ENERGY BASED MODELING AND CONTROL OF CONTINUOUS CHEMICAL REACTORS UNDER ISOTHERMAL CONDITIONS

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Abstract: The fundamental concept of energy helps to view any physical dynamical system as an energy transforming system. The energetic representation of chemical reaction systems has been an issue among researchers because of its dynamics, complexity and the difficulties generated by irrereversible thermodynamics. This paper is focusing on the specific case of isothermal chemical reactions in continuous reactors. An energy based model of such systems is proposed in this paper which can be said as quasi Port-Hamiltonian system (PHS) based on physical grounds. The model is taking care of the concentration space and reaction space of a chemical reaction. Reaction networks and stoichiometry have been given special importance to define these formulations. The use of physical energy terms in the design of controller for open chemical systems is also achieved. Stoichiometric and Reaction interconnection and damping assignment passivity based controllers (IDA-PBC) are derived in this paper from the proposed Stoichiometric and Reaction energy based models respectively by physically giving the energy function a desired form. The energetic point of view in enzymatic world has been shown to be quite relevant by application of this model and passivity based control to basic enzyme reaction example in open reactors. Real application of enzymatic hydrolysis of cellulose in continuous reactor is being taken and different possibilities to control the enzymatic hydrolysis are simulated and explained at the end.

Keywords: Port-Hamiltonian, IDA-PBC, Reaction Networks, Enzyme Reaction, Gibbs Free energy, Entropy, Continuous reactors.

1. INTRODUCTION

Energy based modeling (EBM) provides a unified framework for prediction, classification and control of systems. Bond Graph (BG) famous for pictorial representation of power flows in systems and Port-Hamiltonian (PH) framework famous for its integrated interconnection and damping properties are the most popular EBM techniques. Both have been very successful in modeling dynamics of electromechanical systems (Maschke et al. (2000)). Hamiltonian function, also called Hamiltonian, refers to an energy function. For electro-mechanical systems the Hamiltonian is its total energy, i.e. sum of its kinetic energy and potential energy. Unfortunately in the case of irreversible thermodynamic systems like chemical processes, the links between thermodynamics and system theory are quite difficult to exhibit from a geometrical point of view (Eberard et al. (2007)). In chemical processes, the Legendre transform helps to define a function as a first order derivative of energy, using this transformation one can try to fit the different energy functions in the Hamiltonian structure.

Different Hamiltonians used were, internal energy (Ramirez

et al. (2013)), ectropy (Hoang and Dochain (2013)), enthalpy (Brown (2007)) etc. but the structure matrices are explicitly dependent on the gradient of the Hamiltonian (intensive variables) destroying the linearity between the flows and efforts (geometry of the system). This implies that all formulations of thermodynamic systems as port-Hamiltonian systems (PHS) leads to quasi PHS. The dynamics of each one of them did not suit the conditions of the systems chosen which proves that it is not possible to formulate general non-isothermal reactions as true Port-Hamiltonian systems. However, in the particular case of isothermal chemical/biochemichal reaction networks, since the temperature is assumed constant, there are no internal irreversible transformations (no internal irreversible entropy production due to the reaction) and it is possible to model the reaction with a structure similar to that of a true dissipative Port-Hamiltonian system (Otero-Muras et al. (2008)). In Alonso and Erik Ydstie (1996), the Hamiltonian used was availability function (not an energy function). Ould-Bouamama et al. (2012), Couenne et al. (2006) and Zhang et al. (2006) tried to express energetic behavior through BG models of closed chemical reaction systems. Delgado and Pichardo (1999), Roman et al. (2009) and

Roman (2011) contributed through pseudo BG models of batch, fed-batch and continuous reactors depicting chemical affinity for the reaction part.

Van der Schaft and Maschke (2011), Makkar and Dieulot (2014) expressed Gibbs free energy (GFE) as a suitable Hamiltonian function but for a closed chemical system at constant temperature and pressure. It mentions about the energy exchange at the boundary but did not explain it and also did not apply the model to any real system. It is a mathematical interpretation needs to be extended to open systems and validated on the real system. Makkar and Dieulot (2013) extended this work to the enzyme reactions in continuous systems for any random data using Gibbs free energy as Hamiltonian and also did not touch the control part. The work of Otero-Muras et al. (2008) also gave energetic representation in reaction space is also based on some abstract function hence not logical on the physical grounds.

Of different energy functions, the notion of GFE for isothermal systems seems very obvious (Van der Schaft et al. (2013)). The internal energy is associated to a chemical system and under ideal conditions of constant pressure, temperature and volume it reduces to GFE. GFE is more of the energy related to reactions only (Thoma and Bouamama (2000)) and not outside the reactor. It would not be right to express GFE as energy flowing in and out of the system when there is inlet and outlet volume flow. Indeed for open systems, inlet and outlet flow rates can be replaced as entropy energy variation (Favache et al. (2009)). The physical energetic model based on real energy function which is also considering the input and output is needed. An open system completely changes the dynamics of the system and making its model also can have totally different interpretations. This paper will contribute through the new pseudo stoichiometric (concentration space) and reaction (reaction space) PH model for open systems using these energy theories. These models can be said as more physical models than previous ones. The control part of these energy based models can also match to reality through Passivity Based Control (PBC). PBC is one such technique which can be derived from energy based models such as PH models and in comparison with what is more logical and can be interpreted physically. PBC is very interesting and sound because one can actually think on energy terms while choosing the control action (Dörfler et al. (2009)) unlike the nonphysical techniques shown in Caraman et al. (2001) and Chirosca et al. (2013). There exists a lot on PBC of continuous chemical reactors (Hoang et al. (2011a)), but these rely on non-physical Lyapunov functions (e.g. quadratic functions) (Hoang et al. (2011b)). In Otero-Muras et al. (2008), a PBC strategy on biochemical reaction networks is used which took stoichiometry into account but with usual reaction rate terms and not physical energy function. Variation of internal entropy has been used in (Garcia Sandoval et al. (2016)) with an application to gaseous mixtures. Passivity Based Control laws based on the new pseudo-PH formulations will be proposed in this paper.

This paper is showing the new quasi Stoichiometric PH (SPH) formulations and stoichiometric IDA-PBC law of open chemical systems for isothermal systems. The reaction space is also taken into account with the introduc-

tion of new quasi reaction PH (RPH) formulation. The structure of Port-Hamiltonian is not completely satisfied making them quasi models but they can be said as the most physical energy based models. The two models will be used to formulate a set of enzyme reactions with MM kinetics and then SPH formulation will be used to generate the control law from the new models. In the last section, there will be simulations of control of full model of enzymatic hydrolysis of cellulose process in continuous mode and different conditions of control will be examined in simulations. The goal was to obtain the consistent simulation results approaching towards the desired level of concentration which is achieved.

2. PSEUDO PORT-HAMILTONIAN MODEL AND PASSIVITY BASED CONTROL: A CONTINUOUS REACTOR MODELING EXAMPLE

Definiton 1: (Dörfler et al. (2009)) The general port Hamiltonian systems with dissipation are defined by:

$$\dot{x} = Q(x)\frac{\partial H}{\partial x} + gu, \qquad (1)$$

$$y = g^T \frac{\partial H}{\partial x},\tag{2}$$

where x is the state space, H(x) represents the Hamiltonian. u, y are collocated input and output respectively. They are also called port power variables, their duality product defines the power flows exchanged. Q(x) = J(x) - R(x) where J(x) is an $n \times n$ skew-symmetric interconnection matrix and g is another $n \times m$ interconnection matrix which connects input with the state space. R(x), is an $n \times n$ symmetric dissipation matrix. A dissipation matrix depicts the dissipated energy of the system during the process, it should always be symmetric as energy dissipated cannot be zero or negative.

As discussed in introduction, it is difficult to ideally fit an energy function associated to a chemical reaction in a Port-Hamiltonian structure. However, for reversible reaction networks which is also the case of most of the enzyme processes, Van der Schaft and Maschke (2011) gave one formulation through modification of Hamiltonian as an exponential function of the energy function. This formulation is used in open systems shown in a CSTR example below. The structural properties of Hamiltonian will not be completely satisfied by the formulation so it will be a quasi or pseudo PH model.

Example 1: A CSTR maintaining a constant volume (V) with same and constant dilution rate (d) for both inlet flow x_{in} and outlet flow x_{out} of concentration of chemical x for the reaction:

$$A + B \xrightarrow[k_{r_1}]{k_{r_1}} C, \ C \xrightarrow[k_{r_2}]{k_{r_2}} D + A.$$

Here, A, B, C are the chemical constituents. A reversible

chemical reaction bears a steady state concentration x^* of reactants and products (x^* will be the equilibrium concentration for a Batch process). The rate laws for the two reactions with rate constants $k_1 = \frac{k_{f1}}{k_{r1}}$ and $k_2 = \frac{k_{f2}}{k_{r2}}$ can be given as:

$$v_1 = k_1 \left(\frac{[A][B]}{[A]^*[B]^*} - \frac{[C]}{[C]^*} \right),$$

$$v_2 = k_2 \left(\frac{[C]}{[C]^*} - \frac{[A][D]}{[A]^*[D]^*} \right)$$

In order to fit the model of the system, it is important to express concentration in terms of energy gradient. Van der Schaft et al. (2013) gave the relation connecting the concentration (x) with steady state concentration (x^*) and exponential function of Gibbs free energy at constant temperature and pressure. The relation is:

$$x = x^* \exp\left(\frac{1}{RT} \frac{\partial G}{\partial x}\right). \tag{3}$$

Here, R $(JK^{-1}mol^{-1})$ is the universal gas constant. Using (3), the rate terms can be written as:

$$v_{1} = k_{1} \left(\exp\left(\frac{1}{RT} \frac{\partial G}{\partial A}\right) \exp\left(\frac{1}{RT} \frac{\partial G}{\partial B}\right) - \exp\left(\frac{1}{RT} \frac{\partial G}{\partial C}\right) \right)$$
(4)

$$v_{2} = k_{2} \left(\exp\left(\frac{1}{RT} \frac{\partial G}{\partial C}\right) - \exp\left(\frac{1}{RT} \frac{\partial G}{\partial A}\right) \exp\left(\frac{1}{RT} \frac{\partial G}{\partial D}\right) \right)$$
(5)

