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Identification of a nonlinear model in synthetic microbial systems

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ABSTRACT

To well understand the mechanism of microbial behavior, mathematic models of microbial systems have become a key issue. In particular, it is important for complex microbial systems. Currently, in complex synthetic microbial systems, block oriented nonlinear model can be widely used to represent and approximate many real complex processes. In this paper, the parameter estimation approach for the Hammerstein model is investigated. The basic idea is as follows. Firstly, the nonlinear transfer function of the model can be converted to an intermediate model. Secondly, the estimates of the parameters of the intermediate model are found by using an improved fish swarm optimization algorithm. Thirdly, the relations of the parameters of the intermediate model and those of the Hammerstein model are established. Then, the estimates of the parameters of the Hammerstein model are obtained. Finally, in simulation experiment, compared with other methods, the simulation results show the effectiveness of the proposed algorithm.

KEYWORDS

Microbial system; Complex process; Mathematic model; Identification.

INTRODUCTION

Recently, in synthetic microbial system, the mathematic models of complex processes constituted by a cascade of linear dynamic subsystems with memoryless nonlinearities, also called block oriented nonlinear model, have been extensively studied by many authors[1]. They play an important role in many fields of application owing to their low complexity implying a low computational cost for system identification. Moreover, they often reflect the structure of microbial systems[2-4]. Now, four types of block oriented nonlinear models are commonly used: Wiener model, Hammerstein model, Wiener– Hammerstein model, and Hammerstein–Wiener model.

In real applications, Hammerstein models have been used for representing a vast kind of microbial systems with nonlinearities in many real complex processes, whereas Wiener models allow taking sensor's nonlinearities into account. At present, these block oriented nonlinear model have been widely applied to denote nonlinear systems in many practical applications in the areas of microbial fields[5-7], chemical processes[8], biological processes and physiological systems[9], control[10], Nonlinear aeroelastic/aeroservoelastic modeling[11], and many others.

Nowadays, block model has been widely used in complex synthetic microbial system to describe microbial behavior. Consequently, in this paper, the parameter estimation approach of block nonlinear Hammerstein model is studied. At First, the nonlinear transfer function of the model can be changed into an intermediate model by the function expansion. Secondly, the parameters of the intermediate model are found based on the improved fish swarm optimization algorithm. Thirdly, through the relations of the intermediate model and the Hammerstein model, the parameters of the Hammerstein model are obtained simultaneously. Finally, the results of simulation experiments are adopted to show the feasibility of the proposed method.

IMPROVED FISH SWARM OPTIMIZATION ALGORITHM

Basic fish swarm optimization algorithm

Fish swarm optimization algorithm (FSOA), first proposed in 2002, is a new population-based optimization technique inspired by the natural feeding behavior of fish[12]. It has been proved in function optimization[12], least squares support vector machine[13] and geotechnical engineering problems [14], among others. FSOA imitates three typical behaviors, defined to include "searching for food", "swarming in response to a threat", and "following to increase the chance of achieving a successful result". Three major parameters involved in FSOA include visual distance (visual), maximum step length (step), and a crowd factor. A fish is represented by its D-dimensional position $X_i = (x_1, x_2, \cdots, x_k, \cdots, x_D)$, and food satisfaction for the fish is represented as FS_i. This paper targets FS minimization. The relationship between two fish is denoted by their Euclidean distance $d_{ij} = \|X_i - X_j\|$. Other parameters include: visual, step, and δ. n is used to represent the size of the fish population. All fish try to identify locations able to satisfy their food needs using three distinct behaviors. These include:

(a) Searching behavior: Searching is a basic biological behavior adopted by fish looking for food. It is based on a random search, with a tendency toward food concentration. It is expressed mathematically as:

$$x_{i+1}^k = x_i^k + R(S1)\frac{x_j^k - x_i^k}{\left\|X_j - X_i\right\|}, \quad FS_j < FS_i \tag{1}$$

$$x_{i+1}^k = x_i^k + R(S2) \tag{2}$$

where x_i^k represents the kth element of fish position X_i. We randomly select for fish X_i a new position X_j within its visual. If the corresponding FS_j is satisfied, Eq. (1) is then employed at the next position X_{i+1}. Otherwise, a random position within the step range will be directly adopted as Eq. (2). $R(S1)$ and $R(S2)$ represent random variables within [0, step] and [-step, step], respectively.

