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Passivity Based Control of Continuous Bioreactors

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Abstract: In this paper, a passivity based model of a general set of bio-reactions in open reactors with new energy functions is derived. A change of coordinates is done, based on the stoichiometric invariance principle, which simplifies the number of equations to be taken care of and shows directly the passivity of the system. The passivity based control will be obtained in terms of systematic controller design techniques. The energy functions can be said to be in close proximity with the Gibbs free energy function used in port-Hamiltonian model of enzymatic reactions and are far from the traditional non-physical quadratic functions.

Keywords: *Port-Hamiltonian systems; passivity; nonlinear control; bioreactors.*

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1 Introduction

Passivity is a fundamental property of physical systems which are able to transform and dissipate energy. For such systems, passivity balances the energy of a system quantifying the external input and generated output. Hence, passivity is also related to the stability of the system by the fact that the system is said to be passive if the input energy is always more than or equal to the stored energy (closed systems) or output energy (open systems). Port-Hamiltonian (PH) modelling has been one of the most physical passivity based modelling technique which has inherent structural properties clearly defining the interconnection and dissipation of energy. Bond graph (BG) modelling technique can be considered as the graphical representation of the PH models . However, it is possible to propose only quasi-port-Hamiltonian representations for chemical and enzymatic systems using different energy functions and subsequent controllers (entropy, enthalpy, Gibbs free energy, etc., see e.g. [1], [2]) or pseudo bond graph models, e.g. [3].

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When it comes to bioreactions, a true energetic representation becomes impossible, as these involve a high number of microbial reactions, which are generally lumped into a mathematical reaction term without any thermodynamical meaning. On a macroscopic level, different kinetics are being proposed based on empirical data fitting, e.g. Monod kinetics, which reflect energy dissipation phenomena and can contribute to passivity based structure. [4] have tried different coordinate transformations allowing a generic but artificial obtention of a passive system where the examples use again quadratic energy functions. [5] explored different possibilities of unphysical Hamiltonian functions such as constant, logarithmic and quadratic functions. Nevertheless, adequate coordinate transformation is needed for better understanding of the mechanisms. The authors in this paper contributed through a new specific passivity based model taking advantage of the structure, based on decoupling of dynamics and the use of invariants extended to continuous reactors in [6]. It is shown that the passivity-based model involves non quadratic storage functions. A general formulation leads to easy application for a large number of systems. The case of multiple equilibria and bifurcation analysis can be seen e.g. in [7].

Passivity based control (PBC), as discussed above, exploits system's physical properties while exploring the possibilities of managing its energy and takes into account physical terms while choosing the control action. PBC of continuous chemical reactors generally relies on non-physical energy functions (e.g. quadratic functions) [1] . Subsequently, in [4] the authors proposed a systematic design of a real PH structure with an efficient control design. However, the energy function is given as a pure meaningless quadratic form, and the PH model is given by an artificial decomposition of the nonlinear model without any real world insight. In [8] it was shown that internal entropy production can be used as a storage function and also, a quasi port-controlled Hamiltonian representation of chemical reactors was formulated. Hence, an original and physical-based control design presented in this paper exploits the new passive model and is applied to aniline degradation by *Pseudomonas putida* cells.

2 The General Dynamical Model of a Single Stream Bioreactor

Suppose there are j independent reactions involving n components, taking place inside a perfectly mixed continuous reactor at constant volume and temperature. The bioreactor has only one single stream for all the concentrations coming in or going out (e.g. wastewater treatment). The inlet dilution rate is equal to outlet dilution rate to maintain constant volume. Dilution rate D is the control parameter. The state space of the concentrations is:

$$[\boldsymbol{z}] = [\xi_1, \xi_2 \cdots \xi_n]^T.$$

$[\boldsymbol{z}]$ comprises a set of $\begin{bmatrix} S & X & P \end{bmatrix}^T$. S represent substrates, X are biomasses, P are products of reaction. The general dynamical model (GDM) of bioreactions is as follows:

$$\left[\frac{d\boldsymbol{z}}{dt}\right] = [\boldsymbol{c}]\,[\boldsymbol{r}(\boldsymbol{z})] + [\boldsymbol{F}] - [D\boldsymbol{z}]\,, \tag{1}$$

where $\boldsymbol{z}$ represents the concentration of components, $\boldsymbol{F}$ represents the inlet flow rate of component $\boldsymbol{z}$, $\boldsymbol{c}$ represents the yield coefficients and $\boldsymbol{r(z)}$ is the rate of reaction.

Remark 2.1 The GDM in this paper can be said to be a specific case of the GDM shown in (1) in which there is only single inlet stream $D\boldsymbol{z}$ with only one feed instead of multiple inlet flow rates ($\boldsymbol{F}$).

A generalised first order time derivative of concentration model of a set of bioreactions in an open reactor with single dilution rate at constant volume and temperature can be written as:

$$\left[\frac{d\boldsymbol{z}}{dt}\right] = [\boldsymbol{c}]\,[\boldsymbol{r}(\boldsymbol{z})] + [D\boldsymbol{z_{in}} - D\boldsymbol{z_{out}}], \tag{2}$$

where $\boldsymbol{z}$ are the n components, $\boldsymbol{c}$ is the matrix of constant yield coefficients associated with the reaction. $\boldsymbol{r}$ are the rates of reaction. $\boldsymbol{z_{in}}$ and $\boldsymbol{z_{out}}$ are the inlet and outlet concentrations of n components. $\boldsymbol{z_{in}}$ are mostly substrates altogether coming in one stream with dilution rate D. For the concentrations not fed from outside, such as products and biomasses, $\boldsymbol{z_{in}}$ will be zero. Similarly, $\boldsymbol{z_{out}}$ is the concentration coming out of the reactor which will be the same as the concentration inside the reactor i.e. $\boldsymbol{z}$. The model (2) is valid for all types of microbial kinetics. The inputs $\boldsymbol{u}$ will be: $\boldsymbol{u} \in [D, D\boldsymbol{z_{in}}]$.

2.1 A useful coordinate transformation

This coordinate transformation is chosen to simplify the model by finding invariants, making it easier to passivate. The important point here is that the new set of coordinates will be independent of kinetics which are restricted to appear in the kinetics, extending the work of [6] to the general dynamical model of bioreactors [9].