Now the whole system can be modeled as:

$$\begin{bmatrix} \frac{dA/dt}{dB/dt} \\ \frac{dC/dt}{dC/dt} \\ \frac{dD/dt}{dD/dt} \end{bmatrix} = \begin{bmatrix} -v_1 + v_2 \\ -v_1 \\ v_1 - v_2 \\ v_2 \end{bmatrix} + \begin{bmatrix} d(A_{in} - A_{out}) \\ d(B_{in} - B_{out}) \\ d(C_{in} - C_{out}) \\ d(D_{in} - D_{out}) \end{bmatrix}.$$
(6)

The inlet and outlet concentration terms can be seen as an entropy change in the system:

$$\underbrace{\sum_{\substack{system\\entropy\\change}} dS_{sys}}_{system} = \underbrace{\sum_{\substack{inlet\\flow}} x_{insin}}_{inlet} - \underbrace{\sum_{\substack{voutsout\\flow}} z_{outlet}}_{flow} - \underbrace{\frac{dG}{T}}_{entropy}.$$
(7)

Also, outgoing concentration will be equal to the concentration inside the reactor $(x_{out} = x)$. Now, through integration of equation (3) for Gibbs free energy provides the required Hamiltonian. Hamiltonian H will be:

$$H = G = \sum \left(zRTx \log \frac{x}{x^*} - zRT(x - x^*) \right), \quad (8)$$

 $z = \pm 1$, as G will be actually the difference between the GFE of reactants and products. The general quasi Port-Hamiltonian form for a CSTR will be:

$$[\dot{x}] = -[K] \exp\left[f\left(\frac{\partial G}{\partial x}\right)\right] + (D(x_{in} - x)) \qquad (9)$$

 $f\left(\frac{\partial G}{\partial x}\right)$ is the function of state space gradient of Gibbs free energy. [K] is the diagonal matrix of equilibrium rate constants. (9) will be elaborated later in the paper using an example.

2.1 Passivity Based Control

Definition 2: (Ortega et al. (2002)) Consider the dissipative Port-Hamiltonian system given in (1), then an asymptotically stable Port Controlled Hamiltonian (PCH) system with desired steady state point x_d , assigned interconnection matrix $J_d = -J_d^T$, damping matrix $R_d = R_d^T \ge 0$ and a

smooth function H_d bounded from below will verify the equation (Ortega et al. (2002)):

$$\dot{x} = (J_d - R_d) \frac{\partial H_d}{\partial x}.$$
(10)

where,

$$u = \left(g^T g\right)^{-1} g^T \left(\left(J_d - R_d\right) \frac{\partial H_d}{\partial x} - \left(J - R\right) \frac{\partial H}{\partial x} \right) \quad (11)$$

such control method is called IDA-PBC. When it comes to control of a continuous chemical process, it is controlled by either dilution rate or by chemical (substrate) concentration. In this paper it is the chemical concentration which is the control input. There is only one chemical which is the control input in the example shown below.

The control propositions 1,3 and 5 below are showing the general method of control law with chemical concentration as a control parameter but for the specific case these general formulations reduce to single equation. For controlling one parameter (product concentration) there is only one control input (substrate concentration) so the system is neither over-actuated nor under-actuated.

Proposition 1: For a chemical process in (9) with constant dilution rate and the port controlled equation as:

$$\dot{x} = -\left[J_d - R_d\right] f\left(\frac{\partial H_d}{\partial x}\right),\tag{12}$$

the net input $d(x_{in} - x)$ will be equal to:

$$d(x_{in} - x) = -(J_d - R_d) f\left(\frac{\partial H_d}{\partial x}\right) + (K) f\left(\frac{\partial G}{\partial x}\right) \quad (13)$$

Proof: Matching equation (9) with (1) provides the information that g is an identity matrix. Equating equation (9) with (12), the value of net input will be same as (13). \Box The important task is to choose the desired Hamiltonian and assign values to the elements of desired interconnection and dissipation matrices. The compulsory conditions of stability and passivity put some constraints in choosing them as discussed in the next section.

2.2 Passivity and Stability

Passivity is a property of physical systems which preserves the energy conservation of a system. A passive component defines dissipation and transformation of energy. It is an inherent Input-Output property of the system. Passivity enforces stability in an input-output sense, i.e., one can say that the system is stable if bounded input energy supplied to the system, yields bounded output energy. Mathematically, a PH system with storage function H can be said to be passive if it holds the following inequality:

$$\frac{dH}{dt} \le u^T y$$

For the PH system given in (1) with output same as (2), the time derivative of Hamiltonian can be written as:

$$\begin{aligned} \frac{dH}{dt} &= -\frac{1}{2} \left(\frac{\partial H}{\partial x} \right)^T \left(Q(x) + Q^T(x) \right) \frac{\partial H}{\partial x} \\ &+ \left(\frac{\partial H}{\partial x} \right)^T g u \end{aligned}$$

A general PH system with zero input given in (1) can be said to be passive and will have an asymptotically stable equilibrium point x^* under the following conditions $(D\ddot{o}rfler et al. (2009)):$

i. H(x) has an isolated minimum at equilibrium point x^* ii. $-(Q(x) + Q(x)^T)$ is negative definite.

PBC defines a controller methodology whose aim is to render the closed-loop passive. The control objective of PBC is to preserve the energy conservation property but with desired energy and dissipation functions.

In the same way as PH system, a general Port Controlled Hamiltonian (PCH) system given in (10) guarantees stability at desired equilibrium point x_d if:

I. $H_d(x)$ has an isolated minimum at x_d

II. $-((J_d - R_d) + (J_d - R_d)^T)$ is negative definite.

The chosen desired Hamiltonian for PBC of chemical process discussed in (12) is:

$$H_d = \sum \left(zRTx \log \frac{x}{x^d} - zRT(x - x^d) \right).$$
(14)

The elements of J_d and R_d serve as tuning parameters to achieve the desired level of chemical concentration.

Proposition 2: Consider the PH and PCH form for a chemical process in continuous reactors given in (9) and (12) respectively. The PH system is said to be passive and has an asymptotic stability towards x^* if the square matrix of -[K] is positive definite and H is minimum at steady state point x^* . For the input given in (13), The PCH system is said to be stable if H_d is minimum at desired steady state point x_d and for a system with zero input, the time derivative of Hamiltonian $\frac{dG}{dt} \leq 0$.

Proof: With reference to conditions i, ii or I, II given above for the general dissipative PH and PCH systems respectively and comparing the equations of General PH and PCH model with chemical process model, the negative definiteness of -k and $-(J_d - R_d)$ can be justified. Now, K is the diagonal matrix of equilibrium rate constants, rate constants are positive, hence -K is negative definite. Also, the elements of $(J_d - R_d)$ are chosen such that it satisfies the necessary conditions. (8) and (14) are clearly showing that H(x) will have its minimum at x^* and the chosen function H_d will be strictly minimum at desired concentration x_d respectively.

Lastly, the time derivative of Hamiltonian G corresponding to respective models with zero input yields the following dissipation equality:

$$\frac{dG}{dt} = -\frac{\partial G}{\partial x} K f\left(\frac{\partial G}{\partial x}\right).$$

Hence, for the system to be passive, $-\frac{\partial G}{\partial x}f\left(\frac{\partial G}{\partial x}\right) \leq 0$. On substitution (*Section 4.2 in Van der Schaft et al. (2013)*) and expansion:

$$\frac{dG}{dt} = -\sum \left[\mu_p - \mu_r\right] \left[exp\left(\mu_p\right) - \exp\left(\mu_r\right)\right] K \le 0.$$

Here, μ_p is the chemical potential of products and μ_r is the chemical potential of the reactants,

$$\mu = \frac{\partial G}{\partial x} = RT \log\left(\frac{x}{x^*}\right).$$

Hence, the system is passive and asymptotically stable towards $x = x^*$ and in the similar way stability conditions can be proved at the desired $x = x_d$ using H_d . \Box

The next section will show a physical Port-Hamiltonian model of the reversible reaction networks.

3. STOICHIOMETRIC PORT-HAMILTONIAN FORMULATION AND PASSIVITY BASED CONTROL OF OPEN REACTION NETWORKS

In the series of reactions where product formation from one reaction acts as the reactant in the other reaction, there has to be a basic topological structure showing the effect of one reaction with the other. The speed of final product formation depends on the speed of individual reaction. This structure is called stoichiometry expressing the conservation laws of chemical reaction.

3.1 Stoichiometry

Example 2: In the following chemical reaction:

$$aM \rightleftharpoons bN, \ bN \rightleftharpoons cO,$$

a, b, c are the Stoichiometric coefficients of chemical M, N, O. The concentration x_i of each chemical i is related to the rate of reaction v_j of chemical reaction j through the following relation:

$$\dot{x} = S_t \times v, \tag{15}$$

 S_t is the $i \times j$ Stoichiometric matrix which captures the basic conservation laws of chemical reaction. For this reaction:

$$S_t = \begin{bmatrix} -a & 0\\ b & -b\\ 0 & c \end{bmatrix}$$

The Stoichiometric matrix (S_t) connects all the individual concentrations with the rates of reaction. In concentration space, S_t should be treated as a different entity. It is a connection matrix which should not be a part of classical PH formulation. This calls for a new PH form of chemical reaction networks by introducing stoichiometric matrix in it and can be called as Stoichiometric-PH (SPH) form.

3.2 Stoichiometric Port-Hamiltonian Formulation of Chemical Reaction Networks in a Continuous Reactor

The state space model for the network of chemical reactions taking place at constant temperature and pressure can be given by (15) where state space are the concentration of the constituents. (3) will help to write concentration terms of Gibbs free energy.

Definition 3: (Van der Schaft and Maschke (2011)) For a continuous reactor at constant temperature and pressure with concentration inflow (x_{in}) , outflow (x_{out}) , a constant dilution rate d, the SPH form can be written as:

$$\dot{x} = -S_t K \exp\left(f\left(\frac{\partial G}{\partial x}\right)\right) + d(x_{in} - x_{out}) \tag{16}$$

$$y = \frac{\partial G}{\partial x} = -T \frac{\partial S_{sys}}{\partial x}.$$
 (17)

Here, more emphasis is given on the fact that stoichiometry of the set of reactions is not part of the system for fitting in to the structure and does not have any impact on stability and passivity properties. It should be taken as separate entity though it is also not having any impact on input and output as well. Only individual concentrations are to being dealt here.

