Parameter Estimation of the Acidogenic Reactor of Two-Stage Anaerobic Digestion ⋆

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Abstract: Based on the models AM2 and AM2HN the dynamics of the hydrolytic-acidogenic bioreactor of a two-stage anaerobic digestion configuration, an online parameter indentifier based on recursive linear least squares is presented and discussed.

Keywords: acidogenesis, anaerobic digestion, parameter estimation, AM2HN, HAM2.

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1. INTRODUCTION

Anaerobic Digestion (AD) is a process where different microorganisms work in order to metabolize organic subtrates. It has successfully been employed to remediate wastewater, sewage sludge, municipal and agricultural solid wastes such as animal manures, while generating renewable energy resources (Nguyen et al., 2015). The major advantages include low energy consumption, less sludge yield, the biomass can remain for a long time without losing its metabolic activity, the ability to stabilize diverse organic wastes with production of renewable energy by the production of biogas, and operational low costs since it does not utilize fossil fuels (Nguyen et al., 2015; Bernard et al., 2001).

Despite the advantages, keeping an optimum operational and stable AD process is highly difficult because it involves biological and biochemical interrelated reactions with diverse microbial communities (Hassam et al., 2015). The principal steps that occur in AD are: hydrolysis, acidogenesis, acetogenesis, and methanogenesis.

For this work we analyze a two-stage anaerobic digestion (TSAD) process, since it has been reported that this configuration has shown improvements over the process. In this configuration, the AD is physically separated in two bioreactors with two different microbial communities based on pH selectivity, as illustrated in Fig 1. This approach increases growth rates, consumes higher organic loads, uses low start-up times, generates high-purity biogas and improves process stability. In the first phase the hydrolysis and acidogenesis of the feeded substrate occur, generating an effluent rich in volatile fatty acids (VFA), which is fed to the second phase, where the methanogenesis occurs and methane-rich biogas is produced. This separation allows a better control of the process (Donoso-Bravo et al., 2011).

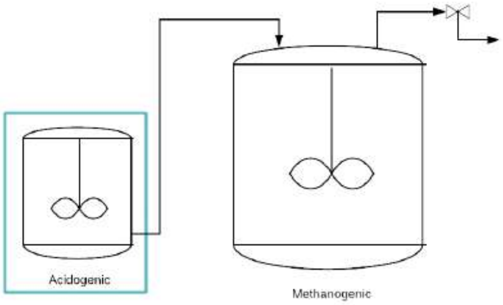

Fig. 1. Two-stage Anaerobic Digestion Diagram

Mathematical models have demonstrated to be proper tools for different purposes. However, modeling biochemical processes is a delicate exercise. The quality of the model and its structure must correspond to the objective for which the model was built (Dochain, 2008). Thus, the model could be used to: reproduce and predict the behavior of a system; help in understanding the mechanisms of the studied system; estimate variables which are not measured; estimate parameters of the process; develop control strategies; select correct optimization of operational conditions, among others (Nguyen et al., 2015; Dochain, 2008).

Through the years several authors have developed different mathematical models for AD, but their use by engineers, process technology providers and operators has been very limited because of the wide variety of models available and their very specific nature. For those reasons, the Anaerobic Digestion Model 1 (ADM1) was developed as a generic model by the International Water Associa-

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tion (IWA) (Batstone et al., 2002). This model is highly complex, since it considers 32 dynamic state variables and other physico-chemical processes. Therefore, it is complicated to carry out a mathematical analysis of the model to propose operation and control strategies. In consequence, several simplified models have been developed, some of them based on the ADM1. The model used in this work is an alternative simplified model, based on the one proposed by Hassam et al. (2015) with modifications that are explained later.

It is important to keep the optimum operation point in each bioreactor, but it is also important to analyze each one individually. This work focuses only in the acidogenic bioreactor, where the hydrolysis and the acidogenesis stages take place. The principal reason to choose this bioreactor is that hydrolysis is a limiting phase for the process (Bajpai, 2017); thus it is also a critical phase for all the process, and hence a bad control in the acidogenic reactor may carry on to several problems in the influent of the methanogenic bioreactor.

The purpose of this work is to verify if it is possible to estimate parameters by the recursive least squares regression method, that is an online method by measuring some of the states of an underlying simplified mathematical model of the hydrolytic-acidogenic process.

