MODELING AND IDENTIFICATION OF HYBRID DYNAMIC SYSTEM IN MICROBIAL CONTINUOUS FERMENTATION

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Abstract. In this paper, a hybrid dynamic model using fuzzy expert system is investigated in the process of glycerol bioconversion to 1,3-PD by Klebsiella pneumoniae (K. pneumoniae). In continuous culture, we assume that 1,3-PD passes the cell membrane of K. pneumoniae by passive diffusion coupling with active transport. To determine the parameters of the proposed system, a parameter identification model is established according to the biological robustness. An optimization algorithm is developed in order to solve the identification model. Numerical simulations indicate that proposed hybrid model adding fuzzy system is more appropriate and the optimization algorithm is effective.

1. Introduction. 1,3-Propanediol (1,3-PD) is an important chemical product which has numerous applications in medicines, cosmetics, lubricants, food and polymers, and its microbial production is recently paid attention to in the world for its low cost, high production and no pollution, etc.\cite{1-4} Glycerol is a low-cost renewable resource appearing in increasing microbial quantities of 1,3-PD, and glycerol bioconversion to 1,3-PD by K. pneumoniae has been widely investigated since the 1980s due to its high productivity\cite{5-7}.

The kinetics models of glycerol bioconversion to 1,3-PD are mainly based on non-structural model. So far, a lot of work had been done to study the fermentation process of producing 1,3-PD by mathematical models, explaining all kinds of phenomena in the fermentation process and realizing the optimal control. Moreover, in 2008, Y. Sun et al.\cite{8} firstly considered the kinetics models of 3-HPA, glycerols transmembrane transport and intracellular 1,3-PD during glycerol metabolism and constructed a nonlinear enzyme-catalytic dynamical system to describe the continuous and batch fermentations of glycerol. Considering the material concentration in the cell is difficult to test and the substrate and the product of transmembrane transport mechanism is not clear, J. Ye et al.\cite{9-11} constructed corresponding dynamical systems, respectively, and inferred the most reasonable metabolic mechanism on the basis of a criterion that the most robust dynamical system is the most reasonable

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This paper is dedicated to Professor Enmin Feng for his important contributions in control and optimization and on the occasion of his 75th birthday. The reviewing process of the paper was handled by Gao Yan as Guest Editor.
one. Recently, J. Gao et al.\textsuperscript{[12]} considered Modeling and identification of microbial batch fermentation using fuzzy expert system, C. Liu et al.\textsuperscript{[13–14]} analyzed the sensitivity and parameter identification for a nonlinear time-delay system in microbial fed-batch process. L. Wang et al.\textsuperscript{[15–17]} considered robust optimal control of a microbial batch culture process.

Based on the related results of batch culture, we study the modeling of glycerol bioconversion to 1,3-PD in continuous culture. We assume that 1,3-PD passes the cell membrane of \textit{K.pneumoniae} by passive diffusion coupling with active transport. Based on qualitative heuristic knowledge from biochemists, a hybrid model is constructed to describe the continuous culture by introducing a fuzzy expert system into the enzyme-catalytic dynamical system. Under certain conditions, we discuss the nature of the velocity vector function of the system to ensure the existence and uniqueness of the solution. To determine the parameters of the proposed system, a parameter identification model is established according to the biological robustness. To solve the identification model, an optimization algorithm is developed on the basis of constrain transcription and smoothing approximation techniques. Numerical simulations indicate that the proposed hybrid model is proper.

2. Nonlinear dynamical system of continuous cultures. During glycerol metabolism, glycerol is firstly transported to the intracellular environment from the extracellular across membrane, and then further catabolized. In this process, reactions are catalyzed by enzymes to generate intermediates and final product, 3-HPA, 1,3-PD, acetate, ethanol. Finally, 1,3-PD is transported to the extracellular environment. Because present experimental research can not confirm the mode of transportation of glycerol and 1,3-PD, in this paper, we assume that 1,3-PD passes the cell membrane of \textit{K.pneumoniae} by passive diffusion coupling with active transport. There are three possible modes of transportation that glycerol passes cell membrane active transport, passive diffusion, active transport together with passive diffusion. In terms of settled dilution rate and concentration of substrate flow, every mode of transportation corresponds to a complex dynamical system. In this paper, we establish a hybrid dynamic model to conduct parameter identification in consideration of passive diffusion coupling with active transport of glycerol.