Example 3: Consider a simple enzyme reaction with single enzyme-substrate (ES) complex. In an Enzyme reaction after the substrate (S) has been transformed into product (P), the enzyme is free to catalyze the next reaction. Below is the reaction:

$$E + S \xrightarrow[k_{r_1}]{k_{r_1}} ES, ES \xrightarrow[k_{r_2}]{k_{r_2}} E + P.$$

The stoichiometric matrix (S_t) for this reaction will be:

$$S_t = \begin{bmatrix} -1 & 1\\ -1 & 0\\ 1 & -1\\ 0 & 1 \end{bmatrix}$$

and the rates of reaction will be:

$$v_1 = k_1 \left(\frac{x_E x_S}{x_E^* x_S^*} - \frac{x_{ES}}{x_{ES}^*} \right), \ v_2 = k_2 \left(\frac{x_{ES}}{x_{ES}^*} - \frac{x_E n_P}{x_E^* x_P^*} \right).$$
(18)

where $k_1 = \frac{k_{f1}}{k_{r1}}$, $k_2 = \frac{k_{f2}}{k_{r2}}$. Using (3), the expanded SPH form (Van der Schaft et al. (2013)) for this reaction can be written as follows:

$$\begin{bmatrix} \dot{x}_E \\ \dot{x}_S \\ \dot{x}_{ES} \\ \dot{x}_P \end{bmatrix} = -\begin{bmatrix} -1 & 1 \\ -1 & 0 \\ 1 & -1 \\ 0 & 1 \end{bmatrix} \begin{bmatrix} k_1 & 0 \\ 0 & k_2 \end{bmatrix} B_m$$

$$\exp\left(Z\frac{1}{RT}\begin{bmatrix} \frac{\partial G}{\partial x_E} \\ \frac{\partial G}{\partial x_S} \\ \frac{\partial G}{\partial x_{ES}} \\ \frac{\partial G}{\partial x_P} \end{bmatrix}\right) + \begin{bmatrix} d(x_{inE} - x_E) \\ d(x_{inE} - x_E) \\ d(x_{inE} - x_E) \\ d(x_{inP} - x_P) \end{bmatrix}.$$
(19)

 B_m is called the incidence matrix and Z is called the complex stoichiometric matrix, their values for this case are:

$$B_m = \begin{bmatrix} -1 & 1 & 0 \\ 0 & -1 & 1 \end{bmatrix}$$
$$Z = \begin{bmatrix} 1 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 1 & 0 & 0 & 1 \end{bmatrix}$$

There is a close relation of the two matrices with the stoichiometry of the reaction network (Van der Schaft et al. (2013)) which is $S_t = Z \times B_m$

Reaction Simplex

In closed reaction system, overall concentration is fixed. The set of algebraic equations corresponds to this mass conservation is called reaction simplex. The reaction simplex for a given initial condition x_0 can be written as:

$$\Omega(n_0) = c_i (x - x_0) = 0$$

where the entries of the vector c_i are the units of the building block C_i^0 and $C_i^0 = c_i^0 \cdot x$. The elements of C_i represent the coefficient of complex *i* taking part in reaction. For the reaction in *Example 3*:

$$[C_i^o] = \begin{bmatrix} C_{is}^0\\ C_{ip}^o \end{bmatrix} = \begin{bmatrix} 0 \ 1 \ 1 \ 0 \\ 1 \ 0 \ 1 \ 1 \end{bmatrix}$$

The reaction simplex is unique for each closed system which implies that there exist a unique and asymptotically stable steady state in each reaction simplex for constant external conditions (Otero-Muras et al. (2008)).

Property 1: (Otero-Muras et al. (2008)) For an open chemical reaction network with a given initial conditions and given inlet conditions there exist a unique reaction simplex and will progress towards it exponentially.

3.3 Passivity Based Control of Stoichiometric Port-Hamiltonian Systems

Proposition 3: Given the SPH system in (16) and a desired steady state point x_d , Assume there are matrices $J_d = -J_d^T, R_d = R_d^T \ge 0$ and a smooth function H_d in a closed-loop system with input $d(x_{in} - x) = \beta(x)$, such that:

$$\beta(x) = -S_t \left((J_d - R_d) f\left(\frac{\partial H_d}{\partial x}\right) - K f\left(\frac{\partial G}{\partial x}\right) \right) \quad (20)$$

leads to an asymptotically stable IDA-PBC design of the form (20)

Proof: Substituting the value of $\beta(x)$ in (16), The IDA-PBC design of SPH system can be written as:

$$\dot{x} = -S_t \left(J_d - R_d \right) f\left(\frac{\partial H_d}{\partial x} \right).$$
(21)

Passivity and Stability of Stoichiometric Port-Hamiltonian Systems

The Stoichiometric matrix describes the basic chemical structure of the reactions. It is necessary to introduce the stoichiometric system in order to account for the passage from the concentration space to the reaction space, which governs the inner dynamics. Hence, the Stoichiometric matrix does not influence the passivity and stability properties. Therefore, the properties in *proposition 2* can be applied on SPH systems.

In the next section, the SPH form, which belonged to concentration space, will be transformed in to the reaction space.

4. REACTION PORT-HAMILTONIAN FORMULATION AND CONTROL OF OPEN REACTION NETWORKS

A complex reaction network possesses an underlying potential structure on a state space that will be referred to as the reaction space. The Reaction space is the state space where one is not talking about individual concentration and views the reaction as a whole. It was important to reformulate the structure in to reaction terms and yet maintaining the physical essence of the formulation plus huge concern was to justify the change in input and output terms. In this section, the reaction space's PH structure will be produced using matrix transformations and referred to as a RPH formulation.

4.1 Reaction Port-Hamiltonian Form

Proposition 4: The Reaction Port-Hamiltonian structure of an open chemical system can be written as:

$$\underbrace{\eta}_{\substack{\text{Reaction}\\\text{state space}}} = \underbrace{v}_{\substack{\text{Reaction}\\rate}} + \underbrace{(w_{in} - w)}_{\substack{\text{Reaction}\\input}}$$
(22)

Proof: The link which connects the two spaces is the stoichiometric matrix (S_t) . One can mathematically find the left inverse of a rectangular matrix. The rate equation can also be written as:

$$v = -Kf\left(\frac{\partial G}{\partial \xi}\right),\tag{23}$$

where ξ is the extent of reaction. Replacing this rate equation in SPH form (16) and on pre-multiplication by S_t^{-1} , one obtains:

$$\underbrace{S_t^{-1}\dot{x}}_{\substack{\text{Beaction}\\\text{statespace}}} = -\underbrace{Kf\left(\frac{\partial G}{\partial \xi}\right)}_{\substack{\text{Reaction}\\\text{rate}}} + \underbrace{S_t^{-1}(d(x_{in} - x))}_{\substack{\text{Reaction}\\\text{input}}}.$$
 (24)

 $\xi = S_t^{-1}\dot{x}, \ (w_{in} - w) = S_t^{-1}(d(x_{in} - x)). \ \Box \Box$

The reaction state space and the reaction input and output is the sum of concentrations multiplied by some coefficients. These coefficients solely depend on the stoichiometric matrix as $S_t S_t^{-1} = I$. The extent of reaction will vary with individual concentration but will be calculated collectively as is expected to be in reaction space. Now, one can have the desired extent of reaction as its controlled parameter and can have the combination of concentrations in a specified manner as its input but such case is possible when there is more than one input concentrations. Normally, it is only one substrate which will reduce the input to one concentration only but controlled parameter will still be the extent of reaction. This formulation is justifying the physical meaning behind the input concentration. For the enzyme reaction example, The inverse stoichiometric matrix will be:

$$S_t^{-1} = \frac{1}{5} \left[\begin{array}{cc} -3 & -2 & 0 & 3 \\ 3 & -1 & 2 & 4 \end{array} \right]$$

The RPH form for these reactions in a CSTR can be written as:

$$[S_{t}]^{-1} \begin{bmatrix} x_{E} \\ \dot{x}_{S} \\ \dot{x}_{ES} \\ \dot{x}_{P} \end{bmatrix} = -\begin{bmatrix} k_{1} & 0 \\ 0 & k_{2} \end{bmatrix}$$
$$\exp\left(\frac{1}{RT} \begin{bmatrix} \partial G/\partial\xi_{1} \\ \partial G/\partial\xi_{2} \end{bmatrix}\right)$$
$$+[S_{t}]^{-1} \begin{bmatrix} d(x_{inE} - x_{E}) \\ d(x_{inS} - x_{S}) \\ d(x_{inES} - x_{ES}) \\ d(x_{inP} - x_{P}) \end{bmatrix}.$$
(25)

4.2 Passivity Based Control of Reaction Port-Hamiltonian Systems

Proposition 5: Given the RPH system in (24) and a desired steady state point ξ_d , Assume there are matrices $J_d = -J_d^T, R_d = R_d^T \ge 0$ and a smooth function H_d in a closed-loop system with input $S_t^{-1}d(x_{in} - x) = \beta(x)$, such that:

$$\beta(x) = -(J_d - R_d) f\left(\frac{\partial H_d}{\partial \xi}\right) + K f\left(\frac{\partial G}{\partial \xi}\right)$$
(26)

leads to an asymptotically stable IDA-PBC design of the form (27).

Proof: Substituting the value of $\beta(x)$ in (24), the IDA-PBC design of RPH system can be written as:

$$S_t^{-1}\dot{x} = -\left(J_d - R_d\right)f\left(\frac{\partial H_d}{\partial \xi}\right).$$
 (27)

The stability and passivity conditions of concentration space are also valid for the reaction space.

5. STOICHIOMETRIC PORT-HAMILTONIAN AND REACTION PORT-HAMILTONIAN MODEL OF ENZYMATIC HYDROLYSIS OF CELLULOSE IN AN OPEN REACTOR

Application to a real system is very important to validate the model. At first, this section is explaining about the problem in details and the assumptions used. Then the simulations based on real data are presented.

Biological conversion of fermentable reducing sugars to fuels and chemicals offers the high yields of these products at low costs. (Gan et al. (2005)) Enzymatic hydrolysis of cellulosic material is a way of producing these sugars. However, commercial application of enzymic cellulose hydrolysis may be the most difficult step in this process due to lack of an effective reactor system to cater for the interfacial heterogeneous catalysis and complex reaction kinetics.

