Biochemical Engineering Journal 128 (2017) 63–75

Contents lists available at ScienceDirect

Biochemical Engineering Journal

journal homepage: www.elsevier.com/locate/bej

Regular article

Model predictive control with on-line model identification for anaerobic digestion processes

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ARTICLE INFO

Article history:
Received 26 December 2016
Received in revised form 20 July 2017
Accepted 6 August 2017
Available online 12 September 2017

Keywords:
Anaerobic digestion process
Model predictive control
Model reduction
State estimation
Optimal control

ABSTRACT

This paper presents a nonlinear model predictive control approach for the anaerobic digestion process. A new model reduction strategy with estimation of the model parameters is proposed for the anaerobic digestion process. The reduced model is then used to predict future plant states in the nonlinear model predictive control. We develop a terminal feasible set to constrain terminal states in the prediction horizon, such that the controlled process beyond the horizon lies within a stable region and the predictive controller is recursively feasible. In addition, to make the predictive controller more practical, we design a predictive control algorithm that explicitly considers the influence of process disturbances and satisfies given constraints. Numerical simulations on the benchmark model ADM1 demonstrate the performance of the proposed method.

1. Introduction

Anaerobic digestion (AD) process has been extensively studied for wastewater treatment and bio-energy production due to its ability of transforming the organic waste or energy crops into biogas in the absence of oxygen [1]. The anaerobic conversion of organic matter is a complex bio-chemical process involving numerous bacterial populations, which makes the process nonlinear and uncertain, therefore, hard to predict and control. For this reason, the design, analysis, and control of anaerobic systems have attracted a considerable amount of attention over decades.

As a basis for designing and controlling the AD process, many kinetic models have been developed and studied to improve the process stability and reduce the operational cost [2–8]. Among these models, Anaerobic Digestion Model No. 1 (ADM1) [6] is a very general mathematical model applicable for a lot of kinetics. It includes 19 bioconversion processes and describes the dynamics of 24 model components. Due to its generality and flexibility, ADM1 has became a common platform for anaerobic process modeling and simulation. However, ADM1 describes in detail the main dynamics involved in the AD process and may not be appropriate for control purposes under limited computational resources. In such cases, a simplified model that covers main dynamical characteristics is preferred. Among many simplified models, the one proposed by Bernard [5] (AM2) is widely used. AM2 contains two reaction dynamics (the acidogenesis step and the methanogenesis step) and 6 state variables (acidogenic bacteria, methanogenic bacteria, organic substrate, volatile fatty acids, inorganic carbon, and total alkalinity). The growth of acidogens is assumed to follow Monod kinetics and the growth of methanogens is assumed to follow Haldane kinetics. García-Diéguez [9] proposed another reduction methodology for control and supervision purposes. The number of reactions was determined by a principal component analysis (PCA) technique. More recently, Hassam [10] proposed a modified version AM2HN of AM2. The modification includes relevant processes including hydrolysis and the concomitant release of ammoniacal nitrogen. However, the kinetic parameters in these reduced models are actually varying drastically because of their abstraction of many complex reaction dynamics. The difficulty in effectively determining values of these parameters hinders the use of these models in control applications. This motivates us to improve the modeling strategy and develop on-line parameter estimation methods. An improved reduced model is proposed in this paper where all the states and many parameters can be estimated by Kalman filter on-line. The maximum substrate degradation rates are defined as state variables to be estimated rather than the biomass concentrations which could not be measured. Moreover, like in ADM1, we define the process rates as substrate degradation rates which enables on-line estimation of kinetic parameters.

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http://dx.doi.org/10.1016/j.bej.2017.08.004
1369-703X/

Control is essential to achieve the required treatment efficiency of AD plants and a considerable amount of effort has been devoted to monitoring and control of the AD process in recent years. A traditional proportional-integral (PI) feedback controller, where the effluent chemical oxygen demand (COD) concentration and the dilution rate are taken respectively as the regulation and the manipulation variable, is presented by Alcaraz-González [11]. Many researchers have developed adaptive control strategies to account for the nonlinearities of the AD process [12–17]. However, such strategies often require complete knowledge of the system, which can be difficult to obtain when dealing with bioprocesses such as AD plants where the parameters of system can change greatly over time. To overcome this problem, robust and rule based expert approaches have been proposed [18–22]. Garcia [23] proposed a fuzzy logic-based system for diagnosis and control of AD process where intermediate/total alkalinity ratio was selected for organic overload identification. However, its performance is strongly dependent on the expertise of operators and phenomenological information, which makes it difficult to apply to different types of wastewater.

With the development of numerical computing technology, nonlinear model predictive control (NMPC) has become an attractive control scheme for nonlinear systems [24–26]. A few studies can be observed in the literature where NMPC has been used to control the AD process [27–30]. However, the structural complexity and poor measurability of the AD process still present a barrier to apply NMPC strategy for its ideal operation.

In this work we propose NMPC algorithms for the AD process based on the reduced model whose parameters are identified online. The control problems are formulated to reflex the control objective including a requirement on the process stability. A terminal feasible set is developed to constrain terminal states, such that the controlled process beyond the prediction horizon lies within its stable region and the predictive controller is recursively feasible. In addition, to make the predictive controller more practical, we design an NMPC that explicitly considers the influence of process disturbances and satisfies given constraints. Numerical simulations on the benchmark model ADM1 demonstrate the performance of the proposed predictive control method.