We make the following assumptions on the basis of the actual fermentation process and the fermentation mechanism:

- (H1) The material composition are uniform in reactor and intracellular, while nonuniform space distribution are ignored.
- (H2) Oxidation path can provide restore path with enough energy and reducing equivalent.

Under assumptions (H1) and (H2), we establish the following complex dynamic model denoted as HNDS, which is described as follows:

\[
\begin{align*}
\dot{x}_1(t) &= (\mu - D_j)x_1 \\
\dot{x}_2(t) &= D_j(C_{s0,j} - x_2) - q_2x_1 \\
\dot{x}_3(t) &= q_3x_1 - D_jx_3 \\
\dot{x}_4(t) &= q_4x_1 - D_jx_4 \\
\dot{x}_5(t) &= q_5x_1 - D_jx_5 \\
\dot{x}_6(t) &= \frac{1}{k_j^8}(k_j^6 \frac{x_2}{x_2 + k_j^{10}} + k_j^{10}(x_2 - x_6)N_+(x_2 - x_6) - q_2^0) - \mu x_6
\end{align*}
\]
\[
\dot{x}_7(t) = \frac{k_{11} x_6}{K_m^G + K_m^G x_7} + \frac{k_{13} x_7}{K_m^P + x_7 + \frac{x_7}{K_P^P}} - \mu x_7
\]

\[
\dot{x}_8(t) = \frac{k_{13} x_7}{K_m^P + x_7 + \frac{x_7}{K_P^P}} - k_{j}^{15} \frac{x_8}{x_8 + k_{j}^{15}} + k_{j}^{17} (x_8 - x_3) N_+(x_8 - x_3) - \mu x_8
\]

where \(x_1(t), x_2(t), \ldots, x_8(t)\) denote the concentrations of biomass, extracellular glycerol, extracellular 1,3-PD, acetate, ethanol, intracellular glycerol, 3-HPA and intracellular 1,3-PD at time \(t\), respectively. \(K_m^G\) and \(K_m^P\) are the Michaelis constants of GDHT and PDOR, respectively, the value of which are 0.53 and 0.14 mmol\(^{-1}\). \(D_j\) and \(C_{s0,j}\) denote dilution rate and concentration of glycerol at the \(j^{th}\) continuous fermentation experiment, \(j \in I_N := \{1, 2, \ldots, N\}\), where \(N\) denotes the total test times. According to the actual fermentation process, parameter vector \(v_j := (D_j, C_{s0,j})^T\) is controlled in \(D_c := [0.1, 15] \times [500, 2000] \subset R^2_+\).

In consideration of the 3-HPA inhibition effect to microbial growth, the expression of the specific growth rate of microbial in equation (1) is modified as follows.

\[
\mu = (1 - \frac{x_7}{x_7^*}) \mu_{max} \frac{x_2}{x_2 + K_s} \prod_{s=2}^{5} (1 - \frac{x_s}{x_s^*})
\]

(1)

It is well known that the specific growth rate of microbial \(\mu_{max}\) is 0.67 h\(^{-1}\) under anaerobic conditions at 37°C and pH7.0. \(K_s\) is Monod constant, which value is 0.28 mmol\(^{-1}\). \(x_s^*(s = 1, 2, \ldots, 8)\) denote the critical concentrations of various state variables, according to the actual experiment. Biomass, glycerol, metabolic intermediate and product cannot exceed its critical concentrations. Where \(x_7^*\) is 10 gL\(^{-1}\), the values of \(x_s^*(s = 2, 3, \ldots, 8)\) are successively 2039 mmolL\(^{-1}\), 939.5 mmolL\(^{-1}\), 1026 mmolL\(^{-1}\), 360.9 mmolL\(^{-1}\), 2039 mmolL\(^{-1}\), 300 mmolL\(^{-1}\), 939.5 mmolL\(^{-1}\). According to Monod equation and Fick scattering law, the specific consumption rate of substrate \(q_2\) and the specific growth of product \(q_3\) in equation (1) are modified as follows.