2. MATHEMATICAL MODEL DESCRIPTION

2.1 Assumptions

As several authors have taken into account (Donoso-Bravo et al., 2011; Hassam et al., 2015; Bernard et al., 2001), the variables are measured on a Chemical Oxygen Demand (COD) basis.

One simplification is that compounds are grouped in several generic macromolecules: the S_0 is equal to the sum of carbohydrates, proteins, and lipids; the S_1 is the sum of aminoacids, monosaccharides and fatty acids; and the S_2 is equal to the sum of valerate, butyrate, propionate, and acetate (Hassam et al., 2015). Despite the fact that each VFA (Volatile Fatty Acids) has its own degradation rate, a global variable grouping all the VFA (S_2) is more commonly reported in real applications (Bernard et al., 2001).

On the other hand, ammonia, a compound produced in the acidogenesis of aminoacids, was not considered since experimentally is has been observed that very low concentrations of ammonia are produced. Also, in the acidogenic reactor very little production of biogas has been observed, both of CO_2 and H_2, and for this reason the biogases are not yet included in the model.

2.2 Model description

The chosen model is based on the simplified model proposed by Bernard et al. (2001), known as AM2, which, years later, was adjusted by Hassam et al. (2015), who added the hydrolysis with a first order reaction rate. This change is quite convenient for our work since we work with winery wastewater, which brings a significant amount of particulate substrate (S_0). The adjustment in the model of Hassam et al. (2015) showed results comparable to the ADM1 model in simulations. Nevertheless, in the case where the hydrolysis is the limiting reaction (as in our case), the first order rate can be a problem. For that reason, we also considered the work of Donoso-Bravo et al. (2011), where they use a Contois kinetic rate for hydrolysis. This model explains better the hydrolysis phenomena since it takes both the substrate and the biomass concentrations into account (Donoso-Bravo et al., 2011). Those considerations were made in order to be able to represent in a better way the behavior of the real system.

Thus, for the acidogenic reactor, this model involves two reactions and one bacterial population (acidogenic bacteria, X_1). In the first reaction, the acidogenic bacteria (X_1) hydrolyzes the particulate organic matter (S_0) into soluble compounds (S_1). Afterwards, the same bacteria population, X_1, consumes the soluble substrate (S_1) and produces VFA (S_2). The biological reactions are as follows (Hassam et al., 2015):

$$S_0 \overset{\rho_0}{\to} X_1 + k_1 S_1, \tag{1}$$

$$k_1 S_1 \overset{\mu_1}{\to} X_1 + k_2 S_2, \tag{2}$$

where k_i are stoichiometric coefficients, also referred as yield coefficients. The hydrolysis rate ρ_0 is of Contois type, whereas the acidogenic reaction is decribed by a Monod law. It is important to note that the total COD is composed of S_1 and S_2 (Bernard et al., 2001).

The mass balance for each state variable (ξ) in the liquid phase is shown in Eq. (3). This equation is valid for the acidogenic reactor. The differences between each state are the input conditions and the value of the parameters (Mogens et al., 2000).

$$\dot{\xi_i} = D(\xi_{in,i} - \xi_i) + \sum_{j=1}^{m} a_{i,j} r_j \tag{3}$$

$$Acumulation = (Input - Output) + Reaction$$

The right-side term of Eq. (3) represents the sum of the input, output and the kinetic rate expressions, described by the multiplication of their stoichiometric coefficient ($a_{i,j}$) and the reaction rate (r_j) (Donoso-Bravo et al., 2011).

For better understanding, the kinetic rate expressions and coefficients are shown in the Petersen matrix on Table 1. The biological processes occuring in the system are listed in the leftmost column of the matrix (hydrolysis, acidogenesis, and decay of X_1). The index j is assigned to each process. The kinectic rate equations for each process are recorded in the rightmost column of the matrix. Last, the elements within the matrix comprise the stoichiometric coefficients (Mogens et al., 2000).

