

On-line maximization of biogas production in an anaerobic reactor using a pseudo-super-twisting controller^{*}

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Abstract: We consider an apparently oversimplified first order model of an anaerobic digester operated as a CSTR, where the dilution rate is the controlled input and the biogas production rate is the measured output. The parameters of this model are considered slowly time-varying. The output function depends on the only state (the substrate), and at any instant has a unique maximum. We propose a simple output-feedback controller based on the super-twisting algorithm combined with a state machine, which converges in a practical sense to this maximum. The controller was tested by simulations of an anaerobic digester, maximizing the biogas production rate, showing very good results.

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1. INTRODUCTION

Anaerobic digestion of biomass is a very complex process involving several types of microorganisms in various linked reactions, from the hydrolysis of complex carbohydrates to the methanization of volatile fatty acids (VFA); additionally, there are also physico-chemical reactions involved (Antonelli et al., 2003). Probably the most used model for describing this complexity in a tractable way is IWA's anaerobic digestion model 1 (ADM1) (Batstone et al., 2002). Although this model is useful for simulation, it is too complicated for designing controllers, since it involves 19 reactions and 24 states, plus some algebraic constraints. However, a simplification that has found applications in the design of controllers is the so-called AM2 model (Bernard et al., 2001). Still, to use it in a model-based controller, calibration of many parameters may be needed (Méndez-Acosta et al., 2010). Furthermore, in these developments the need for on-line measuring some states or estimating them with an observer has sometimes hindered real-life applications.

In this report, we tackle the problem in another way. Instead of designing a controller based on a model and assuming the measurement of critical state variables, we assume a simplified first order model (possibly the simplest one for bioreactors) and consider that an output function is indeed on-line measurable. Very little assumptions are made on the model, but a critical one is that the output function depends on the unique state and has a maximum value defined by a set of parameters that are allowed to

be time-varying. This is general enough to capture the main input-output dynamics of many bioreactors, such as a biogas producing anaerobic digester.

The controller proposed is based on the well known super-twisting controller (STC) (Levant, 1998; Moreno, 2011), which has already been used for bioreactor rate estimation (Lara-Cisneros et al., 2014; Vargas et al., 2014; De Battista et al., 2012). Instead of assuming the measurement of the state and thus building a reference error signal to be used by the controller, we use an approach that uses only the available output measurements. With them we are able to compute an approximation of the absolute value of the error and to use a state-machine that estimates its sign; furthermore, it provides an estimate of a needed parameter, in a similar manner as has previously been done by Moreno et al. (2006). The main result is showing that although we implement a pseudo-super-twisting controller (PSTC) in this sense, we recover the desired properties of the STC in a practical sense. We show its applicability for the AM2 model of anaerobic digestion, maximizing the biogas production rate.

The paper is organized as follows. The next section introduces the AM2 model equations and a proposal about how to view that system as 1-dimensional with time-varying parameters. Section 3 introduces the first part of the PSTC, giving its proof of convergence, followed by a section that complements the design with the state-machine implementation of the error's sign estimator. Section 5 presents and discusses simulation results and finally conclusions are made.

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2. THE ANAEROBIC DIGESTION MODELS

Anaerobic digestion is a complex process, involving several linked reactions, but it has been simplified to a two-reaction four-parameter model, called the AM2 model (Bernard et al., 2001):

$$\dot{X}_1 = \mu_1 X_1 - a X_1 D_{\text{in}}, \quad (1a)$$

$$\dot{S}_1 = -k_{11} \mu_1 X_1 + (S_1^{\text{in}} - S_1) D_{\text{in}}, \quad (1b)$$

$$\dot{X}_2 = \mu_2 X_2 - a X_2 D_{\text{in}}, \quad (1c)$$

$$\dot{S}_2 = k_{12} \mu_1 X_1 - k_{22} \mu_2 X_2 + (S_2^{\text{in}} - S_2) D_{\text{in}}, \quad (1d)$$

$$G = k_G \mu_2 X_2, \quad (1e)$$

with

$$\mu_1(S_1) = \frac{\mu_1^{\text{max}} S_1}{K_{S_1} + S_1}, \quad (1f)$$

$$\mu_2(S_2) = \frac{\mu_2^* S_2^* S_2}{S_2^* S_2 + \beta_2 (S_2^* - S_2)^2}. \quad (1g)$$

Two reactions take place: organic substrate S_1 is consumed by acidogenic bacteria X_1 under Monod kinetics to grow and to produce volatile fatty acids (VFA) S_2 , which in turn are consumed by methanogens X_2 to grow and to produce biogas, mainly methane and carbon dioxide; the reaction is of Haldane type (this is an alternative, but equivalent representation¹). The biogas production rate G is proportional to the growth rate of methanogens. The two types of biomass may be partially fixed and $a \in [0, 1]$ ($a = 1$ represents a perfectly mixed CSTR and $a = 0$ a perfect fixed-mass bioreactor).

The model has three inputs: the dilution rate D_{in} and the two inflow substrate concentrations: S_1^{in} and S_2^{in} , but we consider that only the first one is a manipulated variable, while the latter are perturbations.

The start-up of such a reactor is no easy task, but let us assume that the bioreactor is already at a steady state $\bar{\xi} = [\bar{X}_1, \bar{S}_1, \bar{X}_2, \bar{S}_2]^T$, with input $\bar{u} = \bar{D}_{\text{in}}$ and perturbations \bar{S}_1^{in} and \bar{S}_2^{in} constant. It is known that a steady-state for this process that is neither the washout of methanogens nor acidogens is only achievable for certain values of \bar{u} , and the region of convergence for the coexistence of the two species with this constant input may be relatively small (Sbarcio et al., 2012).