\[
q_2 = k_1 \frac{x_2}{x_2 + k_2} + k_3 (x_2 - x_6) N_+(x_2 - x_6)
\]

(2)

\[
q_3 = k_4 \frac{x_8}{x_8 + k_5} + k_6 (x_8 - x_3) N_+(x_8 - x_3)
\]

(3)

Where

\[
N_+(y) = \begin{cases} 
1, & y > 0 \\
0, & y \leq 0
\end{cases}
\]

is the indicator function.

Considering intracellular environment as black box model, the specific consumption rate of glycerol \(q_2^0\), the specific growth rate of acetate and ethanol \((q_4, q_5)\) is formulated as follows.

\[
q_2^0 = m_2 + \frac{\mu}{Y_2} + \Delta q_2 \frac{x_2}{x_2 + K_2^*}
\]

(4)

\[
q_4 = m_4 + \mu Y_4 + \Delta q_4 \frac{x_2}{x_2 + K_4^*}
\]

(5)

\[
q_5 = m_5 + \mu Y_5
\]

(6)

Where parameter \(m_2, m_4, m_5, Y_2, Y_4, Y_5, \Delta q_2, \Delta q_4, K_2^*, K_4^*\) in (5-7) are given in Table 1.

Let \(x := (x_1, x_2, \ldots, x_8)^T, u'(j) := (k_1^j, k_2^j, \ldots, k_7^j)^T\), let \(U'(j)\) be admissible set of parameters, so \(u'(j) \in U'(j) \subset R^{17}_+\).
Table 1. The constants and the values of critical concentrations.

<table>
<thead>
<tr>
<th>NO.</th>
<th>$\triangle q_l$</th>
<th>$m_l$</th>
<th>$Y_l$</th>
<th>$K_l^*$</th>
<th>$x_l$</th>
<th>$x^l$</th>
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<tr>
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<td>0.47</td>
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<td>-</td>
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<td>0.001</td>
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<td>2039</td>
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<tr>
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<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>0</td>
<td>940</td>
</tr>
<tr>
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<td>33.07</td>
<td>85.71</td>
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<td>1026</td>
</tr>
<tr>
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<td>5.26</td>
<td>5.26</td>
<td>-</td>
<td>0</td>
<td>361</td>
</tr>
<tr>
<td>6</td>
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<td>-</td>
<td>-</td>
<td>0</td>
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<tr>
<td>8</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>0.14</td>
<td>0</td>
<td>940</td>
</tr>
</tbody>
</table>

Continuous fermentation begins with batch fermentation. Then substrate glycerol is put into fermentation cylinder continuously. In the meantime, fermentative broth flows out by a certain rate. It is required that keeping the volume of fermentative broth constant in the entire biochemical process. So the whole continuous fermentation process consists of two stages: the former batch fermentation and the latter continuous fermentation.

Let $f_s(x, v_j, u'(j)) = \dot{x}_s(t) (s = 1, 2, \ldots, 8)$, so the velocity field of continuous stage in dynamic model HNDS can be noted as:

$$f_c := (f_{c,1}, f_{c,2}, \ldots, f_{c,8})^T$$

Let $D_j$ in equation (1) be zero, and accordingly denote $f_c$ by $f_b$, we obtain the velocity field of batch stage in dynamic model HNDS as follows.

$$f_b := (f_{b,1}, f_{b,2}, \ldots, f_{b,8})^T$$

Let $[t_0, t_b]$ and $[t_b, t_f]$ be batch and continuous fermentation time generating 1,3-PD, respectively. Where $[t_0, t_b] \subset R_+, [t_b, t_f] \subset R_+$, and $t_0 < t_b < t_f < \infty$. So dynamic model HNDS can be simply noted as follows.

$$\begin{cases} 
\dot{x}(t) = f_b(x(t), v_j, u'(j)), t \in [t_0, t_b] \\
x(t_0) = x^0 
\end{cases}$$

$$\begin{cases} 
\dot{x}(t) = f_c(x(t), v_j, u'(j)), t \in [t_b, t_f] \\
x(t_b) = x^b 
\end{cases}$$

Where $x^0 \in R_8^+$ is the initial state of batch fermentation. $x^b \in R_8^+$ is the initial state of continuous fermentation. meanwhile, it is the state of end time $t = t_b$ in batch fermentation.