Table 1. Petersen matrix

	State Variable ($i \rightarrow$)				
Process ($j \downarrow$)	S_0	S_1	S_2	X_1	**Kinetic Rate**
Hydrolysis	-1	1			$\rho_0(S_0,X_1)$
Acidogenesis		-k_1	k_2	1	$\mu_1(S_1) \cdot X_1$
Decay of X_1				-1	$k_{d1} \cdot X1$

Based on the mass balance described previously, the following differential equations describe the four state variables of the system:

$$\dot{S_0} = (S_0^{in} - S_0)D - \rho_0(S_0, X_1) \tag{4}$$
$$\dot{S_1} = (S_1^{in} - S_1)D - k_1\mu_1(S_1)X_1 + \rho_0(S_0, X_1) \tag{5}$$
$$\dot{S_2} = (S_2^{in} - S_2)D + k_2\mu_1(S_1)X_1 \tag{6}$$
$$\dot{X_1} = -X_1\alpha D + (\mu_1(S_1) - k_{d1})X_1 \tag{7}$$

where the subscript "in" refers to influent concentrations. The parameter α was introduced by the authors to model biomass retention: $\alpha = 0$ corresponds to an ideal fixed-bed reactor while $\alpha = 1$ corresponds to an ideal reactor with no biomass retention (Hassam et al., 2015; Vargas and Sepúlveda-Gálvez, 2018).

2.3 Kinetics growth models

The modeling of biological kinetics is a difficult task. For effects of this work the following models for bacterial kinetics were considered:

Contois type Contois kinetics better explains the hydrolysis phenomena since it takes both the substrate and biomass concentrations into account (Donoso-Bravo et al., 2011):

$$\rho_0(S_0, X_1) = \frac{k_{hyd}S_0X_1}{X_1 + S_0/K_T} = f_1 \tag{8}$$

where k_{hyd} is the hydrolysis degradation rate and K_T is the Contois affinity constant.

Monod type It is considered Monod-type kinetics for the growth of acidogenic bacteria (Donoso-Bravo et al., 2011; Hassam et al., 2015):

$$\mu_1(S_1) = \frac{\mu^* S_1}{K_{S1} + S_1} = f_2 \tag{9}$$

where μ^* is the maximum bacterial specific growth rate, and K_{S1} is the half-saturation constant associated with the substrate S_1.

3. PARAMETRIC MODEL

Parameter-estimation can be formulated as an optimization problem. There exists a large number of different identification methods available; however, it is true that there is no universally best method. One broad distinction is between on-line and off-line methods. For this work it is used the classic least-squares method (LSM), which is an on-line method that can be used to identify parameters in dynamic systems. The on-line methods give estimates recursively as the measurements are obtained and it is an alternative to use for adaptive controllers or if the process is time-varying, which is the case of our model (Aström and Wittenmark, 1997).

In the LSM it is assumed that the calculated variable, y, is given by the following model

$$y = \theta_1\Phi_1^T(x) + \theta_2\Phi_2^T(x) + ... + \theta_n\Phi_n^T(x) \tag{10}$$

where φ_i are known functions and θ_i are unknown parameters. In order to be able to give an analytic solution, the model must be a linear function of the unknown parameters.

3.1 Linearization

At the equations (8) and (9), it is observed that K_T and K_{S1} appear as non-linear parameters. In order to obtain an estimation of a linear parametric model we take a Taylor expansion of $\rho_0(S_0, X_1)$ about K_T at the estimate $\hat{K}_T$ and $\mu_1(S_1)$ about K_{S1} at the estimate $\hat{K}_{S1}$, which yields:

$$\begin{aligned}
\rho_0(S_0, X_1) &\approx f_1(\hat{K}_T) + \frac{\partial f_1(\hat{K}_T)}{\partial K_T}K_T - \hat{K}_T) \\
&\approx \frac{(k_{hyd}\hat{K}_T^2X_1^2S_0) + (K_Tk_{hyd}X_1S_0^2)}{(X_1\hat{K}_T + S_0)^2} \\
&\approx \frac{(k_{hyd})\hat{K}_T^2X_1^2S_0}{(X_1\hat{K}_T + S_0)^2} + \frac{(K_Tk_{hyd})X_1S_0^2}{(X_1\hat{K}_T + S_0)^2}
\end{aligned} \tag{11}$$

$$\begin{aligned}
\mu_1(S_1) &\approx f_2(\hat{K}_{S1}) + \frac{\partial f_2(\hat{K}_{S1})}{\partial K_{S1}}(K_{S1} - \hat{K}_{S1}) \\
&\approx \frac{\mu^* S_1(2\hat{K}_{S1} + S_1)}{(\hat{K}_{S1} + S_1)^2} - \frac{\mu^* K_{S1}S_1}{(\hat{K}_{S1} + S_1)^2}
\end{aligned} \tag{12}$$