By determining the possible steady states for given values of constant \bar{u} we get can build an input/output steady-state map (\bar{u}, \bar{y}) , considering $y = G$, and find that there is a unique point $(\bar{u}_{\text{opt}}, \bar{y}_{\text{opt}})$ where the biogas production rate is maximal.

¹ For the Monod equation its two parameters have relevant meaning: μ_{max} is the maximal rate as $S \rightarrow \infty$ and K_S is the concentration where $\mu = \mu_{\text{max}}/2$. For the Haldane equation in its usual form as an extension of the Monod equation, i.e.

$$\mu(S) = \frac{\mu_{\text{max}} S}{K_S + S + S^2/K_I}$$

the parameters μ_{max} , K_S and K_I have no direct meaning. Instead this alternative representation uses three relevant parameters: the maximum μ^* , the concentration where this maximum occurs S^* , and $\beta > 0$, which defines the steepness of the curve:

$$S^* = \sqrt{K_S K_I}, \quad \mu^* = \frac{\mu_{\text{max}} \sqrt{K_I}}{2\sqrt{K_S} + \sqrt{K_I}}, \quad \beta = \frac{\sqrt{K_S}}{2\sqrt{K_S} + \sqrt{K_I}}.$$

If the system has been operating for a sufficiently long time with $u(t) \geq 0$, it approaches a 2-dimensional manifold in the \mathbb{R}_+^4 space. To see this, consider writing the system as

$$\dot{X} = M(S)X - aX D_{\text{in}}, \quad X(0) = X_0, \quad (2a)$$

$$\dot{S} = -KM(S)X + (S_{\text{in}} - S)D_{\text{in}}, \quad S(0) = S_0. \quad (2b)$$

with the following definitions:

$$X = \begin{bmatrix} X_1 \\ X_2 \end{bmatrix}, \quad K = \begin{bmatrix} k_{11} & 0 \\ -k_{12} & k_{22} \end{bmatrix}, \quad (2c)$$

$$S = \begin{bmatrix} S_1 \\ S_2 \end{bmatrix}, \quad M(S) = \begin{bmatrix} \mu_1(S_1) & 0 \\ 0 & \mu_2(S_2) \end{bmatrix}. \quad (2d)$$

Let us make the coordinate change

$$Z = KX + S$$

so that

$$\dot{Z} = (-Z + S_{\text{in}} + KX(1 - a)) D_{\text{in}}.$$

If $D_{\text{in}}(t) > 0$, then after some time (e.g. for $t \geq t_s$, where $\int_0^{t_s} D_{\text{in}}(\tau) d\tau = 5$), with $\delta(t)$ a small delay or error,

$$Z(t) = S_{\text{in}} + KX(t)(1 - a) + \delta(t). \quad (3)$$

If we equate this with the definition $Z = KX + S$, then

$$X(t) = \frac{1}{a} K^{-1} (S_{\text{in}} - S(t) + \delta(t)), \quad (4)$$

which we substitute in the differential equation for $S(t)$:

$$\dot{S} = -\frac{1}{a} KM(S)K^{-1} (S_{\text{in}} - S + \delta) + (S_{\text{in}} - S) D_{\text{in}}$$

Since $M(S)$ is diagonal, we notice that

$$KM(S)K^{-1} = \begin{bmatrix} \mu_1(S_1) & 0 \\ (\mu_2(S_2) - \mu_1(S_1))k_3 & \mu_2(S_2) \end{bmatrix}, \quad k_3 = \frac{k_{12}}{k_{11}}$$

has as one of its eigenvalues $\mu_2(S_2)$, with right eigenvector $b^T = [k_3, 1]$, so if we define $S_3 = b^T S = k_3 S_1 + S_2$ we get

$$b^T KM(S)K^{-1} = \mu_2(S_2) b^T$$

and thus $\dot{S}_3 = b^T \dot{S}$ is given by

$$\dot{S}_3 = -\rho(S_3, S_1) + (S_3^{\text{in}} - S_3) D_{\text{in}} \quad (5)$$

where we have defined

$$\rho(S_3, S_1) = \frac{1}{a} \mu_2(S_3 - k_3 S_1) (S_3^{\text{in}} - S_3 + \delta_3), \quad (6a)$$

$$S_3^{\text{in}} = k_3 S_1^{\text{in}} + S_2^{\text{in}}, \quad k_3 = \frac{k_{12}}{k_{11}}, \quad \delta_3 = k_3 \delta_1 + \delta_2. \quad (6b)$$

In fact, S_3 is the total dissolved substrate in the bioreactor, expressed in VFA units. We can view this as a scalar system driven by two inputs: D_{in} , which we can control, and S_1 , which is the state of another scalar system with the same input, namely

$$\dot{S}_1 = -\frac{1}{a} \mu_1(S_1) (S_1^{\text{in}} - S_1 + \delta_1) + (S_1^{\text{in}} - S_1) D_{\text{in}} \quad (7)$$

However, we can view ρ also as a function solely of S_3 with S_1 a time-varying parameter.

From (4), we see that $X_2 = \frac{1}{a k_{22}} (S_3^{\text{in}} - S_3 + \delta_3)$, so the output $G = k_G \mu_2(S_2) X_2$ then can also be written as:

$$G = k_y \rho(S_3), \quad k_y = \frac{k_G}{k_{22}} \quad (8)$$

It is important to notice that indeed $\rho(S_3)$ has a unique maximum for every time-varying ‘‘parameter’’ S_1 ; its domain is defined by $S_3 \geq k_3 S_1$ and its range is bounded in \mathbb{R}_+ . Therefore, we have come up with an alternative representation of the AM2 model, considering only one

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