Earlier, hydrolysis process used to take place in conventional batch reactors. (Gan et al. (2003)) Recent modifications such as using purpose-built integrated membrane reactors featuring simultaneous and continuous product removal have shown promising results. The integrated operation improves reaction kinetics, reducing enzyme inhibition and immobilization of enzymes which leads to high product yield.

Kinetics of cellulose hydrolysis also involves action of several cellulase components. Cellulose materials are insoluble, structured, and comprised of multi-components which arise complexities like composition of cellulosic materials, the mechanism of the enzymes and inhibition by intermediates and end product. A lot of research has been done but the current understanding of overall mechanism is still limited.

In this paper, the mechanism given in Gan et al. (2003) is being taken and modeled and then IDA-PBC is applied. The integrated membrane reactor is assumed similar to a continuous stirred tank reactor. Also, the perfect mixing in the reactor and zero rejection of reducing sugar by the membrane assures that outgoing concentration of reducing sugar and substrate is same as the concentration inside the reactor.

In real life, low and concentration sensors exhibit measurement noises. A study of stochastic Hamiltonian Processes is beyond the scope of this paper as it would need a specific study, using Stochastic Generalized Canonical Transformations (SGCT's) as in (S. and K. (2013)). Some specific results on damping for linear or PDE systems can be found in (Matignon and Hélie (2013)), but further approaches would be needed to adapt these results to other classes of systems. Nevertheless, a small noise has been added to show the robustness of the approach, and a short comment in the paper.

5.1 Reaction Mechanism

There have been plenty of assumptions made before finally arriving to the mathematical representation of hydrolysis process (Gan et al. (2003)). The assumptions are:

1. Multi components of Enzyme E are combined and assumed to have a unified catalytic effect and multiple reducing sugars produced are also supposed as single product P.

2. The different reaction intermediates are divided in to two types: Enzyme-substrate complexes E_{Sc} which leads to final product formation and other act as inhibitors E_{Sx} . 3. The substrate concentration taken in to account will be measured according to the surface concentration of active cellulose enzyme.

4. Final product is also inhibiting enzyme through a reversible reaction leading to EP complex.

5. All the reactions are reversible.

6. The operation is assumed to be smooth and rate of change of interfacial inert and appearance of new cellulose is ignored. The following set of reactions represent the series of events in the process:

$$E + S_c \frac{k_{Sc1}}{k_{Sc2}} ES_c, E + S_x \frac{k_{Sx1}}{k_{Sx2}} ES_x,$$
$$ES_c \frac{k_{P1}}{k_{P2}} E + P, E + P \frac{k_{EP1}}{k_{EP2}} EP.$$

E is the cellulase system, S_c is cellulose, S_x is cellobios and *P* is glucose. k_{Sc1} and k_{Sc2} are the primary rate constants for the reversible formation of active ES_c intermediate, k_{Sx1} and k_{Sx2} are the primary rate constants for the reversible formation of non-productive ES_x complex, k_{P1} and k_{P2} are the rate constants of reversible product formation, and k_{EP1} and k_{EP2} are the forward and reverse reaction rate constants for the formation of the EP complex.

The kinetics of the process is seen to have followed the basic Michaelis-Menten (MM) kinetics with no inhibition to the initiation reaction forming complex ES_c . which in this case will be helpful to find the correct values of steady state concentrations. So, the basic MM kinetics leads to the following equality for the closed system:

$$k_{Sc1}C_E C_{Sc} = k_{Sc2}C_{ESc} \tag{28}$$

Also, the total enzyme concentration E^{tot} at any time will be:

$$E^{tot} = C_E + C_{ES_c} + C_{ES_x} + C_{EP}$$
(29)

The mass action reaction rates for the four reactions are as follows:

$$v_1 = k_{Sc1} C_E C_{S_c} - k_{Sc2} C_{ES_c}, \tag{30}$$

$$v_2 = k_{Sx1} C_E C_{Sx} - k_{Sx2} C_{ESx}, \tag{31}$$

$$v_3 = k_{P1} C_{ES_c} - k_{P2} C_E C_P, \tag{32}$$

$$v_4 = k_{EP1} C_E C_P - k_{EP2} C_{EP}.$$
 (33)

In terms of steady state concentrations, the rate equations become:

$$v_1 = k_1 \left(\frac{C_E}{C_E^*} \frac{C_{S_c}}{C_{S_c}^*} - \frac{C_{ES_c}}{C_{ES_c}^*} \right),$$
(34)

$$v_{2} = k_{2} \left(\frac{C_{E}}{C_{E}^{*}} \frac{C_{S_{x}}}{C_{S_{x}}^{*}} - \frac{C_{ES_{x}}}{C_{ES_{x}}^{*}} \right),$$
(35)

$$v_{3} = k_{3} \left(\frac{C_{ES_{c}}}{C_{ES_{c}}^{*}} - \frac{C_{E}}{C_{E}^{*}} \frac{C_{P}}{C_{P}^{*}} \right),$$
(36)

$$v_4 = k_4 \left(\frac{C_E}{C_E^*} \frac{C_P}{C_P^*} - \frac{C_{EP}}{C_{EP}^*} \right).$$
(37)

Here, $k_1 = \frac{k_{Sc1}}{k_{Sc2}}$, $k_2 = \frac{k_{Sx1}}{k_{Sx2}}$, $k_3 = \frac{k_{P1}}{k_{P2}}$ and $k_4 = \frac{k_{EP1}}{k_{EP2}}$. For the state space of concentrations in this order:

$[\boldsymbol{x}] = \begin{bmatrix} c_E & c_{S_c} & c_{ES_c} & c_{S_x} & c_{ES_x} & c_P & c_{EP} \end{bmatrix}^T,$

Stoichiometric matrix S_t will be:

$$S_t = \begin{bmatrix} -1 & -1 & 1 & -1 \\ -1 & 0 & 0 & 0 \\ 1 & 0 & -1 & 0 \\ 0 & -1 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & -1 \\ 0 & 0 & 0 & 1 \end{bmatrix}.$$
 (38)

Its inverse for the reaction space is:

j

$$S_t^{-1} = \begin{bmatrix} -1 & 0 & 0 & 0 & 1 & 1 & 0 \\ -1 & 1 & 0 & 0 & 0 & 1 & 0 \\ 1 & -1 & 0 & -1 & 0 & 0 & 1 \\ -1 & 1 & 0 & 1 & 0 & 1 & 1 \end{bmatrix}$$
(39)

The incidence matrix (B_m) and complex stoichiometric matrix (Z) are as follows:

$$B_m = \begin{bmatrix} -1 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & -1 & 1 & 0 & 0 \\ 0 & -1 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & -1 & 1 \end{bmatrix}$$
$$Z = \begin{bmatrix} 1 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 1 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix}$$

The SPH form for an open system with dilution rate d and net input as $x_{in} - x$ will be:

$$[\dot{x}]_{7\times1} = -[S_t]_{7\times4} \begin{bmatrix} k_1 & 0 & 0 & 0\\ 0 & k_2 & 0 & 0\\ 0 & 0 & k_3 & 0\\ 0 & 0 & 0 & k_4 \end{bmatrix} [B_m]_{4\times6}$$

$$(40)$$

$$\exp\left[[Z]_{6\times7} \frac{1}{RT} \left[\frac{\partial G}{\partial x} \right]_{7\times1} \right] + [d(x_{in} - x)]_{7\times1}$$

The RPH form can be formulated as:

ex

$$[S_t]_{4\times7}^{-1}[\dot{x}]_{7\times1} = -\begin{bmatrix} k_1 & 0 & 0 & 0\\ 0 & k_2 & 0 & 0\\ 0 & 0 & k_3 & 0\\ 0 & 0 & 0 & k_4 \end{bmatrix}$$
(41)

$$\exp\left[\frac{1}{RT}\left[\partial G_{\partial\xi}\right]_{2\times 1}\right] + [S_t]_{4\times 7}^{-1}[d(x_{in}-x)]_{7\times 1}$$

6. INTERCONNECTION AND DAMPING ASSIGNMENT-PASSIVITY BASED CONTROL OF ENZYMATIC HYDROLYSIS OF CELLULOSE IN CONTINUOUS BIOREACTOR

Assigning the desired interconnection and damping matrices which also satisfy their structural conditions, the matrices are as follows:

$$J_{d} = \begin{bmatrix} 0 & x' & y' & z' \\ -x' & 0 & w' & v' \\ -y' & -w' & 0 & t' \\ -z' & -v' & -t' & 0 \end{bmatrix}$$
(42)
$$R_{d} = \begin{bmatrix} a' & e' & f' & g' \\ e' & b' & h' & i' \\ f' & h' & c' & j' \\ g' & i' & j' & d' \end{bmatrix}$$
(43)

The IDA-PBC controlled input for the chemical system modeled through SPH form will be:

$$d(x_{in} - x) = -S_t$$

$$\left(\begin{bmatrix} -a' & x' - e' & y' - f' & z' - g' \\ -x' - e' & -b' & w' - h' & v' - i' \\ -y' - f' & -w' - h' & -c' & t' - j' \\ -z' - g' & -v' - i' & -t' - j' & -d' \end{bmatrix} B_m$$

$$\exp\left(Z \frac{1}{RT} \left[\frac{\partial G_d}{\partial x} \right] \right) -$$

$$\left[\begin{pmatrix} k_1 & 0 & 0 & 0 \\ 0 & k_2 & 0 & 0 \\ 0 & 0 & k_3 & 0 \\ 0 & 0 & 0 & k_4 \end{bmatrix} B_m \exp\left(Z \frac{1}{RT} \left[\frac{\partial G}{\partial x} \right] \right) \right)$$
(44)

(44) is the generalized control law. The derivation of the control law for this application is shown in Appendix B. For a 4×4 $J_d - R_d$ matrix, the constraints of positive definiteness are very complex in which one parameter depending on the value of many parameters therefore few parameters are assigned 0 value to reduce the complexity maintaining the symmetricity and skew-symmetricity of R_d and J - d matrices. The next section will show the simulation results of the Enzymatic Hydrolysis of Cellulose based on control law shown in (5).

6.1 Simulations

There are broadly two control variables, dilution rate and inlet concentration. Only one parameter can be controlled at a time. Although dilution rate is kept same for the whole system so changing dilution rate gives only one degree of freedom for the manifold of various parameters to be controlled. As their is only one substrate as inlet, the control variable will be either substrate concentration or dilution rate. Usually the concentration of inert material Sx depend on cellulosic material Sc through a variable relation depending on their concentration but in this case it is assumed to be constant.