(b) Swarming behavior: Fish assemble in several swarms to minimize danger. Mathematically,

$$x_{i+1}^{k} = x_{i}^{k} + R(S1)\frac{x_{c}^{k} - x_{i}^{k}}{\left\| X_{c} - X_{i} \right\|}, \quad FS_{c} < FS_{i} \ \left(\frac{n_{s}}{n}\right) < \delta \tag{3}$$

A fish located at X_i has neighbors within its visual. X_c identifies the center position of those neighbors and is used to describe the attributes of the entire neighboring swarm. If the swarm center has a greater concentration of food than is available at the fish's current position X_i, i.e., $FS_c < FS_i$, and if the swarm (X_c) is not overly crowded ($n_s/n < \delta$), the fish will move from X_i to next X_{i+1}, toward X_c. Here, n_s represents number of individuals within the X_c's visual. Swarming behavior is executed for a fish based on its associated X_c; otherwise, searching behavior guarantees a next position for the fish.

(c) Following behavior: When a fish locates food, neighboring individuals follow. Mathematically,

$$x_{i+1}^{k} = x_{i}^{k} + R(S1)\frac{x_{\min}^{k} - x_{i}^{k}}{\left\| X_{\min} - X_{i} \right\|}, \quad FS_{\min} < FS_{i} \ \left(\frac{n_{f}}{n}\right) < \delta \tag{4}$$

Within a fish's visual, certain fish will be perceived as finding a greater amount of food than others, and this fish will naturally try to follow the best one ($X_{\min}$) in order to increase satisfaction. n_f represents number of fish within the visual of $X_{\min}$.

Basic particle swarm optimization algorithm

Particle swarm optimization (PSO) is a population-based stochastic optimization algorithm, firstly introduced by Kennedy and Eberhart in 1995**[15]**. Suppose that search space is D-dimensional, then the i-th particle of the swarm can be denoted by a D-dimensional vector, $X_i = (x_{i1}, x_{i2}, \cdots, x_{iD})^{\mathrm{T}}$. The velocity can be denoted by another D- dimensional vector $V_i = (v_{i1}, v_{i2}, \cdots, v_{iD})^{\mathrm{T}}$. The best previously visited position of the i-th particle is denoted as $P_i = (p_{i1}, p_{i2}, \ldots, p_{iD})^{\mathrm{T}}$. Defining g as the index of the best particle in the swarm, and let the superscripts denote the iteration number, then the swarm is manipulated according to the following two equations:

$$v_{id}^{n+1} = v_{id}^{n} + cr_{1}^{n}(p_{id}^{n} - x_{id}^{n}) + cr_{2}^{n}(p_{gd}^{n} - x_{id}^{n}) \tag{5}$$

$$x_{id}^{n+1} = x_{id}^{n} + v_{id}^{n+1} \tag{6}$$

where $d = 1, 2, \cdots, D$; $i = 1, 2, \cdots, N$, and N is the size of the swarm; c is a positive constant, in general, $c = 2$; r_1, r_2 are random numbers, uniformly distributed in [0, 1]; and $n = 1, 2, \cdots$, determines the iteration number.