Now, the system is linear in the unknown parameters, but noting that $\hat{K}_T$ and $\hat{K}_{S1}$ are estimates of those parameters. Substituting Eq. (11) into Eqs. (4) and (5) and substituting Eq. (12) into Eqs. (5), (6), and (7) yields the following:

$$\dot{S_0} = (S_0^{in} - S_0)D - \frac{(k_{hyd})\hat{K}_T^2X_1^2S_0}{(X_1\hat{K}_T + S_0)^2} - \frac{(K_Tk_{hyd})X_1S_0^2}{(X_1\hat{K}_T + S_0)^2} \tag{13}$$

$$\begin{aligned}
\dot{S_1} = (S_1^{in} - S_1)D &- \frac{\mu^* k_1X_1S_1(2\hat{K}_{S1} + S_1)}{(\hat{K}_{S1} + S_1)^2} + \frac{\mu^* k_1K_{S1}X_1S_1}{(\hat{K}_{S1} + S_1)^2} \\
&+ \frac{(k_{hyd})\hat{K}_T^2X_1^2S_0}{(X_1\hat{K}_T + S_0)^2} + \frac{(K_Tk_{hyd})X_1S_0^2}{(X_1\hat{K}_T + S_0)^2}
\end{aligned} \tag{14}$$

$$\dot{S_2} = (S_2^{in} - S_2)D + \frac{k_2\mu^* X_1S_1(2\hat{K}_{S1} + S_1)}{(\hat{K}_{S1} + S_1)^2} - \frac{k_2\mu^* K_{S1}X_1S_1}{(\hat{K}_{S1} + S_1)^2} \tag{15}$$

$$\dot{X_1} = -\alpha X_1D + \frac{\mu^* X_1S_1(2\hat{K}_{S1} + S_1)}{(\hat{K}_{S1} + S_1)^2} - \frac{\mu^* K_{S1}X_1S_1}{(\hat{K}_{S1} + S_1)^2} - k_{d1}X_1 \tag{16}$$

3.2 Parametric estimation

We use Eqs. (13), (14), (15), and (16) for the parametric model in our identifier design. Now, the four equations are linear in some parameters that are combinations of k_{hyd}, K_T, k_1, μ^*, K_{S1}, k_{d1}, k_2.

However, the model involves derivative signals $\dot{S_0}$, $\dot{S_1}$, $\dot{S_2}$, and $\dot{X_1}$. Filtering those differential equations with stable first order low-pass filters of the form $\frac{\lambda}{s+\lambda}$ creates a suitable parametric model for identification. After filtering, the following parametric model for the four state variables is obtained:

$$\begin{aligned}
\frac{\lambda s}{s + \lambda}S_0 = \frac{\lambda}{s + \lambda}(S_0^{in} - S_0)D &- k_{hyd}\frac{\lambda}{s + \lambda}\frac{S_0\hat{K}_T^2X_1^2}{(X_1\hat{K}_T + S_0)^2} \\
&- k_{hyd}K_T\frac{\lambda}{s + \lambda}\frac{S_0^2X_1}{(X_1\hat{K}_T + S_0)^2}
\end{aligned} \tag{17}$$

$$\frac{\lambda s}{s+\lambda}S_1 = \frac{\lambda}{s+\lambda}(S_1^{in} - S_1)D - k_1\mu^* \frac{\lambda}{s+\lambda}\frac{X_1 S_1(2\hat{K}_{S1} + S1)}{(\hat{K}_{S1} + S_1)^2} + k_1\mu^* K_{S1}\frac{\lambda}{s+\lambda}\frac{X_1 S_1}{(\hat{K}_{S1} + S_1)^2} + k_{hyd}\frac{\lambda}{s+\lambda}\frac{\hat{K}_T^2 X_1^2 S_0}{(X_1\hat{K}_T + S_0)^2} + k_{hyd}K_T\frac{\lambda}{s+\lambda}\frac{S_0^2 X_1}{(X_1\hat{K}_T + S_0)^2} \tag{18}$$