Suppose, state vector $\boldsymbol{z}$ can be divided into two vectors of dimensions j and $k = n - j$, $[\boldsymbol{z}] = \begin{bmatrix} \boldsymbol{\xi} & \boldsymbol{\phi} \end{bmatrix}^T$, $[\boldsymbol{c}] = \begin{bmatrix} \boldsymbol{c_j} & \boldsymbol{c_k} \end{bmatrix}$ so that:

$$\left[\dot{\boldsymbol{\xi}}\right] = [\boldsymbol{c_j}]\,[\boldsymbol{r}(\boldsymbol{z})] + [D\boldsymbol{\xi_{in}} - D\boldsymbol{\xi}], \tag{3}$$

$$\left[\dot{\boldsymbol{\phi}}\right] = [\boldsymbol{c_k}]\,[\boldsymbol{r}(\boldsymbol{z})] + [D\boldsymbol{\phi_{in}} - D\boldsymbol{\phi}]. \tag{4}$$

The coordinate transformation will lead to a new vector of $k = n - j$ elements and will be represented by state $\boldsymbol{W}$, where $[\boldsymbol{A}]$ is a constant matrix:

$$[\boldsymbol{W}]_{n-j\times 1} = [\boldsymbol{A}]_{n-j\times n}\left([\boldsymbol{\xi_{in}} - \boldsymbol{\xi}]_{j\times 1}\right) + [\boldsymbol{\phi_{in}} - \boldsymbol{\phi}]_{n-j\times 1}. \tag{5}$$

Proposition 2.1 *For the relation of* $\boldsymbol{W}$ *proposed in* (5)*,* j *independent reactions* ($\boldsymbol{c_j}$ *is full rank), if matrix* $[\boldsymbol{A}]$ *and functions of* $\boldsymbol{\xi_{in}}$ *and* $\boldsymbol{\phi_{in}}$ *are chosen in a way that* $[\boldsymbol{A}]\,[\boldsymbol{c_j}] + [\boldsymbol{c_k}] = 0$ *and* $[\boldsymbol{A}]\,\dot{\boldsymbol{\xi}}_{\boldsymbol{in}} + \dot{\boldsymbol{\phi}}_{\boldsymbol{in}} = 0$*, the state space model takes the form:*

$$\begin{bmatrix} \dot{\boldsymbol{\xi}} \\ \dot{\boldsymbol{W}} \end{bmatrix} = \begin{bmatrix} [\boldsymbol{c_j}]_{j\times j} & [0]_{j\times n-j} \\ [\boldsymbol{0}]_{n-j\times j} & [-D\boldsymbol{I}]_{n-j\times n-j} \end{bmatrix}_{n\times n} \begin{bmatrix} \boldsymbol{r}(\boldsymbol{\xi}, \boldsymbol{W}) \\ \boldsymbol{W} \end{bmatrix}_{n\times 1} + \begin{bmatrix} D\boldsymbol{\xi_{in}} - D\boldsymbol{\xi} \\ \boldsymbol{0} \end{bmatrix}. \tag{6}$$

Proof: On differentiating (5) with respect to time we get:

$$\left[\dot{\boldsymbol{W}}\right] = [\boldsymbol{A}]\left(\dot{\boldsymbol{\xi}}_{\boldsymbol{in}} - \dot{\boldsymbol{\xi}}\right) + \left(\dot{\boldsymbol{\xi}}_{\boldsymbol{in}} - \dot{\boldsymbol{\phi}}\right). \tag{7}$$

Further substitution for $\left[\dot{\boldsymbol{\xi}}\right]$, $\left[\dot{\boldsymbol{\phi}}\right]$ from (3) and (4) respectively will lead to:

$$\begin{aligned} \left[\dot{\boldsymbol{W}}\right] = [\boldsymbol{A}]_{n-j\times j}\Big(&-[\boldsymbol{c_j}]_{j\times j}[\boldsymbol{r}(\boldsymbol{\xi}, \boldsymbol{W})]_{j\times 1} + [D\boldsymbol{\xi_{in}} - D\boldsymbol{\xi}]_{j\times 1}\Big) \\ &-[\boldsymbol{c_k}]_{n-j\times j}[\boldsymbol{r}(\boldsymbol{\xi}, \boldsymbol{W})]_{j\times 1} + [D\boldsymbol{\phi_{in}} - D\boldsymbol{\phi}]. \end{aligned} \tag{8}$$

Substituting $[\boldsymbol{A}][\boldsymbol{c_j}] = -[\boldsymbol{c_k}]$ and $[\boldsymbol{A}]\dot{\boldsymbol{\xi}}_{\boldsymbol{in}} = -\dot{\boldsymbol{\phi}}_{\boldsymbol{in}}$ in (8) will give:

$$\dot{\boldsymbol{W}} = -D\boldsymbol{W}. \tag{9}$$

With state space as $\begin{bmatrix} \boldsymbol{\xi} & \boldsymbol{W} \end{bmatrix}^T$, the bioreactor model becomes same as shown in (6).

Note that this solution necessarily needs $\boldsymbol{c_j}$ to be a full rank square matrix by careful choice of the components of $\boldsymbol{\xi}$. It is always possible to find such a matrix A by the stoichiometric invariance principle if the j reactions are truly independent. Further, other assumptions on inlet concentrations $\boldsymbol{\phi_{in}}, \boldsymbol{\xi_{in}}$ are weak, since they are always verified when these are constant, which will be assumed in the sequel.

Corollary 2.1 *If* $\forall D : D > 0$, $\boldsymbol{W}$ *is a reaction invariant, i.e.* $\boldsymbol{W}$ *will exponentially converge to zero.*

Proof: Consider a continuously differentiable non-negative storage function $H = \frac{1}{2}\boldsymbol{W}^2$ and $H : \boldsymbol{W} \to R$ with $H(0) = 0$. Differentiating H w.r.t. time and substituting (9) will give $\dot{H} = -D\boldsymbol{W}^2 = -2DH$. Hence for $D > 0$, H and $\boldsymbol{W} \to 0$ as $t \to \infty$.

Remark 2.2 For the general model (1), the representation after coordinate transformation, originated from the stoichiometric invariance principle, was independent of kinetics and was referred to as a "'nice" representation in [9]. However, the model in (9), which considers the case of a single stream input flow, also allows to find a reaction invariant. Hence, the model splits the dynamics into a stable bilinear subsystem ($\boldsymbol{W}$) and a control affine subsystem ($\boldsymbol{\xi}$) which are weakly coupled. The convergence of $\boldsymbol{W}$ to zero extends the so-called "useful" change of coordinates in [9].