Improved fish swarm optimization algorithm

The basic FSOA visual provides local search attributes. A small visual restricts a fish to interaction with a relatively small number of companions. The basic FSOA step limits maximum step length, with a small step limiting fish to searching a small area and increasing the risk of wasting time. The step values are set based on Euclidean distance calculations and are sensitive to basic FSOA performance (refer to Eqs. (1), (3), and (4)). As settings are difficult, this paper employs the basic PSO formulation to minimize the impact of the step factor. As a result, artificial fish are able to swim like a particle in the basic PSO, subject to the visual factor, but not the step. All the basic FSOA equations have been modified:

(1) Searching behavior:

$$x_{i+1}^{k} = x_{i}^{k} + c_{3}r_{3}^{k}(x_{j}^{k} - x_{i}^{k}), \quad FS_{j} < FS_{i} \tag{7}$$

$$x_{i+1}^{k} = x_i^{k} + R(V1) \tag{8}$$

where c_3 is 2, and r_3 is a random variables generated uniformly within [0, 1]. X_j is still a new position within X_i's visual. Therefore, Eq. (7) uses the basic PSO formulae to releases step settings in Eq. (1). Since Eq. (7) is free to step, this paper further modified Eq. (2) as Eq. (8), providing such with a visual range. $R(V1)$ is a random variable within [-visual, visual]. When step is smaller than visual in the basic PSO, the improved fish swarm optimization algorithm (IFSOA) allows fish to swim for greater lengths than permitted by the basic FSOA.

(2) Swarming behavior:

$$x_{i+1}^{k} = x_i^{k} + c_4 r_4^{k} (x_c^{k} - x_i^{k}) \, , \; FS_c < FS_i \, , \left(\frac{n_s}{n}\right) < \delta \tag{9}$$

where c_4 is 2, and r_4 is a random variables generated uniformly within [0, 1] and the definition of X_c is same as that in the basic FSOA.

(3) Following behavior:

$$x_{i+1}^{k} = x_i^{k} + c_5 r_5^{k} (x_{\min}^{k} - x_i^{k}) \, , \; FS_{\min} < FS_i \, , \left(\frac{n_f}{n}\right) < \delta \tag{10}$$

where c_5 is 2, and r_5 is a random variables generated uniformly within [0, 1] and the definition of $X_{\min}$ is same as that used in the basic FSOA.

In summary, the IFSOA is free of the step parameter of the basic FSOA. All positions of X_j, X_c, $X_{\min}$, and the next position X_j are dependent upon visual only. The major advantage of this is to release a step parameter. In order to execute the aforementioned behaviors, the IFSOA mechanism must follow the process shown in Figure 1.

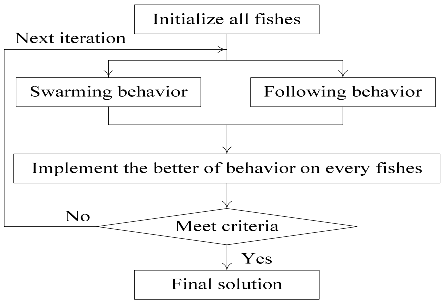

Figure 1 : Flow chart of the IFSOA

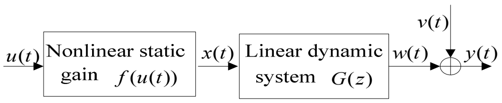

Figure 2: Studied hammerstein model

PARAMETER ESTIMATION PROCESS

In this paper, we are interested in microbial systems that can be described by Hammerstein model shown in Figure 2. Where $u(t)$ is a measurable input signal, $y(t)$ is a measurable output signal, $v(t)$ is an noise, $x(t)$ is an unmeasurable intermediate signal.