This paper is organized as follows: In Sections 2 and 3 we describe process modeling and state estimation methods. The design of two NMPC controllers based on the proposed reduced model is described in Section 4. In Section 5 the effectiveness of the proposed methods is validated by simulations.

2. Modeling the AD process

2.1. Preliminary results on AM2 model

The AM2 model [5] has been widely used for monitoring and control purpose, due to its simplicity and capability to represent the dynamics of various AD reactors. Assuming that the reactor is an ideal continuous stirred tank reactor (CSTR), the mass balance for the six state variables in the AM2 can be described by the following differential equations:

$$\frac{dX_1}{dt} = (\mu_1(S_1) - D)X_1 \tag{1}$$

$$\frac{dX_2}{dt} = (\mu_2(S_2) - D)X_2 \tag{2}$$

$$\frac{dS_1}{dt} = D(S_{1,in} - S_1) - k_{S_1,1}\mu_1(S_1)X_1 \tag{3}$$

$$\frac{dS_2}{dt} = D(S_{2,in} - S_2) + k_{S_2,1}\mu_1(S_1)X_1 - k_{S_2,2}\mu_2(S_2)X_2 \tag{4}$$

$$\frac{dZ}{dt} = D(Z_{in} - Z) \tag{5}$$

$$\frac{dC}{dt} = D(C_{in} - C) - q_c + k_{C,1}\mu_1(S_1)X_1 + k_{C,2}\mu_2(S_2)X_2 \tag{6}$$

$$q_M = k_{ch4}\mu_2(S_2)X_2 \tag{7}$$

where X_1, X_2, S_1, S_2, Z, C denote, respectively, the concentrations of acidogenic bacteria ($kgCOD\,m^{-3}$), methanogenic bacteria ($kgCOD\,m^{-3}$), primary organic substrate ($kgCOD\,m^{-3}$), volatile fatty acids (VFA, $kmol\,m^{-3}$), total alkalinity ($kmol\,m^{-3}$), and total inorganic carbon ($kmol\,m^{-3}$). D is the dilution rate (d^{-1}), q_c and q_M are the molar flow rate of CO_2 and CH_4. $k_{S_1,1}$, $k_{S_2,1}$, $k_{S_2,2}$, $k_{C,1}$, $k_{C,2}$, k_{ch4} are constant yield coefficients. The subscript *in* denotes the influent concentrations of each component. The bacterial growth rate of the acidogenic bacteria is of the Monod type, whereas Haldanes kinetics describes the methanogenic bacterial growth rate, which takes into account the inhibitory effects of VFA accumulation, i.e.,

$$\mu_1(S_1) = \mu_{1,\max}\left(\frac{S_1}{S_1 + K_{S1}}\right) \tag{8}$$

$$\mu_2(S_2) = \mu_{2,\max}\left(\frac{S_2}{S_2 + K_{S2} + (S_2/K_{I2})^2}\right) \tag{9}$$

where $\mu_{1,\max}$ (d^{-1}), $\mu_{2,\max}$ (d^{-1}), K_{S1}($kgCOD\,m^{-3}$), and K_{S2}($kmol\,m^{-3}$) are the maximum bacteria growth rates, half-saturation constants associated to S_1, S_2, respectively. K_{I2}($kmol\,m^{-3}$) is the inhibition constants associated to S_2. While AM2 is successful in characterizing the nonlinear dynamics of AD processes, the changing nature of its parameters brings difficulty with the model prediction and performance optimization in NMPC. We will discuss this further in the next section and propose a simplified model more suitable for NMPC.

2.2. Model reformulation

Because a large variation of the parameters in AM2 is unavoidable over the process, the on-line estimation of the model parameters, especially the kinetic parameters, is often necessary. The inefficiency of AM2 for NMPC mainly comes from the fact that some of its parameters are unable to be measured in a real-time fashion. In the following, we analyze this problem and introduce our reformulation approach.

(i) Redefine process rates as the substrate uptake rates.
The mass balance equation of AM2 is based on the bacteria growth rates. However, the growth rates may not be known precisely since the individual bacteria concentration is unable to be reliably measured, especially in the solid digestion reactors. By defining the process rates as the substrate uptake rates, the yield coefficients $k_{S_1,1}$, and k_{S_2}, 2 are fixed as -1. Meanwhile, it is known that the methane and the primary organic substrate (COD) are not produced by acidogenic and methanogenic processes, respectively. Therefore, these yield coefficients can be fixed such that the identification procedure [31] can be implemented.

(ii) Introduce the maximum substrate degradation rates as state variables.
The maximum substrate degradation rate corresponds to the multiplication of maximum specific uptake rate and biomass concentration.

(iii) Consider ammonium's contribution to the alkalinity of the solution.
In AM2, it is assumed that the total alkalinity is not affected by process rates. This assumption provides a good approximation of alkalinity when treating substrate does not contain protein or amino acids. However, as the substrate in the