$$\frac{\lambda s}{s+\lambda}X_1 = -\frac{\lambda}{s+\lambda}\alpha X_1 D + \mu^* \frac{\lambda}{s+\lambda}\frac{X_1 S_1(2\hat{K}_{S1} + S_1)}{(\hat{K}_{S1} + S_1)^2} - \mu^* K_{S1}\frac{\lambda}{s+\lambda}\frac{S_1 X_1}{(\hat{K}_{S1} + S_1)^2} - k_{d1}\frac{\lambda}{s+\lambda}X_1 \tag{19}$$

$$\frac{\lambda s}{s+\lambda}S_2 = \frac{\lambda}{s+\lambda}(S_2^{in} - S_2)D + k_2\mu^* \frac{\lambda}{s+\lambda}\frac{S_1 X_1(2\hat{K}_{S1} + S_1)}{(\hat{K}_{S1} + S_1)^2} - k_2\mu^* K_{S1}\frac{\lambda}{s+\lambda}\frac{S_1 X_1}{(\hat{K}_{S1} + S_1)^2} \tag{20}$$

3.3 Identifier Design

The parameter identification is now separated into one nine-dimensional identification problem. From the equation (17) we estimate $k_{hyd}K_T$ and k_{hyd}. From Eq. (18) we estimate the parameters $k_{hyd}K_T$, k_{hyd}, $k_1\mu^*$, and $k_1\mu^* K_{S1}$. From equation (19) we estimate the parameters μ^*, $\mu^* K_{S1}$, and k_{d1} and finally from the equation (20) we estimate the parameters k_2, and $k_2\mu^* K_{S1}$. Thus, the parameter vector is

$$\theta = \begin{bmatrix} k_{hyd} \\ k_{hyd}K_T \\ k_1\mu^* \\ k_1\mu^* K_{S1} \\ \mu^* \\ \mu^* K_{S1} \\ k_{d1} \\ k_2\mu^* \\ k_2\mu^* K_{S1} \end{bmatrix} = \begin{bmatrix} \theta_1 \\ \theta_2 \\ \theta_3 \\ \theta_4 \\ \theta_5 \\ \theta_6 \\ \theta_7 \\ \theta_8 \\ \theta_9 \end{bmatrix} \tag{21}$$

The regressor matrix Φ^T is defined as follows:

$$\Phi^T = \frac{\lambda}{s+\lambda}\begin{bmatrix} \Phi_1^T & 0 \\ 0 & \Phi_2^T \end{bmatrix} \tag{22}$$

where

$$\Phi_1 = \begin{bmatrix} -\frac{\hat{K}_T^2 X_1 S_0}{(X_1\hat{K}_T + S_0)^2} & -\frac{X_1 S_0^2}{(X_1\hat{K}_T + S_0)^2} \\ \frac{\hat{K}_T^2 X_1 S_0}{(X_1\hat{K}_T + S_0)^2} & \frac{X_1 S_0^2}{(X_1\hat{K}_T + S_0)^2} \\ 0 & -\frac{X_1 S_1(2\hat{K}_{S1} + S_1)}{(\hat{K}_{S1} + S_1)^2} \\ 0 & \frac{X_1 S_1}{(\hat{K}_{S1} + S_1)^2} \end{bmatrix} \tag{23}$$

$$\Phi_2 = \begin{bmatrix} \frac{X_1 S_1(2\hat{K}_{S1} + S_1)}{(\hat{K}_{S1} + S_1)^2} & 0 \\ -\frac{X_1 S_1}{(\hat{K}_{S1} + S_1)^2} & 0 \\ -X_1 & 0 \\ 0 & \frac{X_1 S_1(2\hat{K}_{S1} + S_1)}{(\hat{K}_{S1} + S_1)^2} \\ 0 & -\frac{X_1 S_1}{(\hat{K}_{S1} + S_1)^2} \end{bmatrix} \tag{24}$$

As it was defined in (10), the parameterization is given by the product of the regressor and the unknown parameter vector; therefore, it can be written as follows

$$y = \Phi^T\theta \tag{25}$$

with

$$y = \frac{\lambda s}{s+\lambda}\begin{bmatrix} S_0 \\ S_1 \\ X_1 \\ S_2 \end{bmatrix} - \frac{\lambda}{s+\lambda}\begin{bmatrix} (S_0^{in} - S_0)D \\ (S_1^{in} - S_1)D \\ -\alpha X_1 D \\ (S_2^{in} - S_2)D \end{bmatrix} \tag{26}$$