3 Passivity Based Model

A passive system is a system which cannot store more energy than is supplied by some source. The difference between the stored energy and supplied energy is the dissipated energy:

Definition 3.1 [4] Consider the system:

$$\dot{\boldsymbol{x}} = \boldsymbol{f}(\boldsymbol{x}) + \boldsymbol{g}(\boldsymbol{x})\,\boldsymbol{u}, \quad \boldsymbol{y} = \boldsymbol{h}(\boldsymbol{x}), \tag{10}$$

where $\boldsymbol{u}$, $\boldsymbol{y}$ are the input and output of the system respectively, $\boldsymbol{f(x)}$, $\boldsymbol{g(x)}$ and $\boldsymbol{h(x)}$ are matrices and vector fields that define the interconnection between physical-meaning elements (state, inputs, and outputs). With a storage function $V(\boldsymbol{x})$:$V(\boldsymbol{x}^*) = 0$, where $\boldsymbol{x}^*$ is the steady state value of $\boldsymbol{x}$ and $V(\boldsymbol{x}) > 0$ at $\boldsymbol{x} \neq \boldsymbol{x}^*$, this system is passive if:

$$\frac{dV}{dt} \leq \boldsymbol{u}^T\boldsymbol{y}. \tag{11}$$

The passive system satisfying the condition presented in Definition 3.1 is written as:

$$\dot{\boldsymbol{x}} = \boldsymbol{Q}(\boldsymbol{x},\boldsymbol{u})\frac{\partial V}{\partial \boldsymbol{x}} + \boldsymbol{\gamma}(\boldsymbol{x})\boldsymbol{v}, \quad \boldsymbol{y} = \boldsymbol{\gamma}^T(\boldsymbol{x})\frac{\partial V}{\partial \boldsymbol{x}}. \tag{12}$$

Here $\boldsymbol{v}$ is the modified input, $\boldsymbol{Q}$ and $\boldsymbol{\gamma}$ are the modified interconnection matrices.

Lemma 3.1 *[4], Consider the system shown in equation (12), which with a storage function $V(\boldsymbol{x})$: $V(\boldsymbol{x}^*) = 0$, where $\boldsymbol{x}^*$ is the steady state value of $\boldsymbol{x}$ and $V(\boldsymbol{x}) > 0$ at $\boldsymbol{x} \neq \boldsymbol{x}^*$, will be passive if $\boldsymbol{Q} \prec 0$.*

In biochemistry, most of the microbial reactions are coupled but can be turned into decoupled reactions either as a linear combination of functions of single state variable or such a transformation can be achieved through decoupling process. The proposed passivization methodology is suitable for such reactions in terms of physical and structural understanding. Decoupling also leads to further simplification of the model by getting rid of many complex terms using minor assumptions without considerable change in the actual kinetics. The following section will explain the general process of decoupling of coupled bioreactions and derive their passivity based model.

3.1 Decoupling of coupled bioreactions

A decoupled reaction has its rate terms depending only on single state or many states if they can be separated (decoupled) algebraically so that they become a linear combination of functions of single state only. It is supposed that there exist j independent reactions with a full rank stoichiometric $\boldsymbol{c_j}$ which allow for the nice representation described above. It would also be possible to achieve a partial stabilization of the system using passivity properties [10], [11].

The bioreactor systems chosen here are single stream bioreactors having inlet concentration of each component to be constant. Dilution rate D is the only control input in such systems. We assume that we can split the rate term of $\boldsymbol{\xi}$, i.e. $\boldsymbol{c_j r(\xi, W)}$ into two parts, u and c standing for uncoupled and coupled $\boldsymbol{c_u r_u(\xi_u, W)}$ and $\boldsymbol{c_c r_c(\xi, W)}$, where $\boldsymbol{c_u r_u(\xi_u, W)}$ is the sum of decoupled rate terms $\boldsymbol{\bar{c}_u p_u(\xi_u)}$ and function $\boldsymbol{f_u(\xi_u, W)}$, with $\frac{\partial(\boldsymbol{p_u})^i}{\partial(\boldsymbol{x})^j} = \frac{\partial(\boldsymbol{f_u})^i}{\partial(\boldsymbol{x})^j} = 0$ if $j \neq i$, $(.)^i$ standing for the i^{th} component of a vector. $\boldsymbol{c_c r_c(\xi, W)}$ is the sum of a decoupled modified rate term $\boldsymbol{\bar{c}_c r_c(\xi)}$, where $\frac{\partial(\boldsymbol{p_c})^i}{(\partial \boldsymbol{x})^j} = 0$, if $j \neq i$ and a remaining coupled term depends on the whole $\boldsymbol{\xi}$, $\boldsymbol{f_c(\xi, W)}$. Concisely, one can write:

$$\begin{bmatrix} \dot{\boldsymbol{\xi}}_{\boldsymbol{u}} \\ \dot{\boldsymbol{\xi}}_{\boldsymbol{c}} \\ \dot{\boldsymbol{W}} \end{bmatrix} = \begin{bmatrix} \bar{\boldsymbol{C}}_{\boldsymbol{j}} & 0 \\ 0 & -D\boldsymbol{I} \end{bmatrix} \begin{bmatrix} \boldsymbol{p_u}(\boldsymbol{\xi_u}) \\ \boldsymbol{p_c}(\boldsymbol{\xi_c}) \\ \boldsymbol{W} \end{bmatrix} + \begin{bmatrix} \boldsymbol{f_u}(\boldsymbol{\xi_u}, \boldsymbol{W}) \\ \boldsymbol{f_c}(\boldsymbol{\xi}, \boldsymbol{W}) \\ 0 \end{bmatrix} + \begin{bmatrix} D(\boldsymbol{\xi_{uin}} - \boldsymbol{\xi_u}) \\ D(\boldsymbol{\xi_{cin}} - \boldsymbol{\xi_c}) \\ 0 \end{bmatrix}. \tag{13}$$

At this stage, equation (13) shows the decoupling process, as the d first equations are only coupled by the vanishing reaction invariant $\boldsymbol{W}$. In practical applications, the corresponding variables are substrates concentrations, for which the kinetics is only coupled with one or several biomass concentrations. Now, the input concentrations can be controlled to obtain a more interesting configuration for the coupled dynamics $\boldsymbol{\xi_c}$.