In Figure 2, the nonlinear static gain $x(t)$ can be represented by the following p-order polynomial.

$$x(t) = f(u(t)) = \sum_{i=1}^{p} r_i u^i(t) = R^{\mathrm{T}} U(t) \tag{11}$$

The following form of the transfer function can express the linear dynamic system.

$$G(z) = \frac{B(z^{-1})}{A(z^{-1})} = \frac{b_0 + b_1 z^{-1} + \cdots + b_m z^{-m}}{1 + a_1 z^{-1} + \cdots + a_n z^{-n}} \tag{12}$$

where m, n are the order of the polynomial, in general, $m \leq n$. The linear transfer function of Eq. (12) can be described by the following difference equation.

$$A(z^{-1})y(t) = B(z^{-1})x(t) + e(t) \tag{13}$$

where $e(t) = A(z\text{-}1)v(t)$ can be interpreted as a fitting error. From Eqs. (11) and (13), Eq. (14) can be obtained.

$$A(z^{-1})y(t) = \sum_{j=0}^{m}\sum_{i=1}^{p}\alpha_{ij}z^{-j}u^{i}(t) + e(t) \tag{14}$$

where $\alpha_{ij} = r_i b_j$, $i = 1, 2, \cdots, p$, $j = 1, 2, \cdots, m$. From Eq. (14), Eq. (15) can be gotten.

$$y(t) = -\sum_{i=1}^{n}a_i y(t-i) + \sum_{j=0}^{m}\sum_{i=1}^{p}\alpha_{ij}u^{i}(t-j) + e(t) \tag{15}$$

Moreover, Eq. (15) can be further rewritten as the following vectors form.

$$y(t) = \theta\varphi(t) + e(t) \tag{16}$$

Where $\begin{array}{c}\theta = (-a_1, -a_2, \cdots; -a_n, \alpha_{10}, \alpha_{11}, \cdots; \alpha_{1m}, \alpha_{20}, \\ \alpha_{21}, \cdots; \alpha_{2m}, \cdots; \alpha_{p0}, \alpha_{p1}, \cdots; \alpha_{pm})\end{array}$, $\begin{array}{c}\phi(t) = (y(t-1), y(t-2), \cdots, y(t-n), u(t), u(t-1), \cdots, u(t-m), \\ u^2(t), u^2(t-1), \cdots, u^2(t-m), \cdots, u^p(t), u^p(t-1), \cdots, u^p(t-m))^{\mathrm{T}}\end{array}$.

It can be seen that $y(t)$ is a function of $u(t)$. It is called as an intermediate model throughout this paper. Here θ is a parameter vector of the intermediate model. Assume that the estimate of the vector θ in the intermediate model is $\hat{\theta} = (-\hat{a}_1, -\hat{a}_2, \cdots, -\hat{a}_n, \hat{\alpha}_{10}, \hat{\alpha}_{11}, \cdots, \hat{\alpha}_{1m}, \hat{\alpha}_{20}, \hat{\alpha}_{21}, \cdots, \hat{\alpha}_{2m}, \cdots, \hat{\alpha}_{p0}, \hat{\alpha}_{p1}, \cdots, \hat{\alpha}_{pm})$. Then, the deviation of the estimation can be judged by the following cost function**[16]**.

$$J_h = \sum_{k=k_0}^{k_0+h}[y(k) - \hat{y}(k)]^2 \tag{17}$$

where h is the window width of the identification, $\hat{y}(k)$ are the input of the obtained identification model. One can solve the minimum of Eq. (17) and obtain the vector θ of the intermediate model by the IFSOA, because minimizing Eq. (17) is an optimization problem. The parameters of the Hammerstein model are obtained by those of the intermediate model as follows. Suppose that the final gain of the linear dynamic subsystem is 1, and then we have

$$G(\infty) = \frac{b_0 + b_1 + \cdots + b_m}{1 + a_1 + a_2 + \cdots + a_n} = 1 \tag{18}$$

Consequently, Eq. (18) can be expressed via the following matrix form.

$$C^{\mathrm{T}}B = C^{\mathrm{T}}A \tag{19}$$

where $C=(1,1,\cdots,1)^{\mathrm{T}}$, $A=(1,a_1,\cdots,a_n)^{\mathrm{T}}$, $B=(b_0,b_1,\cdots, b_m)^{\mathrm{T}}$. Thus it follows from $\alpha_{ij} = r_i b_j$ that

$$H = RB^{\mathrm{T}} \tag{20}$$

where $R=(r_1,r_2,\cdots,r_p)^{\mathrm{T}}$, and $H=\begin{pmatrix} \alpha_{10} & \alpha_{11} & \cdots & \alpha_{1m} \\ \alpha_{20} & \alpha_{21} & \cdots & \alpha_{2m} \\ \vdots & \vdots & \cdots & \vdots \\ \alpha_{p0} & \alpha_{p1} & \cdots & \alpha_{pm} \end{pmatrix}$