In order to estimate values of the unknown parameters, we use the recursive least-squares algorithm as follows:

$$\dot{\hat{\theta}} = -P\Phi\varepsilon \tag{27}$$

$$\dot{P} = -P\Phi\Phi^T P \tag{28}$$

$$\varepsilon = \hat{y} - y \tag{29}$$

$$\hat{y} = \Phi^T\hat{\theta} \tag{30}$$

$$\hat{\theta}(0) = \hat{\theta}_0 \tag{31}$$

$$P(0) = I \tag{32}$$

4. SIMULATIONS

The process was simulated in the software Matlab with the Simulink tool. For the simulation, the parameters were taken from those reported by Bernard et al. (2001), Hassam et al. (2015) and Donoso-Bravo et al. (2011), while the initial conditions are real measurements taken in the laboratory using winery wastewater influent. It is important to mention that the parameters were taken mainly from Bernard et al. (2001) because the influent used in this work was also winery wastewater. The parameters used are those shown in Table 2, while the corresponding 9 parameter values are shown on Table 3.

Table 2. Experimental Parameters

Sym	Units	Reference
k_{hyd}	$0.12\ d^{-1}$	Donoso-Bravo et al. (2011)
K_T	$1.5\ \frac{kgCODs}{kgCODx}$	Donoso-Bravo et al. (2011)
k_1	42.14	Bernard et al. (2001)
μ^*	$1.2\ d^{-1}$	Bernard et al. (2001)
K_{S1}	$7.1 kgm^{-3}$	Bernard et al. (2001)
k_{d1}	$0.033\ d^{-1}$	Hassam et al. (2015)
k_2	$116.5\ molkg^{-1}$	Bernard et al. (2001)

Table 3. Reference Parameters

Parameter		Exp. Value	Unit
θ_1	k_{hyd}	0.12	d^{-1}
θ_2	$k_{hyd}K_T$	0.18	$\frac{kgCODs}{kgCODx}d^{-1}$
θ_3	$k_1\mu^*$	50.58	d^{-1}
θ_4	$k_1\mu^* K_{S1}$	359.03	$kg\,m^{-3}d^{-1}$
θ_5	μ^*	1.2	d^{-1}
θ_6	$\mu^* K_{S1}$	8.52	$kg\,m^{-3}d^{-1}$
θ_7	k_{d1}	0.033	d^{-1}
θ_8	$k_2\mu^*$	139.8	$mol\,kg^{-1}d^{-1}$
θ_9	$k_2\mu^* K_{S1}$	992.58	$mol\,m^{-3}d^{-1}$

In the simulation, the recursive least-squares algorithm was implemented. Several simulations with different conditions were performed, but here only two are presented: the first one was run with values near to zeros as initial conditions, shown in Figure 2; the second one with initial values close to the experimental values, shown in Figure 3. On the other hand, Figure 4 shows the evolution of the state variables.

The first graph of Figure 4 has an acceptable prediction of how S_2 is produced as S_1 is up-taken and it can be observed that the biomass is stable, just as expected in the real process. The behavior of the states is according to a real dilution rate in a laboratory acidogenic reactor ($1\ d^{-1}$).

For the estimated parameters, we can notice several results: applying the LSM, it is observed that most of

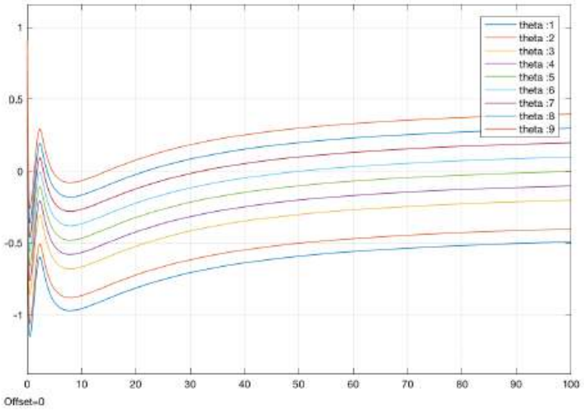

Fig. 2. Estimation with parameters starting near to zeros.