In this paper the IDA-PBC control simulations are obtained for the desired concentration of reducing sugars. Before it, the steady state concentrations (x_{eq}) are obtained at given initial conditions (x_0) of various substituents taking part in reaction and dilution rate. The values of initial concentration, steady state concentration, desired concentration of all the constituents and dilution rate and rate constants are given in the Table A.1. The desired concentration is chosen from the steady state model for a constant value of inlet substrate concentration. The desired inlet concentration (Sc_{ind}) and the manifold of desired concentration (x_d) is then obtained through the IDA-PBC control methodology explained above. As only substrate is fed from outside the reactor so inlet substrate concentration will be the parameter to control. This will reduce (44) to a single algebraic equation in which inlet substrate concentration S_{cin} will be linear function of desired rate laws and actual rate laws having tuning parameters as multiplying coefficients to these rate laws. The final equation of Sc_{in} derived from equation (44) can be seen in Appendix B. The simulations obtained for the various concentrations with respect to time and inlet substrate concentration are shown below:

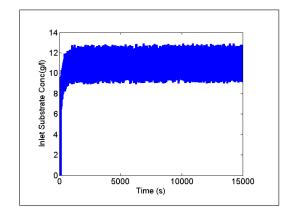


Fig. 1. Inlet Substrate Concentration with Time.

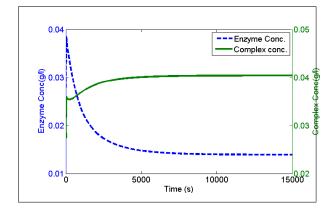


Fig. 2. Enzyme and Active Cellulose Substrate Concentration with Time.

Discussion

The full kinetics of the process is modeled and controlled without any reduction. The results obtained are actual and smooth hence prove the potential of the modeling and controlling technique for open systems. The SPH and RPH model can be made of almost all reactions in chemical and biochemical world with very few neglectable assumptions. The IDA-PBC is very much physical, easy to understand and apply. It can be used to generate the control law of the real processes through simulations. The assumptions taken are from the biochemical kinetics only. The results are quite close to the simulations of (Gan et al. (2003)), still, 38

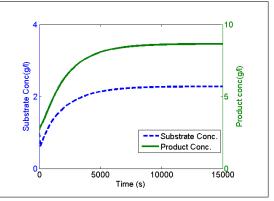


Fig. 3. Active Substrate and Product Concentration with Time.

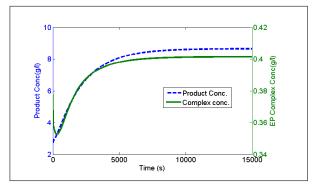


Fig. 4. Product and Enzyme-Product Complex Concentration with Time.

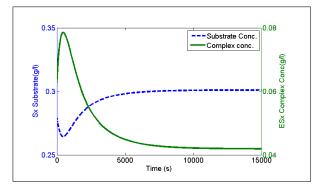


Fig. 5. Inert Substrate and Enzyme-Inert Complex Concentration with Time.

it is difficult to compare with other theories as results can be similar, the approach being original in itself. Note that extensions to no enzymatic and biological, but gaseous mixtures have been addressed from the modelling point of view (Garcia Sandoval et al. (2016)). Still, much is to be done to control efficiently these kinds of other complex chemical systems.

7. CONCLUSION

New energy-based models have been given for isothermal chemical systems in open reactors. These models are related to the port-Hamiltonian theory and exhibit the energy flows and dissipation. Two kinds of models, whether the concentrations or the reaction rates are considered, are given for reversible chemical and enzymatic reactions. The Internal Damping Assignment- Passivity Based Control method, generally applied to Port-Hamiltonian systems, has been used to provide a new framework for a systematic design of these kind of systems. A variety of chemical systems, including bio and enzymatic plants, in batch and continuous modes, can be covered under this approach. In this paper, an enzymatic hydrolysis of cellulose has been addressed. Further studies could include the control of bioreactions under the Reaction-PH form or non-liquid (dilute) reactions.

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Appendix A. TABLE

All the adopted values with notations and units are shown in *Table A.1*.

Appendix B. DERIVATION OF INLET SUBSTRATE CONCENTRATION

As it is known that there are only one or two inlet concentrations and also not all the constituents go out. Specially enzymes stay inside the reactor in most of the Bioreactions which is the case in this example also therefore equation (44) can be reduced to be written in the following form:

$$d[x_{in} - x] = -S_t \left([J_d - R_d] \left[\frac{v_d}{k} \right] - [k] \left[\frac{v_{eq}}{k} \right] \right)$$
(B.1)

Here, v_d and v_{eq} are the rate equations at desired and steady state concentrations respectively. The main concern in this case is to get a relation for the inlet concentration of active cellulose. Solving above equation for x = Sc, substituting S_t given in (38), the equation formed is as follows:

$$d(Sc_{in} - Sc) = a'\left(\frac{v_{1d}}{k_1}\right) + \left(-x' + e'\right)\left(\frac{v_{2d}}{k_2}\right) + \left(-y' + f'\right)\left(\frac{v_{3d}}{k_3}\right) + \left(-z' + g'\right)\left(\frac{v_{4d}}{k_4}\right) + v_{1eq},$$
(B.2)

and Sc_{in} will be:

$$Sc_{in} = \left(\frac{1}{d}\right) \left(a'\left(\frac{v_{1d}}{k_1}\right) + \left(-x'+e'\right)\left(\frac{v_{2d}}{k_2}\right) + \left(-y'+f'\right)\left(\frac{v_{3d}}{k_3}\right) + \left(-z'+g'\right)\left(\frac{v_{4d}}{k_4}\right) + v_{1eq}\right) + Sc.$$
(B.3)