Although many results indicate that glycerin transmembrane transport is in the combination of active and passive way, it is still not clear. By comparing transport mechanisms of glycerol across cell membrane of Escherichia coli with that of K. pneumoniae, we draw a conclusion that glycerol could pass cell membrane of K. pneumoniae by passive diffusion at high glycerol concentration and by active transport significantly only when the concentration of glycerol is at low concentration. So we modify the above dynamical system using a fuzzy expert system more clearly to analyze the glycerol transport.

For active transport and passive diffusion, the specific consumption rate of extracellular glycerol can be respectively described as Eqs. (12) and (13) based on (3).
concentration, fuzzy rules can be given as follows.

\[ q_2^1 = k_j^1 \frac{x_2}{x_2 + k_j^2} \]
\[ q_2^2 = k_j^3(x_2 - x_6)N_+(x_2 - x_6) \]

where \( k_j^1, k_j^2 \) and \( k_j^3 \) are kinetic parameters whose material biological meanings can be referred to the previous literature.

During the continuous fermentation process, extracellular glycerol concentration will gradually descend. So, range of extracellular glycerol concentration can be divided into different phases in which different transport mechanisms of glycerol across cell membrane are dominating. By the actual experiment, we take the interval \([0, x_2]\) as the universe of discourse. We define the fuzzy sets \( A_i (i = 1, 2) \), where the fuzzy sets are complete and consistent. \( A_1 \) and \( A_2 \) characterize high and low two fuzzy concepts of extracellular glycerol concentration, respectively. We can take the membership functions as follows.

\[
\mu_{A_1}(x_2; a, b) = \begin{cases} 
1(0 \leq x_2 < a) \\
\frac{b-a}{b-a}(a \leq x_2 < b) \\
0(b \leq x_2 < x_2^a) 
\end{cases}
\]

\[
\mu_{A_2}(x_2; a, b) = \begin{cases} 
0(0 \leq x_2 < a) \\
\frac{b-a}{b-a}(a \leq x_2 < b) \\
1(b \leq x_2 < x_2^a) 
\end{cases}
\]

where \( a \) and \( b \) are parameters which should be identified. Because that glycerol could pass cell membrane by passive diffusion at high glycerol concentration and by active transport significantly only when the concentration of glycerol is at low concentration, fuzzy rules can be given as follows.

**Rule1** If \( x_2 \in A_1 \), then \( q_2 = q_2^1 \)

**Rule2** If \( x_2 \in A_2 \), then \( q_2 = q_2^2 \)

The **Rule1** states that if the value of \( x_2 \) is high, the specific consumption rate of extracellular glycerol is determined by the equivalent \( q_2^1 \); Similarly, the **Rule2** states that if the value of \( x_2 \) is low, the specific consumption rate of extracellular glycerol is determined by the equivalent \( q_2^2 \). It is noted that the membership functions of consequent part are adapted fuzzy singleton function. We can now use the above fuzzy rules to construct a nonlinear mapping that is input function \( q_2 \) to describe the specific consumption rate of extracellular glycerol expressed as follows.

\[ q_2 = \frac{\mu_{A_1}(x_2)}{\mu_{A_1}(x_2) + \mu_{A_2}(x_2)}q_2^1 + \frac{\mu_{A_2}(x_2)}{\mu_{A_1}(x_2) + \mu_{A_2}(x_2)}q_2^2 = \mu_{A_1}(x_2)q_2^1 + \mu_{A_2}(x_2)q_2^2 \]

