^2)dt \\ \overline{dY_2} &= u_3(1 + \frac{2}{y}u_2)du_2 + (u_2 + \frac{1}{y}u_2^2)du_3 \\ dY_2 &= \overline{dY}_2 - u_3^2(u_2 + \frac{3}{y}u_2^2 + \frac{2}{y^2}u_2^3) - \\ &- m(\mu_m \frac{x_2}{K_S + x_2} - u_3)(u_2 + \frac{1}{y}u_2^2)dt \end{aligned} \tag{19}$$

From the formulae (19) follows the next diffeomorphism:

$$\begin{aligned} Y_1 &= u_2 \\ Y_2 &= \mu(u_2 + ku_2^2) \\ Y_3 &= \mu^2(u_2 + \frac{3}{y}u_2^2 + \frac{2}{y^2}u_2^3) + m(\mu_m \frac{S}{(K_S + S)} - x_3)(u_2 + \frac{1}{y}u_2^2) \\ Y_4 &= u_4 \end{aligned} \tag{20}$$

If we start from different form of the model (1*) with the same mathematical technique we determine the next diffeomorphism:

$$\begin{aligned} Y_1 &= x_1 x_4 \\ Y_2 &= x_3 x_1 x_4 \\ Y_3 &= x_1 x_4 m(\mu_m \frac{x_2}{(K_S + x_2)} - x_3) + x_3^2 x_1 x_4 \\ Y_4 &= x_2 x_4 - S_0 x_4 \end{aligned} \tag{21}$$

The new equivalent model has the form:

$$\begin{aligned} \dot{Y}_1 &= Y_2 \\ \dot{Y}_2 &= Y_3 \\ \dot{Y}_3 &= V \\ \dot{Y}_4 &= -\frac{Y_2}{y} \end{aligned} \tag{22}$$

The main ideas, mathematical formulations and results used in the paper could be seen in the origins [1, 2, 4]. The optimal process is determined by optimization of the criterion Jp=f(F_{opt})=$x_1(T)x_4(T)$, $t\in[0,T]$ [11, 13]. It is evidently that $F\in[0, F_{max}]$. The Hamiltonian H(.) of the model (22) is:

$$H = \Psi_1 Y_2 + \Psi_2 Y_3 + \Psi_3 V + \Psi_4 \frac{-Y_2}{y} \tag{23}$$

The model (22) is a linear and stationary model. That is why the determination of H(.) is easy. We optimise Jp=f(F_{opt})= x_1(T)x_4(T) for a period of 10 hours (K_S=0.1 gl^{-1}, μ_{max}=0.3, S_0=200 gl^{-1}). The bioreactor volume V_0 increases from 5 *l*. to 8 *l*.

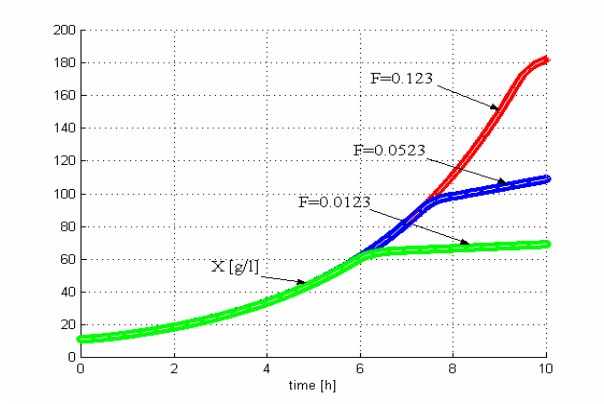

Fig. 5 Optimal system: F=0.0523;(o) F=0.123

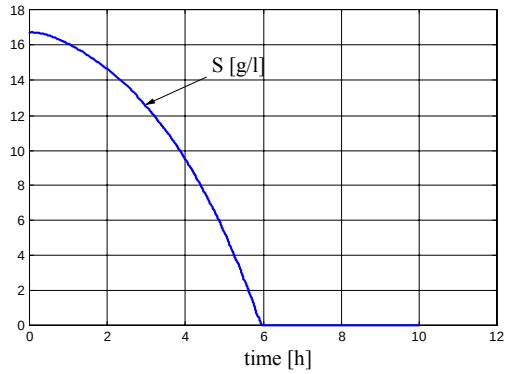

Fig. 6 Substrate concentration F=0.0123

From the Hamiltonian H(.) follows that the F_{opt} is maximum in the period [0 ÷ T] hours (max H). The control V of the model (22) is linked with F with the next formula:

$$V = (m(\mu_m \frac{x_2}{(K_S + x_2)} - x_3) + x_3^2)(x_3 x_1 x_4) + \\ + (x_1)(m\mu_m \frac{K_S}{(K_S + x_2)^2})(S_0 F - \frac{1}{y} x_3 x_1 x_4 - x_2 F) + \\ + (m(\mu_m \frac{x_2}{(K_S + x_2)} - x_3)(2x_3 x_1 x_4 - m x_1 x_4) \tag{24}$$