SYMBOLNAMEUNITVALUE K_{Sc1} Enzyme Adsorption Constant $1/g$ -s.2 K_{Sc2} Enzyme Desorption Constant s^{-1} .05 K_{Sx1} Inert Enzyme Adsorption Constant $1/g$ -s.02 K_{Sx2} Inert Enzyme Desorption Constant s^{-1} .002 K_{P1} Product Formation Constant s^{-1} .002 K_{P2} Product Dissociation Constant $1/g$ -s.1 K_{EP1} Forward Product Inhibition Constant $1/g$ -s.1 d Dilution Rate s^{-1} .0005 d Dilution Rate s^{-1} .0005 E_0 Initial free soluble Enzyme Conc. $g/1$.022759 Sc_0 Initial Active Cellulose Conc. $g/1$.0297 Sx_0 Initial Enzyme-Inert Conc. $g/1$.06275 P_0 Initial Product Conc. $g/1$.06275 P_0 Initial Enzyme-Cellulose Conc. $g/1$.02271 Sc_{eq} Steady state Free Soluble Enzyme Conc. $g/1$.02271 Sc_{eq} Steady state Enzyme-Cellulose Conc. $g/1$.01352 Sx_{eq} Steady state Enzyme-Cellulose Conc. $g/1$.01352 Sx_{eq} Steady state Enzyme-Cellulose Conc. $g/1$.01352 Sx_{eq} Steady state Enzyme-Cellulose Conc. $g/1$.01379 Sc_{eq} Steady state Enzyme-Cellulose Conc. $g/1$.01379 Sc_{eq} Steady state Enzyme-Cellulose Conc. $g/1$.01379 Sc_{ed} <th colspan="5">TABLE OF ADOPTED VALUES WITH NOTATIONS</th>	TABLE OF ADOPTED VALUES WITH NOTATIONS				
K_{Sc2} Enzyme Desorption Constant s^{-1} .05 K_{Sx1} Inert Enzyme Adsorption Constant $1/g$ -s.02 K_{Sx2} Inert Enzyme Desorption Constant s^{-1} .002 K_{P1} Product Formation Constant s^{-1} 9.05 K_{P2} Product Dissociation Constant $1/g$ -s3 K_{EP1} Forward Product Inhibition Constant $1/g$ -s1 K_{EP2} Reverse Product Inhibition Constant s^{-1} .03 d Dilution Rate s^{-1} .005 E_0 Initial free soluble Enzyme Conc. $g/1$.02759 Sc_0 Initial Active Cellulose Conc. $g/1$.0297 Sx_0 Initial Enzyme-Cellulose Conc. $g/1$.02802 ESx_0 Initial Product Conc. $g/1$.06275 P_0 Initial Product Conc. $g/1$.02271 Sc_{eq} Steady state Free Soluble Enzyme Conc. $g/1$.02271 Sc_{eq} Steady state Active Cellulose Conc. $g/1$.02271 Sc_{eq} Steady state Free Soluble Enzyme Conc. $g/1$.02271 Sc_{eq} Steady state Enzyme-Cellulose Conc. $g/1$.0252 Sx_{eq} Steady state Enzyme-Cellulose Conc. $g/1$.01352 Sx_{eq} Steady state Enzyme-Cellulose Conc. $g/1$.01352 Sx_{eq} Steady state Enzyme-Cellulose Conc. $g/1$.01352 Sx_{eq} Steady state Enzyme-Cellulose Conc. $g/1$.0399 Sc_{ind} Desired Inlet Active Cellul	SYMBOL	NAME	UNIT	VALUE	
K_{Sx1} Inert Enzyme Adsorption Constant $1/g$ -s $.02$ K_{Sx1} Inert Enzyme Desorption Constant s^{-1} $.002$ K_{P1} Product Formation Constant s^{-1} 9.05 K_{P2} Product Dissociation Constant $1/g$ -s 3 K_{EP1} Forward Product Inhibition Constant $1/g$ -s 1 K_{EP2} Reverse Product Inhibition Constant s^{-1} $.03$ d Dilution Rate s^{-1} $.005$ E_0 Initial free soluble Enzyme Conc. $g/1$ $.02759$ Sc_0 Initial Active Cellulose Conc. $g/1$ $.0297$ Sx_0 Initial Enzyme-Cellulose Conc. $g/1$ $.0297$ Sx_0 Initial Enzyme-Cellulose Conc. $g/1$ $.02271$ Sx_0 Initial Product Conc. $g/1$ $.02271$ Feq Steady state Free Soluble Enzyme Conc. $g/1$ $.02271$ Sc_{eq} Steady state Active Cellulose Conc. $g/1$ $.02271$ Sc_{eq} Steady state Enzyme-Cellulose Conc. $g/1$ $.02271$ Sc_{eq} Steady state Product Conc. $g/1$ $.01352$ Sx_{eq} Steady state Enzyme-Cellulose Conc. $g/1$ $.01352$ Sx_{eq} Steady state Inert Material Conc. $g/1$ $.00477$ P_{eq} Steady state Enzyme-Cellulose Conc. $g/1$ $.00477$ P_{eq} Steady state Enzyme-Cellulose Conc. $g/1$ $.0399$ Sc_{ind} Desired Inlet Active Cellulose Conc. $g/1$ $.0379$ $Sc_{$		Enzyme Adsorption Constant	l/g-s	.2	
K_{Sx1} Inert Enzyme Adsorption Constant $ lg-s$ $.02$ K_{Sx2} Inert Enzyme Desorption Constant s^{-1} $.002$ K_{P1} Product Formation Constant s^{-1} 9.05 K_{P2} Product Dissociation Constant $l/g-s$ 3 K_{EP1} Forward Product Inhibition Constant $l/g-s$ 3 d Dilution Rate s^{-1} $.03$ d Dilution Rate s^{-1} $.005$ E_0 Initial free soluble Enzyme Conc. g/l $.02759$ Sc_0 Initial Active Cellulose Conc. g/l $.0297$ Sx_0 Initial Enzyme-Cellulose Conc. g/l $.0297$ Sx_0 Initial Enzyme-Inert Conc. g/l $.0227$ P_0 Initial Product Conc. g/l $.02759$ P_0 Initial Enzyme-Cellulose Conc. g/l $.0297$ Sx_0 Initial Product Conc. g/l $.0275$ P_0 Initial Enzyme-Inert Conc. g/l $.0277$ E_{eq} Steady state Free Soluble Enzyme Conc. g/l $.0271$ Sc_{eq} Steady state Enzyme-Cellulose Conc. g/l $.0271$ Sc_{eq} Steady state Enzyme-Cellulose Conc. g/l $.01352$ Sx_{eq} Steady state Enzyme-Cellulose Conc. g/l $.01352$ Sx_{eq} Steady state Enzyme-Cellulose Conc. g/l $.06477$ P_{eq} Steady state Enzyme-Cellulose Conc. g/l $.0399$ Sc_{ind} Desired Inlet Active Cellulose Conc. g/l	K_{Sc2}	Enzyme Desorption Constant	1	.05	
K_{P1} Product Formation Constant s^{-1} 9.05 K_{P2} Product Dissociation Constant $1/g$ -s3 K_{EP1} Forward Product Inhibition Constant $1/g$ -s1 K_{EP2} Reverse Product Inhibition Constant s^{-1} .03 d Dilution Rate s^{-1} .005 E_0 Initial free soluble Enzyme Conc. $g/1$.02759 Sc_0 Initial Active Cellulose Conc. $g/1$.0297 Sx_0 Initial Enzyme-Cellulose Conc. $g/1$.0297 Sx_0 Initial Inert Material Conc. $g/1$.02802 ESx_0 Initial Enzyme-Inert Conc. $g/1$.06275 P_0 Initial Product Conc. $g/1$.02271 E_{eq} Steady state Free Soluble Enzyme Conc. $g/1$.02271 Sc_{eq} Steady state Active Cellulose Conc. $g/1$.02271 Sc_{eq} Steady state Enzyme-Cellulose Conc. $g/1$.01352 Sx_{eq} Steady state Enzyme-Cellulose Conc. $g/1$.02271 Sc_{eq} Steady state Enzyme-Cellulose Conc. $g/1$.0477 P_{eq} Steady state Enzyme-Cellulose Conc. $g/1$.0477 P_{eq} Steady state Enzyme-Cellulose Conc. $g/1$.02471 E_{eq} Steady state Enzyme-Cellulose Conc. $g/1$.0477 P_{eq} Steady state Enzyme-Cellulose Conc. $g/1$.0477 P_{eq} Steady state Enzyme-Cellulose Conc. $g/1$.0477 P_{eq} Desired Inlet Active Cellulose C		Inert Enzyme Adsorption Constant	l/g-s	.02	
K_{P2} Product Dissociation Constant $1/g$ -s3 K_{EP1} Forward Product Inhibition Constant $1/g$ -s.1 K_{EP2} Reverse Product Inhibition Constant s^{-1} .03 d Dilution Rate s^{-1} .0005 E_0 Initial free soluble Enzyme Conc. g/l .02759 Sc_0 Initial Active Cellulose Conc. g/l .0297 Sx_0 Initial Enzyme-Cellulose Conc. g/l .0297 Sx_0 Initial Enzyme-Cellulose Conc. g/l .2802 ESx_0 Initial Enzyme-Inert Conc. g/l .06275 P_0 Initial Enzyme-Cellulose Conc. g/l .0271 Eeq Steady state Free Soluble Enzyme Conc. g/l .02271 Sc_{eq} Steady state Active Cellulose Conc. g/l .02271 Sc_{eq} Steady state Active Cellulose Conc. g/l .02271 Sc_{eq} Steady state Enzyme-Cellulose Conc. g/l .02271 Sx_{eq} Steady state Enzyme-Cellulose Conc. g/l .01352 Sx_{eq} Steady state Product Conc. g/l .0477 P_{eq} Steady state Product Conc. g/l .0477 P_{eq} Steady state Enzyme-Cellulose Conc. g/l .399 Sc_{ind} Desired Inlet Active Cellulose Conc. g/l .01379 Sc_d Desired Inlet Active Cellulose Conc. g/l .01379 Sc_d Desired Free Soluble Enzyme Conc. g/l .01379 Sc_d Desired Free Soluble Enzyme Conc. <td>K_{Sx2}</td> <td>Inert Enzyme Desorption Constant</td> <td></td> <td>.002</td>	K_{Sx2}	Inert Enzyme Desorption Constant		.002	
K_{EP1} Forward Product Inhibition Constant $1/g$ -s.1 K_{EP2} Reverse Product Inhibition Constant s^{-1} .03 d Dilution Rate s^{-1} .0005 E_0 Initial free soluble Enzyme Conc. g/l .02759 Sc_0 Initial Active Cellulose Conc. g/l .0297 Sx_0 Initial Enzyme-Cellulose Conc. g/l .0297 Sx_0 Initial Enzyme-Cellulose Conc. g/l .0297 Sx_0 Initial Enzyme-Inert Conc. g/l .06275 P_0 Initial Product Conc. g/l .06275 P_0 Initial Enzyme-Cellulose Conc. g/l .02271 Sc_{eq} Steady state Free Soluble Enzyme Conc. g/l .02271 Sc_{eq} Steady state Active Cellulose Conc. g/l .02271 Sc_{eq} Steady state Enzyme-Cellulose Conc. g/l .01352 Sx_{eq} Steady state Enzyme-Cellulose Conc. g/l .06477 F_{eq} Steady state Enzyme-Inert Conc. g/l .06477 F_{eq} Steady state Enzyme-Cellulose Conc. g/l .399 Sc_{ind} Desired Inlet Active Cellulose Conc. g/l .01379 Sc_d Desired Free Soluble Enzyme Conc. g/l .01379 Sc_d Desired Enzyme-Cellulose Conc. <t< td=""><td>K_{P1}</td><td>Product Formation Constant</td><td>s^{-1}</td><td>9.05</td></t<>	K_{P1}	Product Formation Constant	s^{-1}	9.05	