Lemma 3.2 *Let us consider the equilibrium point $\boldsymbol{\xi}^*$ of the system* (13)*. If* $(D - D^*)(\boldsymbol{\xi_{cin}} - \boldsymbol{\xi_c}) + D^*\left(\boldsymbol{\xi^*_{cin}} - \boldsymbol{\xi_c}\right) + \boldsymbol{f_c}(\boldsymbol{\xi}, \boldsymbol{W}) - \boldsymbol{f_c}(\boldsymbol{\xi^*}) = 0$,

then system (13) *can be written as:*

$$\begin{bmatrix} \dot{\boldsymbol{\xi}}_{\boldsymbol{u}} \\ \dot{\boldsymbol{\xi}}_{\boldsymbol{c}} \\ \dot{\boldsymbol{W}} \end{bmatrix} = \begin{bmatrix} \bar{\boldsymbol{c}}_{\boldsymbol{j}} & \boldsymbol{0} \\ \bar{0} & -\bar{D}\boldsymbol{I} \end{bmatrix} \begin{bmatrix} \boldsymbol{p_u}(\boldsymbol{\xi_u}) - \boldsymbol{p_u}(\boldsymbol{\xi_u^*}) \\ \boldsymbol{p_c}(\boldsymbol{\xi_c}) - \boldsymbol{p_c}(\boldsymbol{\xi_c^*}) \\ \boldsymbol{W} \end{bmatrix} + \begin{bmatrix} (D - D^*)(\boldsymbol{\xi_{uin}} - \boldsymbol{\xi_u}) + D^*(\boldsymbol{\xi_u^*} - \boldsymbol{\xi_u}) \\ 0 \\ 0 \end{bmatrix}. \tag{14}$$

Proof: At equilibrium, $\boldsymbol{\xi}^* = \begin{bmatrix} \boldsymbol{\xi}_u{}^* & \boldsymbol{\xi_c}^* & 0 \end{bmatrix}$. As $\dot{\boldsymbol{\xi}} = 0$, this in turn implies $\bar{\boldsymbol{c}}_{\boldsymbol{u}}\boldsymbol{p_u}(\boldsymbol{\xi_u}^*) + \boldsymbol{f_u}(\boldsymbol{\xi_u}^*) = -D^*(\boldsymbol{\xi_{uin}} - \boldsymbol{\xi_u}^*)$ and $\bar{\boldsymbol{c}}_{\boldsymbol{c}}\boldsymbol{p_c}(\boldsymbol{\xi_c}^*) + \boldsymbol{f_c}(\boldsymbol{\xi}^*) = -D^*(\boldsymbol{\xi_{cin}}^* - \boldsymbol{\xi_c}^*)$.

Adding and subtracting $\boldsymbol{p_u}(\boldsymbol{\xi_u}^*)$, $\boldsymbol{p_c}(\boldsymbol{\xi_c}^*)$ in the corresponding equation (13) and replacing the compensation yield the final result. The above set of equations will be decoupled if one can cancel the f_c term, using control terms. These control terms can be either the dilution rate D, or the inlet concentrations $\boldsymbol{\xi^*_{cin}}$ (provided that the equation $[\boldsymbol{A}]\dot{\boldsymbol{\xi}}_{\boldsymbol{in}} + \dot{\boldsymbol{\phi}}_{\boldsymbol{in}} = 0$ is verified). The states are only coupled by the stoichiometric matrix $\bar{\boldsymbol{c}}_{\boldsymbol{j}}$ and $\boldsymbol{W}$ ($\boldsymbol{W} \to 0$). The next section will show the passivization procedure using a physical energy (storage) function.

3.2 Passivity based model of a general decoupled bioreactor

Proposition 3.1 *Suppose the system:*

$$\dot{\boldsymbol{\xi}_{\boldsymbol{u}}} = \bar{\boldsymbol{c}}_{\boldsymbol{j}}\boldsymbol{p_u}(\boldsymbol{\xi}_u) - \bar{\boldsymbol{c}}_j\boldsymbol{p_u}(\boldsymbol{\xi_u}^*) + \boldsymbol{f_u}(\boldsymbol{\xi}_u, \boldsymbol{W}) - \boldsymbol{f_u}(\boldsymbol{\xi_u}^*) + \underbrace{(\boldsymbol{\xi}_{uin} - \boldsymbol{\xi_u})}_{\boldsymbol{g}}\underbrace{(D - D^*)}_{u} + D^*(\boldsymbol{\xi_u}^* - \boldsymbol{\xi_u}) \tag{15}$$

is passive with storage function $V(\boldsymbol{\xi_u}, t)$, *input* u *and output* $y : y = \boldsymbol{g}^T \frac{\partial V}{\partial \boldsymbol{\xi_u}}$, *and* $\boldsymbol{f_u}(\boldsymbol{\xi}_u, \boldsymbol{W}) - \boldsymbol{f_u}(\boldsymbol{\xi_u}^*)$ *is a vanishing perturbation:* $\lim_{t\to\infty} \boldsymbol{f_u}(\boldsymbol{\xi}_u, \boldsymbol{W}) - \boldsymbol{f_u}(\boldsymbol{\xi_u}^*) = 0$. *Assume that there exists a neighbourhood* Z *of* $\boldsymbol{\xi_u}^*$ *such that the reduced system:*

$$\dot{\boldsymbol{\xi}}_{\boldsymbol{u}} = \bar{\boldsymbol{c}}_{\boldsymbol{j}}\boldsymbol{p_u}(\boldsymbol{\xi_u}) - \bar{\boldsymbol{c}}_{\boldsymbol{j}}\boldsymbol{p_u}(\boldsymbol{\xi_u}^*) + (\boldsymbol{\xi_{uin}} - \boldsymbol{\xi_u})(D - D^*) \tag{16}$$

has $\boldsymbol{\xi_u}^*$ *as an exponentially stable equilibrium point and for* $\bar{\boldsymbol{\xi}}_{\boldsymbol{u}} = \boldsymbol{\xi_u} - \boldsymbol{\xi_u}^*$, *the storage function* $V(\boldsymbol{\xi_u}, t)$ *satisfies the following conditions:*
$\exists k_3, k_4 > 0, k_3 \parallel \bar{\boldsymbol{\xi}}_{\boldsymbol{u}} \parallel \leq \frac{\partial V}{\partial \boldsymbol{\xi_u}} \leq k_4 \parallel \bar{\boldsymbol{\xi}}_{\boldsymbol{u}} \parallel$,
$\exists \gamma : \gamma + D^* > 0 \parallel f'(\boldsymbol{\xi}_u, \boldsymbol{W}) - \boldsymbol{f_u}(\boldsymbol{\xi_u}^*) \parallel \leq (\gamma + D^*) \parallel \bar{\boldsymbol{\xi}}_{\boldsymbol{u}} \parallel$.

Then the full system (15) *is also locally exponentially stable at* $\boldsymbol{\xi}^*$ *if:*
$(-\lambda_{\min} k_3 - k_3 + k_4(\gamma + D^*)\lambda_{\max}) < 0$, *where* $\lambda_{\min}$, $\lambda_{\max}$ *are the minimum and maximum eigenvalues of* $-\bar{\boldsymbol{c}}_{\boldsymbol{j}}$.