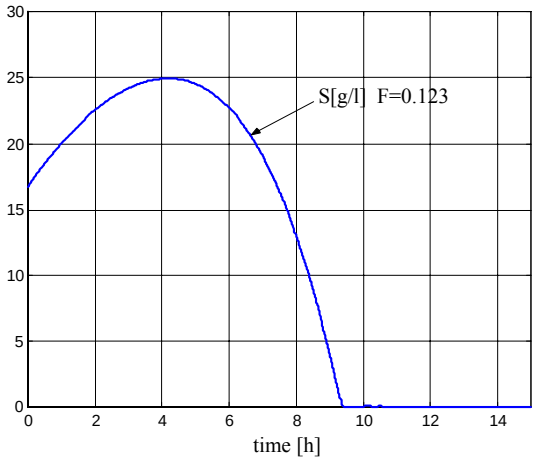

Fig. 7 Substrate concentration F=0.123

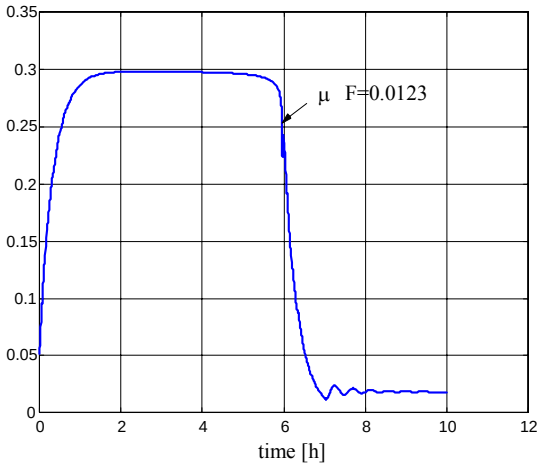

Fig. 8 Specific growth rate μ - F=0.0123

For model (1*) the optimal control is very simple $F=F_{max}$ (Fig 8, 9).

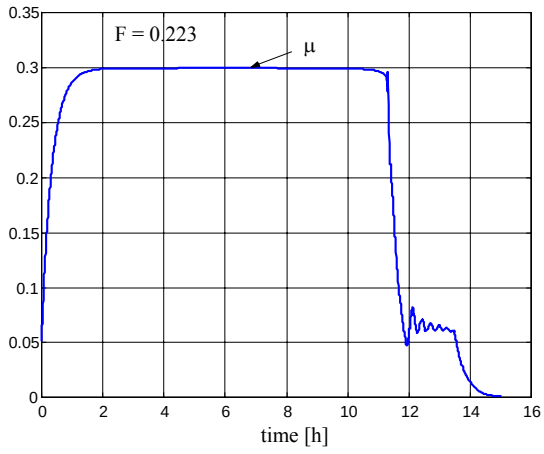

Fig. 9 Specific growth rate μ, F=0.223

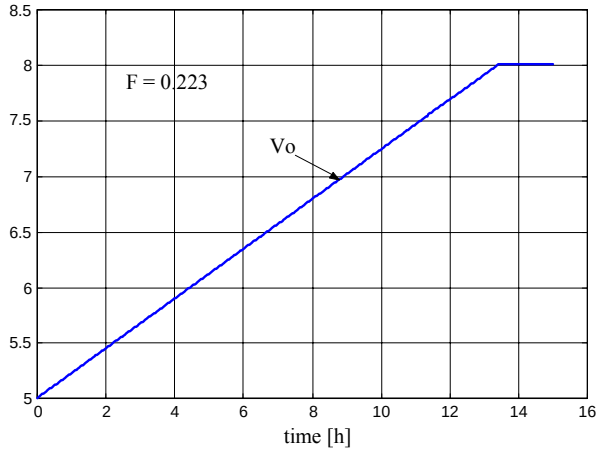

Fig.10 Volume F=0.223

Direct application of the model (18) is the determination of some optimal control conditions in order to reach the maximum $Y_4(T)=\log(x_1(T)x_4(T))$ in the end of the fed-batch process.

$$\dot{Y}_4 = \frac{Y_2}{(Y_1 + kY_1^2)} = x_3 = \mu \qquad (25)$$

The x_3 is the specific growth rate. The maximum $Y_4(T)$ needs continuously maximum of the μ in the process period [0, T].

Conclusions

The Brunovsky normal form of the biotechnological models is very simple and the models are linear with stationary coefficients. This form is convenient for optimization with the Pontryagin maximum principle. Here all linear control theory is possible to be used without restrictions. An advantage is the analytical determination of the optimal control laws like functions of the parameters and the system state vectors. The main disadvantages of the utilized approach are the complex formulas of the state vector **Y**, of the control $V(U,x_1,x_2,x_3)$ and the difficult biotechnological interpretation.

The models (8 and 22) are linear and stationary. The diffeomorphic model (18) is simplified. The tree first differentials equations are linear and stationary. This is of benefit to the control practice.

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