K_{EP1} Forward Product Inhibition Constant $1/g$ -s.1 K_{EP2} Reverse Product Inhibition Constant s^{-1} .03 d Dilution Rate s^{-1} .0005 E_0 Initial free soluble Enzyme Conc. g/l .02759 Sc_0 Initial Active Cellulose Conc. g/l .0297 Sx_0 Initial Enzyme-Cellulose Conc. g/l .0297 Sx_0 Initial Inert Material Conc. g/l .06275 P_0 Initial Enzyme-Inert Conc. g/l .06275 P_0 Initial Product Conc. g/l .02271 Ecq Steady state Free Soluble Enzyme Conc. g/l .02271 Sc_{eq} Steady state Free Soluble Enzyme Conc. g/l .02271 Sc_{eq} Steady state Enzyme-Cellulose Conc. g/l .02271 Sx_{eq} Steady state Enzyme-Cellulose Conc. g/l .01352 Sx_{eq} Steady state Enzyme-Cellulose Conc. g/l .06477 P_{eq} Steady state Enzyme-Inert Conc. g/l .06477 P_{eq} Steady state Product Conc. g/l .399 Sc_{ind} Desired Inlet Active Cellulose Conc. g/l .11 E_d Desired Free Soluble Enzyme Conc. g/l .01379 Sc_d Desired Free Soluble Enzyme Conc. g/l .01379 Sc_{ind} Desired Inlet Active Cellulose Conc. g/l .01379 Sc_{ind} Desired Free Soluble Enzyme Conc. g/l .01379 Sc_d Desired Enzyme-Cellulose Conc. <td>K_{P2}</td> <td>Product Dissociation Constant</td> <td>l/g-s</td> <td>3</td>	K_{P2}	Product Dissociation Constant	l/g-s	3	
d Dilution Rate s^{-1} .0005 E_0 Initial free soluble Enzyme Conc. $g/1$.02759 Sc_0 Initial Active Cellulose Conc. $g/1$ 1.035 ESc_0 Initial Enzyme-Cellulose Conc. $g/1$.0297 Sx_0 Initial Enzyme-Cellulose Conc. $g/1$.0297 Sx_0 Initial Inert Material Conc. $g/1$.2802 ESx_0 Initial Enzyme-Inert Conc. $g/1$.06275 P_0 Initial Enzyme-Cellulose Conc. $g/1$.06275 P_0 Initial Enzyme-Cellulose Conc. $g/1$.02271 Eeq Steady state Free Soluble Enzyme Conc. $g/1$.02271 Sc_{eq} Steady state Enzyme-Cellulose Conc. $g/1$.02271 Sc_{eq} Steady state Enzyme-Cellulose Conc. $g/1$.01352 Sx_{eq} Steady state Enzyme-Cellulose Conc. $g/1$.06477 P_{eq} Steady state Enzyme-Inert Conc. $g/1$.06477 P_{eq} Steady state Enzyme-Cellulose Conc. $g/1$.0399 Sc_{ind} Desired Inlet Active Cellulose Conc. $g/1$.111 E_d Desired Free Soluble Enzyme Conc. $g/1$.01379 Sc_d Desired Free Soluble Enzyme Conc. $g/1$.01379 Sc_{ad} Desired Active Cellulose Conc. $g/1$.01379 Sc_{ad} Desired Free Soluble Enzyme Conc. $g/1$.01379 Sc_d Desired Free Soluble Enzyme Conc. $g/1$.04058 Sx_d Desired Enzyme-Cellulose Conc. $g/1$	K_{EP1}	Forward Product Inhibition Constant	l/g-s	.1	
dDilution Rate s^{-1} .0005 E_0 Initial free soluble Enzyme Conc. g/l .02759 Sc_0 Initial Active Cellulose Conc. g/l 1.035 ESc_0 Initial Enzyme-Cellulose Conc. g/l .0297 Sx_0 Initial Enzyme-Cellulose Conc. g/l .0297 Sx_0 Initial Enzyme-Cellulose Conc. g/l .06275 P_0 Initial Product Conc. g/l .06275 P_0 Initial Enzyme-Cellulose Conc. g/l .02271 Eeq Steady state Free Soluble Enzyme Conc. g/l .02271 Sc_{eq} Steady state Active Cellulose Conc. g/l .01352 Sx_{eq} Steady state Enzyme-Cellulose Conc. g/l .01352 Sx_{eq} Steady state Enzyme-Cellulose Conc. g/l .06477 P_{eq} Steady state Enzyme-Inert Conc. g/l .06477 P_{eq} Steady state Enzyme-Cellulose Conc. g/l .06477 P_{eq} Steady state Enzyme-Cellulose Conc. g/l .399 Sc_{ind} Desired Inlet Active Cellulose Conc. g/l .117 E_d Desired Free Soluble Enzyme Conc. g/l .01379 Sc_d Desired Free Soluble Enzyme Conc. g/l .01379 Sc_d Desired Inlet Active Cellulose Conc. g/l .01379 Sc_d Desired Inlet Active Cellulose Conc. g/l .01379 Sc_d Desired Enzyme-Cellulose Conc. g/l .04058 Sx_d Desired Enzyme-Cellulose Conc. $g/$	K_{EP2}	Reverse Product Inhibition Constant	s^{-1}	.03	
Sc_0 Initial Active Cellulose Conc. g/l 1.035 ESc_0 Initial Enzyme-Cellulose Conc. g/l $.0297$ Sx_0 Initial Inert Material Conc. g/l $.2802$ ESx_0 Initial Enzyme-Inert Conc. g/l $.06275$ P_0 Initial Product Conc. g/l $.2649$ EP_0 Initial Enzyme-Cellulose Conc. g/l $.3777$ E_{eq} Steady state Free Soluble Enzyme Conc. g/l $.02271$ Sc_{eq} Steady state Active Cellulose Conc. g/l $.02271$ Sc_{eq} Steady state Enzyme-Cellulose Conc. g/l $.01352$ Sx_{eq} Steady state Enzyme-Cellulose Conc. g/l $.01352$ Sx_{eq} Steady state Enzyme-Cellulose Conc. g/l $.06477$ P_{eq} Steady state Enzyme-Cellulose Conc. g/l $.399$ Sc_{ind} Desired Inlet Active Cellulose Conc. g/l $.399$ Sc_{ind} Desired Free Soluble Enzyme Conc. g/l $.01379$ Sc_d Desired Free Soluble Enzyme Conc. g/l $.01379$ Sc_d Desired Active Cellulose Conc. g/l $.01379$ Sc_d Desired Active Cellulose Conc. g/l $.04058$ Sx_d Desired Enzyme-Cellulose Conc. g/l $.04058$ Sx_d <td></td> <td>Dilution Rate</td> <td>s^{-1}</td> <td>.0005</td>		Dilution Rate	s^{-1}	.0005	
Sc_0 Initial Active Cellulose Conc. g/l 1.035 ESc_0 Initial Enzyme-Cellulose Conc. g/l $.0297$ Sx_0 Initial Inert Material Conc. g/l $.2802$ ESx_0 Initial Enzyme-Inert Conc. g/l $.06275$ P_0 Initial Product Conc. g/l $.2649$ EP_0 Initial Enzyme-Cellulose Conc. g/l $.3777$ E_{eq} Steady state Free Soluble Enzyme Conc. g/l $.02271$ Sc_{eq} Steady state Active Cellulose Conc. g/l $.02271$ Sc_{eq} Steady state Enzyme-Cellulose Conc. g/l $.02271$ Sc_{eq} Steady state Enzyme-Cellulose Conc. g/l $.01352$ Sx_{eq} Steady state Enzyme-Cellulose Conc. g/l $.01352$ Sx_{eq} Steady state Enzyme-Inert Conc. g/l $.06477$ P_{eq} Steady state Product Conc. g/l $.399$ Sc_{ind} Desired Inlet Active Cellulose Conc. g/l $.3179$ Sc_d Desired Free Soluble Enzyme Conc. g/l $.01379$ Sc_d Desired Free Soluble Enzyme Conc. g/l $.01379$ Sc_d Desired Active Cellulose Conc. g/l $.04058$ Sx_d Desired Enzyme-Cellulose Conc. g/l $.04058$ Sx_d De	E_0	Initial free soluble Enzyme Conc.	g/l	.02759	
ESc_0 Initial Enzyme-Cellulose Conc. g/l .0297 Sx_0 Initial Inert Material Conc. g/l .2802 ESx_0 Initial Enzyme-Inert Conc. g/l .06275 P_0 Initial Product Conc. g/l 2.649 EP_0 Initial Enzyme-Cellulose Conc. g/l .3777 E_{eq} Steady state Free Soluble Enzyme Conc. g/l .02271 Sc_{eq} Steady state Active Cellulose Conc. g/l .02271 Sc_{eq} Steady state Enzyme-Cellulose Conc. g/l .02271 Esc_{eq} Steady state Enzyme-Cellulose Conc. g/l .01352 Sx_{eq} Steady state Enzyme-Cellulose Conc. g/l .06477 P_{eq} Steady state Enzyme-Cellulose Conc. g/l .06477 P_{eq} Steady state Enzyme-Cellulose Conc. g/l .399 Sc_{ind} Desired Inlet Active Cellulose Conc. g/l .3179 Sc_d Desired Free Soluble Enzyme Conc. g/l .01379 Sc_d Desired Active Cellulose Conc. g/l .01379 Sc_d Desired Active Cellulose Conc. g/l .01379 Sc_d Desired Active Cellulose Conc. g/l .04058 Sx_d Desired Enzyme-Cellulose Conc. g/l .04058 Sx_d Desired Inert Material Conc. g/l .3076 ESx_d Desired Enzyme-Inert Conc. g/l .3076 ESx_d Desired Enzyme-Inert Conc. g/l .3076 ESx_d Desired Enzyme-Inert Conc. g/l <td>Sc_0</td> <td>Initial Active Cellulose Conc.</td> <td></td> <td>1.035</td>	Sc_0	Initial Active Cellulose Conc.		1.035	
Sx_0 Initial Inert Material Conc. g/l .2802 ESx_0 Initial Enzyme-Inert Conc. g/l .06275 P_0 Initial Product Conc. g/l 2.649 EP_0 Initial Enzyme-Cellulose Conc. g/l .3777 E_{eq} Steady state Free Soluble Enzyme Conc. g/l .02271 Sc_{eq} Steady state Active Cellulose Conc. g/l .02271 Sc_{eq} Steady state Enzyme-Cellulose Conc. g/l .02271 Sc_{eq} Steady state Enzyme-Cellulose Conc. g/l .01352 Sx_{eq} Steady state Inert Material Conc. g/l .06477 P_{eq} Steady state Product Conc. g/l .06477 P_{eq} Steady state Enzyme-Cellulose Conc. g/l .399 Sc_{ind} Desired Inlet Active Cellulose Conc. g/l .11 E_d Desired Free Soluble Enzyme Conc. g/l .01379 Sc_d Desired Free Soluble Enzyme Conc. g/l .01379 Sc_d Desired Active Cellulose Conc. g/l .01379 Sc_d Desired Free Soluble Enzyme Conc. g/l .04058 Sx_d Desired Enzyme-Cellulose Conc. g/l .3076 ESx_d Desired Inert Material Conc. g/l .3076 ESx_d Desired Enzyme-Inert Conc. g/l .04241 P_d Desired Product Conc. g/l .04241	ESc_0	Initial Enzyme-Cellulose Conc.		.0297	