Proof: One knows from the exponential stability conditions that $\ni k_1, k_2 > 0$,
$k_1 \parallel \bar{\boldsymbol{\xi}}_{\boldsymbol{u}} \parallel \leq V \leq k_2 \parallel \bar{\boldsymbol{\xi}}_{\boldsymbol{u}} \parallel$. Since $\frac{dV}{dt} = \frac{\partial V}{\partial \boldsymbol{\xi_u}} \frac{\partial \boldsymbol{\xi_u}}{\partial t}$, it follows from the assumption:
$\frac{\partial V}{\partial \boldsymbol{\xi_u}}^T \bar{\boldsymbol{c}}_j(\boldsymbol{p_u}(\boldsymbol{\xi_u}) - \boldsymbol{p_u}(\boldsymbol{\xi_u}^*)) \leq (-\lambda_{\min} - 1) k_3 \parallel \bar{\boldsymbol{\xi}}_{\boldsymbol{u}}{}^2 \parallel$,
$\frac{\partial V}{\partial \boldsymbol{\xi_u}}^T (\boldsymbol{f_u}(\boldsymbol{\xi}_u, \boldsymbol{W}) - \boldsymbol{f_u}(\boldsymbol{\xi_u}^*, 0)) \leq k_4(\gamma + D^*)\lambda_{\max} \parallel \bar{\boldsymbol{\xi}}_{\boldsymbol{u}}{}^2 \parallel$.
Now, $\frac{dV}{dt} \leq (-\lambda_{\min} k_3 - k_3 + k_4(\gamma + D^*)\lambda_{\max}) \parallel \bar{\boldsymbol{\xi}}_{\boldsymbol{u}}{}^2 \parallel + \boldsymbol{u}^T \boldsymbol{y} \leq \boldsymbol{u}^T \boldsymbol{y}$ if

$(-\lambda_{\min}k_3 - k_3 + k_4(\gamma + D^*)\lambda_{\max}) < 0$, Hence, the reduced system (16) is exponentially stable and according to *Theorem 3.12* in [12], the full system will be exponentially stable.

Now, *Proposition* 3.1 tells that the full system will be exponentially stable if the reduced unperturbed system is exponentially stable. From *Proposition* 3.1 one can take $\boldsymbol{f_u}(\boldsymbol{\xi}_u, \boldsymbol{W}) - \boldsymbol{f_u}(\boldsymbol{\xi_u}^*, 0) + D^*(\boldsymbol{\xi_u}^* - \boldsymbol{\xi_u}) = 0$ and the system (13) is written as (17).

$$\begin{bmatrix} \dot{\boldsymbol{\xi}}_{\boldsymbol{u}} \\ \dot{\boldsymbol{\xi}}_{\boldsymbol{c}} \\ \dot{\boldsymbol{W}} \end{bmatrix} = \begin{bmatrix} \bar{\boldsymbol{C}}_{\boldsymbol{j}} & 0 \\ 0 & -D\boldsymbol{I} \end{bmatrix} \begin{bmatrix} \boldsymbol{p_u}(\boldsymbol{\xi_u}) - \boldsymbol{p_u}(\boldsymbol{\xi_u^*}) \\ \boldsymbol{p_c}(\boldsymbol{\xi_c}) - \boldsymbol{p_c}(\boldsymbol{\xi_c^*}) \\ \boldsymbol{W} \end{bmatrix} + \begin{bmatrix} (D - D^*)(\boldsymbol{\xi_{uin}} - \boldsymbol{\xi_u}) \\ 0 \\ 0 \end{bmatrix}. \quad (17)$$

This presentation is straightforward and physically linked to passivity.

Proposition 3.2 *Consider the system* (17) *with* $\bar{\boldsymbol{c}}_j \prec 0$. *Assume that there exists a neighbourhood* Z *of* $\boldsymbol{\xi} = \boldsymbol{\xi^*}$ *such that:*

1. $\sum \left(\int_0^{(\boldsymbol{\xi_u})^i} (\boldsymbol{p_u})^{\boldsymbol{i}} \left((\boldsymbol{\xi_u})^{\boldsymbol{i}}\right) - \int_0^{(\boldsymbol{\xi_u})^{\boldsymbol{i}}} (\boldsymbol{p_u})^i \left((\boldsymbol{\xi_u}^*)^{\boldsymbol{i}}\right) \right) > 0$

2. $\sum \left(\int_0^{(\boldsymbol{\xi_c})^i} (\boldsymbol{p_c})^{\boldsymbol{i}} \left((\boldsymbol{\xi_c})^{\boldsymbol{i}}\right) - \int_0^{(\boldsymbol{\xi_c})^{\boldsymbol{i}}} (\boldsymbol{p_c})^i \left((\boldsymbol{\xi_c}^*)^{\boldsymbol{i}}\right) \right) > 0,$

then the storage function $V' = \sum_{i=1}^{n} V'_i = \sum_{i=1}^{n_u} \int \left((\boldsymbol{p_u})^{\boldsymbol{i}}(\boldsymbol{\xi_u})^{\boldsymbol{i}} - (\boldsymbol{p_u})^{\boldsymbol{i}}(\boldsymbol{\xi_u^*})^{\boldsymbol{i}}\right) \partial(\boldsymbol{\xi_u})^{\boldsymbol{i}} + \sum_{i=1}^{n_c} \int \left((\boldsymbol{p_c})^{\boldsymbol{i}}(\boldsymbol{\xi_c})^{\boldsymbol{i}} - (\boldsymbol{p_c})^{\boldsymbol{i}}(\boldsymbol{\xi_c^*})^{\boldsymbol{i}}\right) \partial(\boldsymbol{\xi_c})^{\boldsymbol{i}} + \sum_{i=1}^{n-j} \frac{1}{2}\boldsymbol{W_i}^2$ *will make the reduced system* (17) *asymptotically stable at* $\boldsymbol{\xi} = \boldsymbol{\xi^*}$.