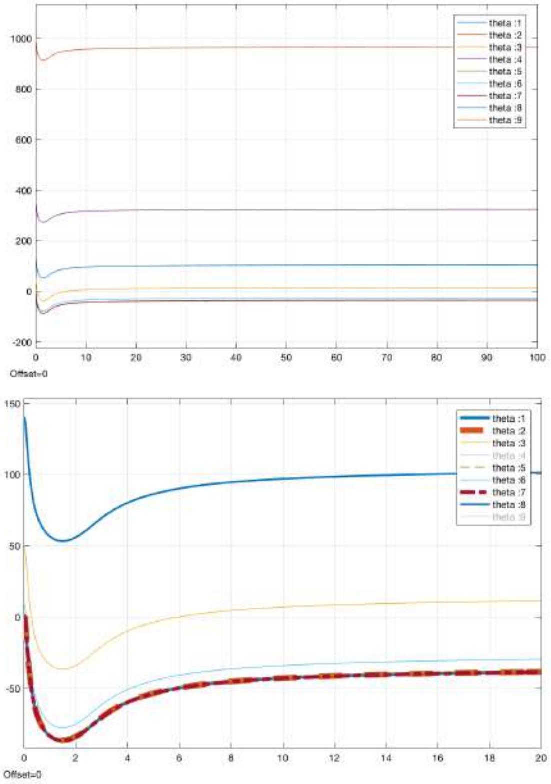

Fig. 3. Estimation with parameters starting close to reference values

them do not converge neither to a value nor to the experimental parameters, when the initial guess of the parameters is far from the true values (in this case all near to zero). This is expected because we have used a linearization to perform the estimation. In contrast, Figure 3 shows the convergence of the algorithm, at least for some of the parameters, which shows the applicability of the procedure.

Another weakness of applying this parameter identification technique is that it is necessary to measure all the state variables on-line. Nowadays this is difficult to do because equipment does not yet exist or is too expensive. Nevertheless, with the recent development of some equipments and current researches, some variables may be measured indirectly, so it can be a good option in a short future, or another option would be to use an observer or estimator.

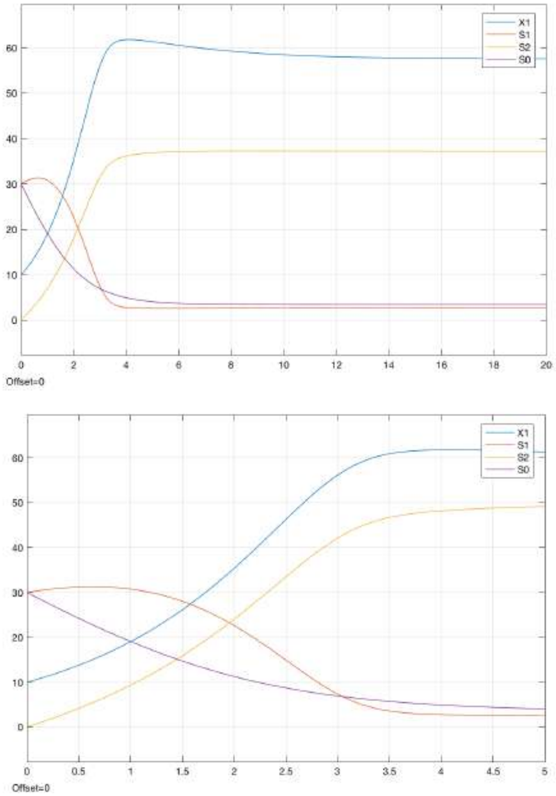

Fig. 4. State Variables. Simulations with different dilution rates.

On the other hand, for biological systems such as the one studied, this method could be important to make the estimation in real time because in these systems the parameters are expected to change in the time, and it is shown how the least squares estimate can be obtained recursively. The method could then also be an option for future applications with adaptive controllers for the biological systems.

5. CONCLUSIONS

For a system model that represents the dynamics of the acidogenic bioreactor in a two-stage anaerobic digestion system, the well-known recursive least squares parameter estimation technique was developed and tested in simulations. The results are encouraging and may allow an on-line estimation of critical process parameters, provided that the state is continually measured. This may well be the basis for future applications in process control of this type of systems.

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Table 4. Nomenclature

AD	Anaerobic Digestion
VFA	Volatile Fatty Acids
TSAD	Two-stage AD
COD	Chemical Oxygen Demand
X_1	Acidogenic bacteria
S_0	Particulate organic matter
S_1	Soluble compounds concentration
S_2	Concentration of VFA
ρ_0	Contois kinetic rate
μ_1	Monod kinetic rate
D	dilution rate coefficient

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