Right-multiplying C in each side of Eq. (20) gives

$$HC = RB^{\mathrm{T}}C \tag{21}$$

Then, it follows from Eq. (21), $B^{\mathrm{T}}C=C^{\mathrm{T}}B$ and Eq. (19) that

$$R=\frac{HC}{C^{\mathrm{T}}A} \tag{22}$$

Transposing each side of Eq. (20) yields

$$H^{\mathrm{T}} = BR^{\mathrm{T}} \tag{23}$$

Right-multiplying C in each side of Eq. (23) gives

$$H^{\mathrm{T}}C = BR^{\mathrm{T}}C \tag{24}$$

Then, by Eq. (24), $R^{\mathrm{T}}C=C^{\mathrm{T}}R$ and Eq. (22), it follows that

$$B=\frac{C^{T}AH^{T}C}{C^{T}HC} \tag{25}$$

In conclusion, firstly, we solve Eq. (17) to get the vector θ of the intermediate model using the above IFSOA, by which the estimates of A and H can be obtained via Eqs. (20) and (19). Then, the estimates of R and B are found by Eqs. (22) and (25). In this way, the estimates of the parameters of Hammerstein model are successfully identified.

SIMULATION EXPERIMENTS

It is supposed that a vast class of microbial system can be described by the following block Hammerstein model with 2-order nonlinear subsystem and 4-order linear dynamic subsystem shown in Figure 1, and mathematical model is

$$x(t)=0.5u(t)+0.8u^{2}(t)\,,\;G(z)=\frac{0.6+1.1z^{-1}+0.7z^{-2}-1.2z^{-3}}{1-0.3z^{-1}-0.1z^{-2}+0.5z^{-3}-0.2z^{-4}}$$

and $v(t)$ is Gaussian noise with zero mean and standard deviation, $\sigma = 0.04$, $u(t)$ is Gaussian noise with zero mean and standard deviation, $\sigma = 1$.

In the estimation process of the vector θ of intermediate model, the parameters of the algorithm are set as follows. Let window width of estimation: h=50, the number of artificial fish is 40, the maximum iterative steps are 1000, step is 4.5, visual is 5, try number is 5, δ is 0.56, maximal rate $V_{\max}$ is 2, and the initial values of model parameters are all picked out randomly from [-0.4, 1.2]. The estimates of the vector θ of the intermediate model can be found based on IFSOA as follows.

$$\theta=(0.3011, 0.1011, -0.4986, 0.1984, 0.3011, 0.5460, 0.3519, -0.6007, 0.4799, 0.8701, 0.5608, -0.9574).$$

Thus, the following parameter matrices H, A are formed according to Eqs. (19) and (20).

$$H = \begin{pmatrix} 0.3011 & 0.5460 & 0.3519 & -0.6007 \\ 0.4799 & 0.8701 & 0.5608 & -0.9574 \end{pmatrix}, \; A = (1 \quad -0.3013 \quad -0.1011 \quad 0.4986 \quad -0.1984)^{\mathrm{T}}.$$

The parameter vector R can be obtained by Eq. (22).

$$R = (0.5011 \quad 0.7986)^{\mathrm{T}}.$$

From Eq. (25), the parameter vector B is obtained.

$$B = (0.6009 \quad 1.0896 \quad 0.7022 \quad -1.1988)^{\mathrm{T}}.$$

From the above experimental results, it can be seen that the estimates of the parameters by IFSOA are almost closer to the true values of the model. Moreover, the step response curves of the real model and the estimated model by IFSOA are both shown in Figure 3, respectively. And the corresponding error curve is shown in Figure 4. From the figures, it can be seen that the two curves are almost overlapped, which illustrates that the estimation results by the proposed algorithm is good.