Proof: One has V' being always positive around $\boldsymbol{\xi^*}$. On partially differentiating V' w.r.t. states $\boldsymbol{\xi_u}$,$\boldsymbol{\xi_c}$ and $\boldsymbol{W}$:

$$\frac{\partial V'}{\partial \boldsymbol{\xi_u}} = \boldsymbol{p_u}(\boldsymbol{\xi_u}) - \boldsymbol{p_u}(\boldsymbol{\xi_u}^*) : \frac{\partial V'}{\partial \boldsymbol{\xi_c}} = \boldsymbol{p_c}(\boldsymbol{\xi_c}) - \boldsymbol{p_c}(\boldsymbol{\xi_c}^*) : \frac{\partial V'}{\partial \boldsymbol{W}} = \boldsymbol{W} \quad (18)$$

the system in (17) can be written in the form:

$$\underbrace{\begin{bmatrix} \dot{\boldsymbol{\xi}}_{\boldsymbol{u}} \\ \dot{\boldsymbol{\xi}}_{\boldsymbol{c}} \\ \dot{\boldsymbol{W}} \end{bmatrix}}_{\dot{\boldsymbol{\xi}}} = \underbrace{\begin{bmatrix} \bar{\boldsymbol{C}}_{\boldsymbol{j}} & 0 \\ 0 & -D\boldsymbol{I} \end{bmatrix}}_{\boldsymbol{Q'}} \underbrace{\begin{bmatrix} \frac{\partial V'}{\partial \boldsymbol{\xi_u}} \\ \frac{\partial V'}{\partial \boldsymbol{\xi_c}} \\ \frac{\partial V'}{\partial \boldsymbol{W}} \end{bmatrix}}_{\frac{\partial V'}{\partial \boldsymbol{\xi}}} + \underbrace{\begin{bmatrix} (\boldsymbol{\xi_{uin}} - \boldsymbol{\xi}_u) & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}}_{\boldsymbol{g}} \underbrace{\begin{bmatrix} (D - D^*) \\ 0 \\ 0 \end{bmatrix}}_{\boldsymbol{u'}}. \quad (19)$$

The output of the system will be $\boldsymbol{y'} = \boldsymbol{g}^T \frac{\partial V}{\partial \boldsymbol{\xi}}$. The time derivative of V' is:

$$\dot{V'} = \frac{\partial V'}{\partial \boldsymbol{\xi}} \dot{\boldsymbol{\xi}} = \frac{\partial V'}{\partial \boldsymbol{\xi}}^T \boldsymbol{Q'} \frac{\partial V'}{\partial \boldsymbol{\xi}} + \frac{\partial V'}{\partial \boldsymbol{\xi}}^T \boldsymbol{g u'} = \frac{\partial V'}{\partial \boldsymbol{\xi}}^T \boldsymbol{Q} \frac{\partial V'}{\partial \boldsymbol{\xi}} + \boldsymbol{y'}^T \boldsymbol{u'}. \quad (20)$$

Since $\bar{\boldsymbol{c}}_j \prec 0$ and $D > 0$ is making matrix $\boldsymbol{Q'}$ negative definite, (19) is passive. V'_i is minimum i.e. 0 at $(\boldsymbol{\xi}^*)^i$, the system (19) has a passive equilibrium point $\boldsymbol{\xi} = \boldsymbol{\xi^*}$.

4 Passivity Based Control

Passivity based control is a generic design method which is extensively used in electro-mechanical systems.

Proposition 4.1 *[4] Consider the passive system of the form:*

$$\dot{\boldsymbol{x}} = \boldsymbol{Q}(\boldsymbol{x},\boldsymbol{u})\frac{\partial V}{\partial \boldsymbol{x}} + \boldsymbol{\gamma}(\boldsymbol{x})\boldsymbol{v}; \boldsymbol{y} = \boldsymbol{\gamma}^T(\boldsymbol{x})\frac{\partial V}{\partial \boldsymbol{x}}, \tag{21}$$

where $V(\boldsymbol{x})$ is the specified closed-loop storage function $V(\boldsymbol{x})$: $V(\boldsymbol{x^d}) = 0$, $\boldsymbol{x^d} \neq 0$ is the desired steady state value of $\boldsymbol{x}$ and $V(\boldsymbol{x}) > 0$, $\boldsymbol{Q} \prec 0$. Suppose that the model is zero state detectable, then the feedback $\boldsymbol{v} = -\boldsymbol{C}(\boldsymbol{x},t)y$ with $\boldsymbol{C}(\boldsymbol{x},t) \geq e\boldsymbol{I} > 0$ and constant e renders $\boldsymbol{x} = \boldsymbol{x^d}$ globally asymptotically stable.

4.1 Passivity based control of a general decoupled bioreactor

The following proposition will give general formulations of passivity based control of a decoupled bioreactor system.

Proposition 4.2 *Consider the desired storage function $\bar{V}$, with conditions following:*

$$\begin{aligned}\bar{V} = \sum_{i=1}^{n}\bar{V}_i = \sum_{i=1}^{n_u}\int \left(\boldsymbol{p_u}(\boldsymbol{\xi_u}) - \boldsymbol{p_u}\left(\boldsymbol{\xi_u^d}\right)\right)^i (\partial \boldsymbol{\xi_u})^i \\ + \sum_{i=1}^{n_c}\int \left(\boldsymbol{p_c}(\boldsymbol{\xi_c}) - \boldsymbol{p_c}\left(\boldsymbol{\xi^d}\right)\right)^i (\partial \boldsymbol{\xi_c})^i + \sum_{i=1}^{n-j}\frac{1}{2}(W^2)^i,\end{aligned} \tag{22}$$

1. $\sum_{i=1}^{n_u}\left(\int_0^{(\boldsymbol{\xi_u})^i} (\boldsymbol{p_u})^i\left((\boldsymbol{\xi_u})^i\right) - \int_0^{(\xi_u)^i} (p_u)^i\left((\boldsymbol{\xi_u^d})^i\right)\right) > 0,$
2. $\sum_{i=1}^{n_c}\left(\int_0^{(\boldsymbol{\xi_c})^i} (\boldsymbol{p_c})^i\left((\boldsymbol{\xi_c})^i\right) - \int_0^{(\xi_c)^i} (p_c)^i\left((\boldsymbol{\xi_c^d})^i\right)\right) > 0,$
3. $\bar{V}\left(\boldsymbol{\xi^d}\right) = 0$

Hence, the system (19) *is passive and the feedback $\bar{\boldsymbol{u}} = -\boldsymbol{C}(\boldsymbol{x},t)\bar{\boldsymbol{y}}$ with $\boldsymbol{C}(\boldsymbol{x},t) \geq e\boldsymbol{I} > 0$ renders* (19) *globally asymptotically stable at $\xi = \xi^d$.*

Proof: After replacing the equilibrium point $\boldsymbol{\xi^*}$ with desired equilibrium point $\boldsymbol{\xi^d}$, the system (19) can take the form:

$$\underbrace{\begin{bmatrix}\dot{\boldsymbol{\xi}}_{\boldsymbol{u}}\\ \dot{\boldsymbol{\xi}}_{\boldsymbol{c}}\\ \dot{\boldsymbol{W}}\end{bmatrix}}_{\dot{\boldsymbol{\xi}}} = \underbrace{\begin{bmatrix}\bar{\boldsymbol{C}}_{\boldsymbol{j}} & 0\\ 0 & -\bar{D}\boldsymbol{I}\end{bmatrix}}_{\boldsymbol{Q'}}\underbrace{\begin{bmatrix}\frac{\partial \bar{V}}{\partial \boldsymbol{\xi_u}}\\ \frac{\partial \bar{V}}{\partial \boldsymbol{\xi_c}}\\ \frac{\partial \bar{V}}{\partial \boldsymbol{W}}\end{bmatrix}}_{\frac{\partial \bar{V}}{\partial \boldsymbol{\xi}}} + \underbrace{\begin{bmatrix}(\boldsymbol{\xi_{uin}} - \boldsymbol{\xi_u}) & 0 & 0\\ 0 & 0 & 0\\ 0 & 0 & 0\end{bmatrix}}_{\boldsymbol{g}}\underbrace{\begin{bmatrix}(D - D^d)\\ 0\\ 0\end{bmatrix}}_{\bar{\boldsymbol{u}}}. \tag{23}$$