So, the enzyme catalyzed glycerol transmembrane transport dynamic model can be modified.

\[ \dot{x}_6(t) = \frac{1}{k_j^3}(k_j^8 \mu_{A_1}(x_2) \frac{x_2}{x_2 + k_j^2} + k_j^{10} \mu_{A_2}(x_2)(x_2 - x_6)N_+(x_2 - x_6) - q_2^0) - \mu x_6 \]

Let \( u(j) := (k_j^1, k_j^2, \ldots, k_j^{17}, a, b)^T \) be parameters vector to be identified. HNDS can be simply denoted as follows.

\[
\begin{cases} 
\dot{x}(t) = f_6(x(t), v_j, u(j)), t \in [t_0, t_b] \\
x(t_0) = x^0 
\end{cases}
\]

\[
\begin{cases} 
\dot{x}(t) = \tilde{f}_6(x(t), v_j, u(j)), t \in [t_b, t_f] \\
x(t_b) = x^b 
\end{cases}
\]
In the dynamic model, let $U(j)$ be admissible range of continuous parameters and $W_a := \prod_{i=1}^{8} [x_i, \pi_i] \subset R_{a_i}^{8}$ be the state variables. We assume that

- (H3) $U(j)$, $D_c$ and $W_a$ are non-empty, closed and bounded sets.

Under the assumption (H3), we can easily obtain the following properties of the system (14).

**Property 1.** The function $\tilde{f}_b : W_a \times D_c \times U(j) \rightarrow R_{a_i}^{8}$ and $\tilde{f}_c : W_a \times D_c \times U(j) \rightarrow R_{a_i}^{8}$ defined in (14) is continuous and bounded for each $t \in [t_0, t_f]$.

**Proof.** This conclusion can be obtained by the expression of $f$ in (14).

**Property 2.** For given $j$ and $u(j) \in U(j)$, vector function $\tilde{f}_b$ and $\tilde{f}_c$ satisfy the following conditions:

1. $\tilde{f}_b$ and $\tilde{f}_c$ are Lipschitz continuous for each $x \in W_a$.
2. There exist positive constants $a_1, a_2, e_1, e_2 > 0$ such that
   \[
   \|\tilde{f}_b(x(t), v_j, u(j))\| \leq a_1 + e_1 \|x(t)\|, \forall t \in [t_0, t_b],
   \]
   \[
   \|\tilde{f}_c(x(t), v_j, u(j))\| \leq a_2 + e_2 \|x(t)\|, \forall t \in [t_b, t_f].
   \]

**Property 3.** Suppose $u(j) \in U(j)$, the system (14) has a unique solution, denoted by $x(t; v_j, u(j))$, and $x(t; v_j, u(j))$ is continuous in $u(j)$ on $U(j)$.

3. Analysis of biological robustness and parameter identification. Robustness is a basic property of biological systems still keeping its biological functions after internal or external disturbance. A traditional analysis method of biological robustness is based on disturbance of systematic parameters. Actually, biological system is not sensitive and robust to parameter perturbation, which is proved by lots of experiments and gradually accepted in the field of biology.

However, it is difficult to test concentration of substances in the cells and the test data are not accurate. According to the concept of robustness, the influence degree of the parameters after disturbance on the intracellular state variable is defined as the robustness of the system. Let $I_N := \{1, 2, ..., N\}$ be the serial number set of experiments in continuous culture, where $N$ is the total experiment times. For the $j^{th}$ experiment, we have measured the substance concentrations at different instants $t_i$, $i \in M_j$, where $M_j$ denote measure times during the $j^{th}$ fermentation process. For given $v_j, j \in I_N$, we have experimental data in continuous cultures and denote the experimental values of the concentrations of reactants in steady state as $y_{j1}, y_{j2}, y_{j3}, y_{j4}, y_{j5}$ correspondingly. Let $y_j = (y_{j1}, y_{j2}, y_{j3}, y_{j4}, y_{j5})^T \in R^5$ be the experimental data of biomass, glycerol, 1,3-PD, acetate and ethanol.