ESx_0 Initial Enzyme-Inert Conc. g/l .06275 P_0 Initial Product Conc. g/l 2.649 EP_0 Initial Enzyme-Cellulose Conc. g/l .3777 E_{eq} Steady state Free Soluble Enzyme Conc. g/l .02271 Sc_{eq} Steady state Active Cellulose Conc. g/l .02271 Sc_{eq} Steady state Active Cellulose Conc. g/l .02271 ESc_{eq} Steady state Enzyme-Cellulose Conc. g/l .01352 Sx_{eq} Steady state Inert Material Conc. g/l .2852 ESx_{eq} Steady state Enzyme-Inert Conc. g/l .06477 P_{eq} Steady state Product Conc. g/l .399 Sc_{ind} Desired Inlet Active Cellulose Conc. g/l .3179 Sc_d Desired Free Soluble Enzyme Conc. g/l .01379 Sc_d Desired Active Cellulose Conc. g/l .01379 Sc_d Desired Enzyme-Cellulose Conc. g/l .01379 Sc_d Desired Free Soluble Enzyme Conc. g/l .01379 Sc_d Desired Active Cellulose Conc. g/l .04058 Sx_d Desired Inert Material Conc. g/l .04058 Sx_d Desired Enzyme-Inert Conc. g/l .04241 P_d Desired Product Conc. g/l .04241	Sx_0	Initial Inert Material Conc.		.2802	
P_0 Initial Product Conc. g/l 2.649 EP_0 Initial Enzyme-Cellulose Conc. g/l $.3777$ E_{eq} Steady state Free Soluble Enzyme Conc. g/l $.02271$ Sc_{eq} Steady state Active Cellulose Conc. g/l $.7291$ ESc_{eq} Steady state Enzyme-Cellulose Conc. g/l $.01352$ Sx_{eq} Steady state Enzyme-Cellulose Conc. g/l $.2852$ ESx_{eq} Steady state Enzyme-Inert Conc. g/l $.06477$ P_{eq} Steady state Product Conc. g/l $.06477$ EP_{eq} Steady state Enzyme-Cellulose Conc. g/l $.399$ Sc_{ind} Desired Inlet Active Cellulose Conc. g/l $.11$ E_d Desired Free Soluble Enzyme Conc. g/l $.01379$ Sc_d Desired Free Soluble Enzyme Conc. g/l $.01379$ Sc_d Desired Free Soluble Enzyme Conc. g/l $.01379$ Sc_d Desired Enzyme-Cellulose Conc. g/l $.04058$ Sx_d Desired Inert Material Conc. g/l $.04058$ Sx_d Desired Inert Material Conc. g/l $.3076$ ESx_d Desired Enzyme-Inert Conc. g/l $.3076$ P_d Desired Product Conc. g/l $.34241$	ESx_0	Initial Enzyme-Inert Conc.		.06275	
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	P_0	Initial Product Conc.		2.649	
E_{eq} Steady state Free Soluble Enzyme Conc. g/l .02271 Sc_{eq} Steady state Active Cellulose Conc. g/l .7291 ESc_{eq} Steady state Enzyme-Cellulose Conc. g/l .01352 Sx_{eq} Steady state Inert Material Conc. g/l .2852 ESx_{eq} Steady state Enzyme-Inert Conc. g/l .06477 P_{eq} Steady state Product Conc. g/l .5271 EP_{eq} Steady state Enzyme-Cellulose Conc. g/l .399 Sc_{ind} Desired Inlet Active Cellulose Conc. g/l .11 E_d Desired Free Soluble Enzyme Conc. g/l .01379 Sc_d Desired Active Cellulose Conc. g/l .01379 Sc_d Desired Free Soluble Enzyme Conc. g/l .01379 Sc_d Desired Active Cellulose Conc. g/l .04058 Sx_d Desired Enzyme-Cellulose Conc. g/l .04058 Sx_d Desired Inert Material Conc. g/l .3076 ESx_d Desired Enzyme-Inert Conc. g/l .3076 ESx_d Desired Enzyme-Inert Conc. g/l .3076 ESx_d Desired Product Conc. g/l .04241 P_d Desired Product Conc. g/l .04241	EP_0	Initial Enzyme-Cellulose Conc.		.3777	
Sc_{eq} Steady state Active Cellulose Conc. g/l .7291 ESc_{eq} Steady state Enzyme-Cellulose Conc. g/l .01352 Sx_{eq} Steady state Inert Material Conc. g/l .2852 ESx_{eq} Steady state Enzyme-Inert Conc. g/l .06477 P_{eq} Steady state Product Conc. g/l .5271 EP_{eq} Steady state Enzyme-Cellulose Conc. g/l .399 Sc_{ind} Desired Inlet Active Cellulose Conc. g/l .01379 Sc_d Desired Free Soluble Enzyme Conc. g/l .01379 Sc_d Desired Enzyme-Cellulose Conc. g/l .01379 Sc_d Desired Enzyme-Cellulose Conc. g/l .04058 Sx_d Desired Enzyme-Cellulose Conc. g/l .04058 Sx_d Desired Enzyme-Inert Conc. g/l .3076 ESx_d Desired Enzyme-Inert Conc. g/l .3076 ESx_d Desired Enzyme-Inert Conc. g/l .04241 P_d Desired Product Conc. g/l 8.773	E_{eq}	Steady state Free Soluble Enzyme Conc.		.02271	
ESc_{eq} Steady state Enzyme-Cellulose Conc. g/l .01352 Sx_{eq} Steady state Inert Material Conc. g/l .2852 ESx_{eq} Steady state Enzyme-Inert Conc. g/l .06477 P_{eq} Steady state Product Conc. g/l 5.271 EP_{eq} Steady state Enzyme-Cellulose Conc. g/l .399 Sc_{ind} Desired Inlet Active Cellulose Conc. g/l .11 E_d Desired Free Soluble Enzyme Conc. g/l .01379 Sc_d Desired Active Cellulose Conc. g/l .01379 Sc_d Desired Enzyme-Cellulose Conc. g/l .01379 Sc_d Desired Enzyme-Cellulose Conc. g/l .04058 Sx_d Desired Enzyme-Cellulose Conc. g/l .04058 Sx_d Desired Inert Material Conc. g/l .3076 ESx_d Desired Enzyme-Inert Conc. g/l .04241 P_d Desired Product Conc. g/l 8.773	Sc_{eq}	Steady state Active Cellulose Conc.		.7291	
$\begin{array}{c cccc} Sx_{eq} & \text{Steady state Inert Material Conc.} & g/l & .2852 \\ \hline ESx_{eq} & \text{Steady state Enzyme-Inert Conc.} & g/l & .06477 \\ \hline P_{eq} & \text{Steady state Product Conc.} & g/l & 5.271 \\ \hline EP_{eq} & \text{Steady state Enzyme-Cellulose Conc.} & g/l & .399 \\ \hline Sc_{ind} & \text{Desired Inlet Active Cellulose Conc.} & g/l & 11 \\ \hline E_d & \text{Desired Free Soluble Enzyme Conc.} & g/l & .01379 \\ \hline Sc_d & \text{Desired Active Cellulose Conc.} & g/l & 2.327 \\ \hline ESc_d & \text{Desired Enzyme-Cellulose Conc.} & g/l & .04058 \\ \hline Sx_d & \text{Desired Inert Material Conc.} & g/l & .3076 \\ \hline ESx_d & \text{Desired Enzyme-Inert Conc.} & g/l & .04241 \\ \hline P_d & \text{Desired Product Conc.} & g/l & 8.773 \\ \hline \end{array}$	ESc_{eq}	Steady state Enzyme-Cellulose Conc.		.01352	
ESx_{eq} Steady state Enzyme-Inert Conc. g/l .06477 P_{eq} Steady state Product Conc. g/l 5.271 EP_{eq} Steady state Enzyme-Cellulose Conc. g/l .399 Sc_{ind} Desired Inlet Active Cellulose Conc. g/l 11 E_d Desired Free Soluble Enzyme Conc. g/l .01379 Sc_d Desired Active Cellulose Conc. g/l .01379 Sc_d Desired Enzyme-Cellulose Conc. g/l .04058 Sx_d Desired Inert Material Conc. g/l .3076 ESx_d Desired Enzyme-Inert Conc. g/l .3076 ESx_d Desired Product Conc. g/l .3076		Steady state Inert Material Conc.	g/l	.2852	
P_{eq} Steady state Product Conc. g/l 5.271 EP_{eq} Steady state Enzyme-Cellulose Conc. g/l $.399$ Sc_{ind} Desired Inlet Active Cellulose Conc. g/l 11 E_d Desired Free Soluble Enzyme Conc. g/l $.01379$ Sc_d Desired Active Cellulose Conc. g/l 2.327 ESc_d Desired Enzyme-Cellulose Conc. g/l $.04058$ Sx_d Desired Inert Material Conc. g/l $.3076$ ESx_d Desired Enzyme-Inert Conc. g/l $.3076$ P_d Desired Product Conc. g/l 8.773	ESx_{eq}	Steady state Enzyme-Inert Conc.		.06477	
EP_{eq} Steady state Enzyme-Cellulose Conc. g/l .399 Sc_{ind} Desired Inlet Active Cellulose Conc. g/l 11 E_d Desired Free Soluble Enzyme Conc. g/l .01379 Sc_d Desired Active Cellulose Conc. g/l 2.327 ESc_d Desired Enzyme-Cellulose Conc. g/l .04058 Sx_d Desired Inert Material Conc. g/l .3076 ESx_d Desired Enzyme-Inert Conc. g/l .04241 P_d Desired Product Conc. g/l 8.773	P_{eq}	Steady state Product Conc.		5.271	
Sc_{ind} Desired Inlet Active Cellulose Conc. g/l 11 E_d Desired Free Soluble Enzyme Conc. g/l .01379 Sc_d Desired Active Cellulose Conc. g/l 2.327 ESc_d Desired Enzyme-Cellulose Conc. g/l .04058 Sx_d Desired Inert Material Conc. g/l .3076 ESx_d Desired Enzyme-Inert Conc. g/l .04241 P_d Desired Product Conc. g/l 8.773	\hat{EP}_{eq}	Steady state Enzyme-Cellulose Conc.		.399	
E_d Desired Free Soluble Enzyme Conc. g/l .01379 Sc_d Desired Active Cellulose Conc. g/l 2.327 ESc_d Desired Enzyme-Cellulose Conc. g/l .04058 Sx_d Desired Inert Material Conc. g/l .3076 ESx_d Desired Enzyme-Inert Conc. g/l .04241 P_d Desired Product Conc. g/l 8.773	Scind	Desired Inlet Active Cellulose Conc.	g/l	11	
Sc_d Desired Active Cellulose Conc. g/l 2.327 ESc_d Desired Enzyme-Cellulose Conc. g/l .04058 Sx_d Desired Inert Material Conc. g/l .3076 ESx_d Desired Enzyme-Inert Conc. g/l .04241 P_d Desired Product Conc. g/l 8.773	E_d	Desired Free Soluble Enzyme Conc.		.01379	
ESc_d Desired Enzyme-Cellulose Conc. g/l .04058 Sx_d Desired Inert Material Conc. g/l .3076 ESx_d Desired Enzyme-Inert Conc. g/l .04241 P_d Desired Product Conc. g/l 8.773		Desired Active Cellulose Conc.		2.327	
Sx_d Desired Inert Material Conc. g/l .3076 ESx_d Desired Enzyme-Inert Conc. g/l .04241 P_d Desired Product Conc. g/l 8.773	ESc_d	Desired Enzyme-Cellulose Conc.		.04058	
ESx_d Desired Enzyme-Inert Conc. g/l .04241 P_d Desired Product Conc. g/l 8.773		Desired Inert Material Conc.		.3076	
P_d Desired Product Conc. g/l 8.773	ESx_d	Desired Enzyme-Inert Conc.		.04241	
		Desired Product Conc.		8.773	
		Desired Enzyme-Cellulose Conc.		.4032	

Table A.1. TABLE OF ADOPTED VALUES WITH NOTATIONS