According to *Proposition* 3.2, this system is passive. The input of the system is $\bar{\boldsymbol{u}}$ and the output $\bar{\boldsymbol{y}}$ is: $\bar{\boldsymbol{y}} = [\boldsymbol{g}]^T\frac{\partial \bar{V}}{\partial \boldsymbol{\xi}}$. By *Proposition* 4.1, the feedback $\bar{\boldsymbol{u}} = -\boldsymbol{C}(\boldsymbol{x},t)\bar{\boldsymbol{y}}$ with $\boldsymbol{C}(\boldsymbol{x},t) \geq e\boldsymbol{I} > 0$ will render (23) globally asymptotically stable at $\boldsymbol{\xi} = \boldsymbol{\xi^d}$.

5 Application to a Single Reaction with Monod Kinetics: Aniline Degradation by *Pseudomonas Putida* in CSTR

Aniline is among the toxic constituents of many industrial effluents (e.g. wastewaters in chemical and dyeing industries). Biological processing for aniline degradation is a cheap and green alternative to chemical removal processes such as solvent extraction, chemical oxidation, etc. In [13] the author has studied the model of aniline degradation by *Pseudomonas putida* ATCC 21812 cells in batch reactors following a Monod model. *Pseudomonas putida* growth X and simultaneous aniline degradation S in a CSTR equations are:

$$\dot{X} = \mu X - DX, \quad \dot{S} = -\frac{\mu X}{Y} + D\,(S_{in} - S)\,, \tag{24}$$

where D is the dilution rate, Y is the cell/substrate yield coefficient and μ is the specific growth rate. For Monod kinetics:

$$\mu = \frac{\mu_m S}{K_s + S}, \tag{25}$$

here μ_m is the maximum specific growth rate and K_s is the half velocity constant. The state space will be $[\boldsymbol{z}] = \begin{bmatrix} S & X \end{bmatrix}^T$ and the model can be represented as:

$$\underbrace{\begin{bmatrix} \dot{S} \\ \dot{X} \end{bmatrix}}_{\dot{\boldsymbol{\omega}}} = \underbrace{\begin{bmatrix} -1 & 0 \\ 0 & 1 \end{bmatrix}}_{\boldsymbol{c}} \underbrace{\begin{bmatrix} \frac{\mu X}{Y} \\ \mu X \end{bmatrix}}_{\boldsymbol{r}} + \underbrace{\begin{bmatrix} DS_{in} - DS \\ -DX \end{bmatrix}}_{D(\boldsymbol{z_{in}} - \boldsymbol{z_{out}})}. \tag{26}$$

5.1 Coordinate transformation and a passivity based model

Divide the state space into two parts ξ_a and ξ_b such that:

$$\left[\dot{\boldsymbol{\xi}}\right] = \left[\dot{S}\right] = \underbrace{[-1]}_{\boldsymbol{c_j}} \underbrace{\left[\frac{\mu X}{Y}\right]}_{\boldsymbol{r}} + \underbrace{[DS_{in} - DS]}_{D(\boldsymbol{\xi_{in}} - \boldsymbol{\xi})}, \left[\dot{\boldsymbol{\phi}}\right] = \left[\dot{X}\right] = \underbrace{[1]}_{\boldsymbol{c_k}} \underbrace{[\mu X]}_{\boldsymbol{r}} + \underbrace{[-DX]}_{D(\boldsymbol{\psi_{in}} - \boldsymbol{\psi})}. \tag{27}$$

The new coordinate W can be written as:

$$W = A\,(S_{in} - S) + Y\,(X_{in} - X)\,, \tag{28}$$

where $A = 1$, $X_{in} = 0$ and S_{in} is a constant. Hence, differentiating (28) w.r.t. time and substituting (27) will give $\dot{W} = -DW$. With the new state space $\begin{bmatrix} S & W \end{bmatrix}^T$ and the substitution $X = S_{in} - S - W$ the bioreactor model becomes:

$$\begin{bmatrix} \dot{S} \\ \dot{W} \end{bmatrix} = \begin{bmatrix} -1 & 0 \\ 0 & -D \end{bmatrix} \begin{bmatrix} \mu \frac{(S_{in} - S)}{Y} \\ W \end{bmatrix} + \begin{bmatrix} \mu \frac{W}{Y} \\ 0 \end{bmatrix} + \begin{bmatrix} D\,(S_{in} - S) \\ 0 \end{bmatrix}. \tag{29}$$

Taking the steady state points of (S, W) as $(S^*, 0)$ and then adding and substracting equilibrium rate term $\mu\,(S^*)\,\frac{(S_{in} - S^*)}{Y}$ in (29), (29) can be written as:

$$\begin{aligned} \begin{bmatrix} \dot{S} \\ \dot{W} \end{bmatrix} = \begin{bmatrix} -1 & 0 \\ 0 & -D \end{bmatrix} & \begin{bmatrix} \mu \frac{(S_{in} - S)}{Y} - \mu\,(S^*)\,\frac{(S_{in} - S^*)}{Y} \\ W \end{bmatrix} + \begin{bmatrix} \mu \frac{W}{Y} \\ 0 \end{bmatrix} \\ & + \begin{bmatrix} (D - D^*)\,(S_{in} - S) + D^*(S^* - S) \\ 0 \end{bmatrix}. \end{aligned} \tag{30}$$

From *Proposition* 3.1, $\mu\frac{W}{Y} + D^*(S^* - S) = 0$. Using the storage function:

$$V' = \int \mu(S)\frac{(S_{in} - S)}{Y}\partial S - \int \mu^*(S^*)\frac{(S_{in} - S^*)}{Y}\partial S + \frac{1}{2}W^2, \tag{31}$$

where μ^*, S^* are the steady state values of μ, S, and doing some algebraic modifications, the bioreactor model can be rewritten as:

$$\underbrace{\begin{bmatrix} \dot{S} \\ \dot{W} \end{bmatrix}}_{\dot{\boldsymbol{\xi}}} = \underbrace{\begin{bmatrix} -1 & 0 \\ 0 & -D \end{bmatrix}}_{\boldsymbol{Q}} \begin{bmatrix} \frac{\partial V'}{\partial S} \\ \frac{\partial V'}{\partial W} \end{bmatrix} + \underbrace{\begin{bmatrix} S_{in} - S & 0 \\ 0 & 1 \end{bmatrix}}_{\boldsymbol{\gamma}} \underbrace{\begin{bmatrix} (D - D^*) \\ 0 \end{bmatrix}}_{u'}. \tag{32}$$

The matrix $\boldsymbol{Q}$ will always be negative definite and it can be seen through careful observation that $V' \geq 0$ and 0 at $S = S^*$, making the system (32) passive.