**Definition 3.1** (Extracellular relative error). For given $j$, if $x_k(t_i; v_j, u(j)), k \in I^5$ is the corresponding computational results by the system HNDS at $t_i \in [t_b, t_f]$, extracellular relative error can be defined as:

\[
SSD(u, j) := \frac{1}{M_j} \sum_{i=1}^{M_j} \sum_{k=1}^{5} \frac{|x_k(t_i; v_j, u(j)) - y_{jk}|^2}{|y_{jk}|^2}
\]

**Definition 3.2.** For given $j$, if $x_k(t_i; v_j, u(j)), k \in I^5$ is the corresponding computational results by the system HNDS at $t_i \in [t_b, t_f]$,
(1) \( \forall u^1(j), u^2(j) \in U(j) \), the average relative deviation of intracellular state variables is defined as:

\[
MSD(u^1, u^2, j) := \sum_{k=6,7,8} \int_{t_h}^{t_f} \frac{|x_k(t; v_j, u^1(j)) - x_k(t; v_j, u^2(j))|^2}{|x_k(t; v_j, u^2(j))|^2} dt \tag{16}
\]

(2) For given \( u(j) \in U(j) \), \( \forall \bar{u}(j) \in U(j) (\bar{u}(j) \neq u(j)) \), the average relative deviation of intracellular state variables is defined as:

\[
MSD_{\text{max}}(u, \bar{u}, j) := \max \{MSD(u, \bar{u}, j)\} \tag{17}
\]

(3) The robustness index of the system HNDS corresponding to \( u(j) \) is defined as:

\[
J^1_j(u(j)) = SSD(u, j) + MSD_{\text{max}}(u, j) \tag{18}
\]

**Definition 3.3.** The robustness index of the system HNDS corresponding to \( U(j) \) is defined as:

\[
R^j := J^1_j(u^*(j)) \tag{19}
\]

where \( u^*(j) := \arg \min \{J^1_j(u(j)) \mid u(j) \in U(j)\} \).

Let system HNDS\((j_1)\) have a higher robustness when \( R^j_1 < R^j_2 \).

The dynamical system HNDS, microbial fermentation product 1,3-PD from intermittent fermentation to continuous fermentation, has two types of performance indicators. One is the relative error of extracellular substance concentration between measured and calculated values and the other is the average relative deviation of parameters corresponding to physical state variables. Then the parameter identification model, denoted by (PIP), can be formulated as

\[
\min J(u(j)) = \frac{1}{t_f - t_h} \sum_{j=1}^{n_j} (SSD(u, j) + MSD_{\text{max}}(u, j)) \tag{20}
\]

s.t. \( x(t; v_j, u(j)) \in W_a \),

\[
\bar{f}_k(x(t), v_j, u(j)) \in [-\varepsilon_f, \varepsilon_f], k \in I_8,
\]

\[
u(j) \in U(j), j \in I_N.
\]

where \( \varepsilon_f \) is computational accuracy.

On the basis of the factual fermentation, we make the following assumptions.

- (H4) For given \( x_0 \in W_a \), the system HNDS is controllable and observable.
- (H5) \( U(j) \) is nonempty in \( R^j_1 \).

Similarly to say, we can prove the following theorem.

**Theorem 3.4.** Under the assumptions (H4)-(H5), there exists an optimal solution \( \hat{u} \) to (PIP), that is, \( \exists \hat{u} \in U(j) \), such that

\[
J(\hat{u}) \leq J(u), \forall u \in U(j). \tag{21}
\]

4. Optimization algorithm and numerical simulation.

4.1. **Optimization algorithm.** The biggest difference between this paper and the original continuous fermentation is that the new model add the fuzzy expert system by increasing two parameters \( a, b (0 < a, b < 1) \). The particle swarm optimization PSO algorithm to identify the optimal solution. The following describes the main steps of PSO algorithm.
• Step 1:
  Initialize: $M$ is the total number of particles, the region of parameters $D_{u,0} \subset \mathbb{R}^{17}$, maximum allowable velocity of particle $V_{\text{max}} = (v_{\text{max},1}, v_{\text{max},2}, \ldots, v_{\text{max},17})$, the maximum iterative times $K_{\text{max}}$ and the cognitive and social scaling parameters $c_{1g}, c_{1b}, c_{2}$ and maximum inertia weight $\omega_{\text{max}}$. $k$ is the iterative time, and set $k = 1$.