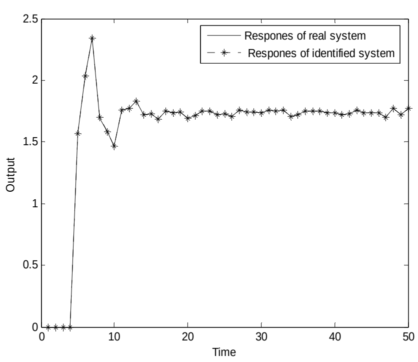

Figure 3 : The step response of the identified model

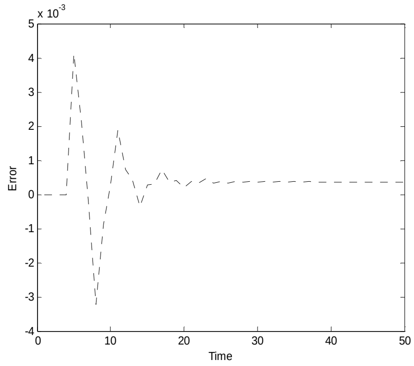

Figure 4 : Error curve

To further show the validity of the presented method, similarly, the estimates of the parameters of the Hammerstein model by the basic FSOA are as follows.

$$\theta = (0.2968, 0.0897, -0.5077, 0.2043, 0.3029, 0.5555, 0.3459, -0.6064, 0.4879, 0.8947, 0.5572, -0.9767),$$

$$H = \begin{pmatrix} 0.3029 & 0.5555 & 0.3459 & -0.6064 \\ 0.4879 & 0.8947 & 0.5572 & -0.9767 \end{pmatrix}, \; A = (1 \quad -0.2968 \quad -0.0897 \quad 0.5077 \quad -0.2043)^{\mathrm{T}},$$

$$R = (0.5029 \quad 0.8100)^{\mathrm{T}}, \; B = (0.6023 \quad 1.1046 \quad 0.6879 \quad -1.2058)^{\mathrm{T}}.$$

The estimates of the parameters of the Hammerstein model by the basic PSO are as follows.

$$\theta = (0.3070, 0.1100, -0.5065, 0.1897, 0.3047, 0.5550, 0.3545, -0.5980, 0.4890, 0.8905, 0.5687, -0.9595),$$

$$H = \begin{pmatrix} 0.3047 & 0.5550 & 0.3545 & -0.5980 \\ 0.4890 & 0.8905 & 0.5687 & -0.9595 \end{pmatrix}, \; A = (1 \quad -0.3070 \quad -0.1100 \quad 0.5065 \quad -0.1897)^{\mathrm{T}},$$

$$R = (0.5027 \quad 0.8066)^{\mathrm{T}}, \; B = (0.6062 \quad 1.1040 \quad 0.7051 \quad -1.1895)^{\mathrm{T}}.$$

When the above simulation results are compared, one can see that the estimation accuracy of the presented method is obviously improved. Moreover, in the simulation experiment, the presented method is easily carried out for the block Hammerstein model. Consequently, the structure of a vast class of microbial system can be well obtained by the presented method.

CONCLUSION

In this paper, the parameter estimation of the Hammerstein model is investigated, which can express a vast class of microbial system. The basic idea is to convert the Hammerstein model to an intermediate model initially. Then, the estimates of the parameters of the intermediate model are obtained by the IFSOA. Next, the estimates of the parameters of the Hammerstein model are gained by the relationship between the intermediate model and the Hammerstein model. Finally, the simulation results demonstrate that the presented method is feasible. Accordingly, this paper presents a new identification for block Hammerstein model in synthetic microbial system. That is to say, the model of a vast class of microbial system can be well obtained by the presented method.

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