5.2 Passivity based control design

Replacing the steady state S^* with desired steady state S^d and the new storage function $\bar{V}$:

$$\bar{V} = \int \mu(S)\frac{(S_{in} - S)}{Y}\partial S - \int \mu^d\left(S^d\right)\frac{\left(S_{in} - S^d\right)}{Y}\partial S + \frac{1}{2}W^2, \tag{33}$$

where μ^d is the desired steady state values of μ, and doing some algebraic modifications, the bioreactor model can be rewritten as:

$$\underbrace{\begin{bmatrix} \dot{S} \\ \dot{W} \end{bmatrix}}_{\dot{\boldsymbol{\xi}}} = \underbrace{\begin{bmatrix} -1 & 0 \\ 0 & -D \end{bmatrix}}_{\boldsymbol{Q}} \underbrace{\begin{bmatrix} \frac{\partial \bar{V}}{\partial S} \\ \frac{\partial \bar{V}}{\partial W} \end{bmatrix}}_{\frac{\partial \bar{V}}{\partial \boldsymbol{\xi}}} + \underbrace{\begin{bmatrix} S_{in} - S & 0 \\ 0 & 1 \end{bmatrix}}_{\boldsymbol{\gamma}} \underbrace{\begin{bmatrix} (D - D^d) \\ 0 \end{bmatrix}}_{\bar{\boldsymbol{u}}}; \bar{\boldsymbol{y}} = \boldsymbol{\gamma}^T \frac{\partial \bar{V}}{\partial \boldsymbol{\xi}}. \tag{34}$$

Matrix $\boldsymbol{Q} \prec 0$ and if $\bar{V} \geq 0$, the system (34) is passive. $\bar{V} = 0$ at $S = S^d$ and $W = 0$. Since the system (34) is zero state detectable if the desired concentration of substrate $S^d = 0$, the feedback $\bar{\boldsymbol{u}} = -\boldsymbol{C}\bar{\boldsymbol{y}}$ ensures asymptotical stability at $S = S^d$.

5.3 Simulations

An industrial incident, where 9 tons of aniline at 70 mg/l leaked from a chemical plant into a river is considered, and 1 mg/l or less must be reached. Monod parameters are $K_s = 3.1\ mg/l$, $\mu_m = .12h^{-1}$, $Y = 0.74$. The dilution rate D is the control input and substrate concentration is the only measurement. The simulation results compare three control strategies i.e. chemostat control with steady state dilution rate, passivity based control and passivity based adaptive control (not discussed here but similar to the control designed in [14]). The new coordinate W converges to zero as shown in Figure 2, ensuring proper control. The cell concentration will obviously increase at a similar rate as substrate concentration will decrease as can be seen in Figure 4.

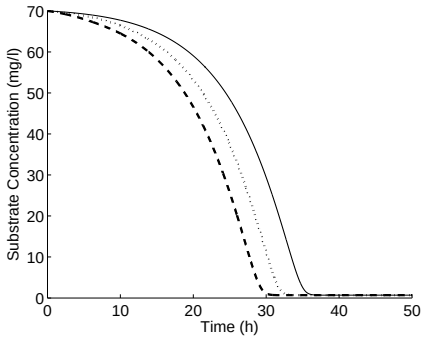

Figure 1: Substrate Concentration; Bold: Chemostat; Dotted: Passivity Based; Dashed: Adaptive.

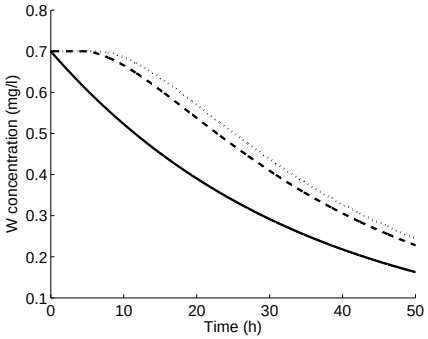

Figure 2: W Concentration; Bold: Chemostat; Dotted: Passivity Based; Dashed: Adaptive.

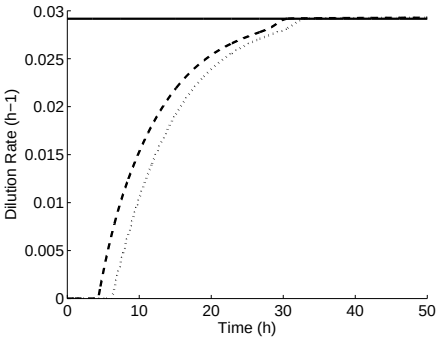

Figure 3: Dilution Rate; Bold: Steady state, Dotted: Passivity Based; Dashed: Adaptive.

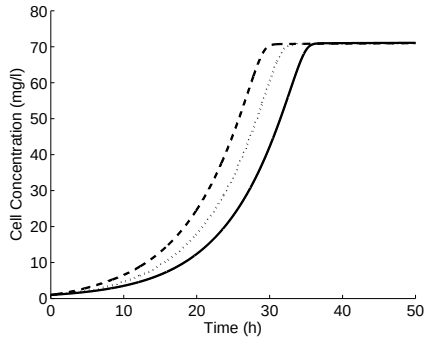

Figure 4: Cell Concentration; Bold: Chemostat; Dotted: Passivity Based; Dashed: Adaptive.

6 Conclusion

This paper is a successful attempt to maintain the structure and physical meaning of the passivity based model of microbial reactions with Monod kinetics in continuous reactors by using meaningful storage functions and obvious coordinate transformation on the grounds of passivity. The general model implies that this technique can be directly applied to a huge set of reactions. This paper is providing a physical view for all issues related to robust control of a bioreaction. Simulations obtained justify and validate the model. In the future, this technique can be extended to other kinetics involved and to different types of reactors such as plug flow, etc. The physical meaning given to the design of observers (as in e.g. [15]) and parameter estimation could be an interesting job to work on.

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