• Step 2:
  Particles from the region $D_{u,0}$ according to the uniform distribution, randomly generate $M$. Memorize the personal best and worst position of $i^{th}$ particle by $p_{\text{best}}^i$ and $p_{\text{worst}}^i$ and the best position of whole population by $g_{\text{best}}$.

• Step 3:
  For every particle, test the value of $\hat{G}_{\varepsilon, \gamma}(u^i)$. If $\hat{G}_{\varepsilon, \gamma}(u^i) > 0$, the position is feasible, otherwise, move the position towards the feasible region in the direction of $-\frac{\partial \hat{G}_{\varepsilon, \gamma}(u^i)}{\partial u^i}$ with Armijo line search.

• Step 4:
  Calculate the fitness value $J_1(u^i(k))$ for every particle $u^i(k)$ according to PIP. If $J_1(u^i(k)) < J_1(p_{\text{best}}^i)$, $p_{\text{best}}^i = u^i(k)$, if $J_1(p_{\text{best}}^i) < J_1(g_{\text{best}})$, $g_{\text{best}} = p_{\text{best}}^i$, if $J_1(u^i(k)) > J_1(p_{\text{worst}}^i)$, $p_{\text{worst}}^i = u^i(k)$.

• Step 5:
  Let $k = k + 1$. If $k > K$, stop. Otherwise, update position of each particle and the velocity, then goto Step 3.

4.2. Numerical results. We derive these parameters after numerous numerical experiments using PSO algorithm. And the list of identification parameters are as follows.

<table>
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<tr>
<th>NO.</th>
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<th>2</th>
<th>3</th>
<th>4</th>
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<td>original model</td>
<td>9.89346</td>
<td>81.4246</td>
<td>1.3443</td>
<td>100</td>
<td>32.2974</td>
<td>300</td>
</tr>
<tr>
<td>modified model</td>
<td>5</td>
<td>62.9608</td>
<td>3</td>
<td>473.571</td>
<td>1</td>
<td>291.299</td>
</tr>
<tr>
<td>original model</td>
<td>13</td>
<td>14</td>
<td>15</td>
<td>16</td>
<td>17</td>
<td></td>
</tr>
<tr>
<td>modified model</td>
<td>278.497</td>
<td>0.946147</td>
<td>1</td>
<td>0.01</td>
<td>0.01</td>
<td></td>
</tr>
</tbody>
</table>

$a = 0.21, b = 0.79$. We simulate the continuous fermentation process based on identified parameters. Figure 1 shows comparison of stimulated results and experimental date of extracellular glycerol, 1,3-PD, acetate and ethanol. Points are experimental data, and the full lines show the simulation curves. Figure 2 shows comparison of the results of the original system and the fuzzy system of 1,3-PD. Define the relative errors between the experimental data and the computational results as follows:

$$e_k = \frac{1}{N} \sum_{j=1}^{N} \frac{\sum_{i=1}^{M_j} |x^j_k(t_i; u) - y^j_k(t_i)|}{\sum_{i=1}^{M_j} |y^j_k(t_i)|}, k \in I_2$$

Table 2. The list of parameter identification.
Figure 1. Comparison of stimulated and experimental results of glycerol, 1,3-PD, acetate and ethanol.

Figure 2. Comparison of the results of the original model and the modified model of 1,3-PD.

By numerical calculation, we obtain the relative errors values for the original system and the fuzzy system of 1,3-PD are \( e_1 = 32.86\% \) and \( e_2 = 17.99\% \). By comparing the relative errors, we can draw a conclusion that the model adding fuzzy expert system is more appropriate to describe the continuous fermentation of glycerol to 1,3-PD by \( K.pneumoniae \). Numerical results also show that the optimization algorithm is effective.

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REFERENCES


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