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An Identification Approach for a Class of Nonlinear Dynamic System

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Abstract: Present study proposed new identification method for the nonlinear dynamic system. Firstly, suppose that the original system is expressed by Hammerstein model then the transfer function of the model can be changed into a linear form, thus generating a middle model. The parameters of the middle model are obtained by a Bacterial Chemotaxis Optimization (BCO) algorithm. Finally, through the relationships of the parameters of middle model and those of Hammerstein model, the parameters of Hammerstein model are derived. Thus, the original system is identified. The feasibility and efficiency of the presented algorithm are demonstrated using numerical simulations.

Key words: Dynamic system, hammerstein model, identification, BCO

INTRODUCTION

The research theories of system identification have been going mature for the linear system. In the existence, the systems, however, are almost nonlinear, so it is very important to research the identification of nonlinear systems (Sjoberg *et al.*, 1995; Anguelova and Wennberg, 2008; Bai and Chan, 2008). Especially, the identification of the nonlinear dynamic system was one of the main topics for the current system identification fields (Hu, 2001; Bentsman *et al.*, 2008).

The identification of nonlinear systems using the artificial neural network (Wang and Cheng, 1996) is one of main methods at present, because the neural network has the capacity of approximating any complicated nonlinear functions. Nevertheless, there are several defects such as over learning, local minimum, etc. At present, due to lack of describing umform theory for different nonlinear systems, identification of systems is often aimed at the specific system. In application, many nonlinear systems are described by Hammerstein model (Bai and Chan, 2008). The purpose of this study is to investigate the identification method of nonlinear dynamic system. Firstly, the model of the original dynamic system is supposed to be expressed by Hammerstein model. Through function expansion, the transfer function of the linear subsystem can be converted to a linear form, thus generating a middle model. Then, identific-ation is changed into a function optimization problem and the BCO algorithm is adopted to obtain parameters of the middle model. Finally, through the relationships of coefficients of the middle model and those of Hammerstein model, the identification of the nonlinear

dynamic system is realized. Simulation results show the feasibility of the presented method.

BCO ALGORITHM

Recently, the BCO algorithm has been received more attention as a novel global random search technique and it has achieved success in solving practical nonlinear optimization problems (Bremermann, 1974; Muller *et al.*, 2002; Zhang and Wu, 2008). The optimization by bacterial chemotaxis was inspired from bacterial foraging behavior, introduced by Bremermann (1974) and Muller *et al.* (2002) extracted bacterial chemotaxis algorithm from the newest production found in biology field. The processing of BCO is presented as follows:

- **Step 1:** Calculate the velocity of a bacterium *v*, which is supposed to be a scalar constant value 1
- **Step 2:** Calculate the duration of the traj-ectory τ, the distribution of which satisfies the probability density function:

$$P(X = \tau) = \frac{1}{T} \exp(-\frac{\tau}{T}) \tag{1}$$

where, the expectation E(X) = T and the variance Var(X) = T. The time T is given by:

$$T = \begin{cases} T_0, & \text{for } \frac{f_{pr}}{l_{pr}} \ge 0 \\ T_0 \left(1 + b \left| \frac{f_{pr}}{l_{pr}} \right| \right), & \text{for } \frac{f_{pr}}{l_{pr}} < 0 \end{cases}$$
 (2)

where, T_0 expresses the minimal mean time, f_{pr} expresses the difference between the actual and previous value, l_{pr} expresses the vector connecting the previous and actual position in parameter space and b is supposed as the dimensionless parameter.

Step 3: Calculate the new direction. The density function of the angle α between the previous and new direction is Gaussian, for turning right or left, respectively as follows:

$$P(X = \alpha, v = \pm \mu) = \frac{1}{\sqrt{2\pi}\sigma} exp \left[-\frac{(\alpha - v)^2}{2\sigma^2} \right]$$
 (3)

where, $\mu E(X)$ and $\sigma = (Var(X)^{1/2})$ are provided by:

- If $(f_p/l_p)<0$ and then $\mu=62^{\circ}(1-\cos\theta); \sigma=26^{\circ}(1-\cos\theta);$ $\cos\theta=\exp(-\tau_c\tau_{pr})$
- Else $(f_{pr}/l_{pr}) = 0$, then $\mu = 62^{\circ}$; $\sigma = 26^{\circ}$

where, τ_c describes the correlation time, τ_{pr} describs the duration of previous step.

The choice of a right or left direction as referring to previous trajectory is determined by a uniform probability density, thereby, yielding a probability density for the angle α :

$$P(X = \alpha) = \frac{1}{2} [P(X = \alpha, v = \mu) + P(X = \alpha, v = -\mu)]$$
 (4)

Step 4: Calculate the new position:

$$X_{\text{new}} = X_{\text{old}} + n_{\text{u}} 1 \tag{5}$$

where, x_{new} expresses the new position of the bacteria; x_{old} expresses previous position; n_o expresses the normalized new direction and l expresses the length of new trajectory.

In summary, the algorithm contains the following parameters to be calculated in advance: T_0 , τ_c and b. Muller *et al.* (2002) gives their detailed formula:

$$T_0 = \epsilon^{0.30} 10^{-1.73}, b = T_0 (T_0^{-1.54} 10^{0.60}) \tau_c = \left(\frac{b}{T_0}\right)^{0.31} 10^{1.16}$$

Step 5: Output the optimization results

IDENTIFICATION PROCESS

Here, the original system is described by the Hammerstein model (Hu, 2001), whose structure is shown in Fig. 1. Let u(t), y(t) and v(t) be the input, output and noise, x(t) be an middle input signal.

The gain of the nonlinear part can be approximately expressed by the p-order polynomial:

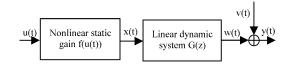


Fig. 1: The structure of Hammerstein model

$$x(t) = \sum_{i=1}^{p} r_{i} u^{i}(t) = R^{T} U(t)$$
 (6)

The linear subsystem can be described by the following transfer function:

$$G(z) = \frac{y(t)}{x(t)} = \frac{B(z^{-1})}{A(z^{-1})} = \frac{b_0 + b_1 z^{-1} + \dots + b_m z^{-m}}{1 + a_1 z^{-1} + \dots + a_n z^{-n}}$$
(7)

where, m, n are the polynomial's order. Eq. 7 can be described by difference equation:

$$A(z^{-1}) y(t) = B(z^{-1})x(t) + e(t)$$
 (8)

where, $e(t) = A(z^{-1})v(t)$ can be taken as a fitting error. From Eq. 6 and 8, it follows that:

$$y(t) = -\sum_{i=1}^{n} a_{i}y(t-i) + \sum_{i=0}^{m} \sum_{j=1}^{p} \alpha_{ij}u^{i}(t-j) + e(t)$$
(9)

where, $\alpha_{ij} = r_i b_j$, i = 1, 2, ..., p, j = 0, 1, ..., m. And it follows that:

$$y(t) = \theta \phi(t) + e(t)$$
 (10)

Where:

$$\theta = (-.a_2,...,-a_n, a_{10}, a_{11},..., a_{1m}, a_{20}, a_{21},...,a_{2m}, a_{n0},a_{n1},...a_{nm})$$

$$\varphi(t) = (y(t-1),...,y(t-2),...,y(t-n), u(t), u(t-1),...u^{2}(t-m), ...u^{2}(t) u^{2}(t-1),...u^{2}(t-m),...u^{p}(t),u^{p}(t-1),...(t-m))^{T}$$

Thus, the deviation of the estimation can be judged by the following cost function:

$$J_{h} = \sum_{k=k_{0}}^{k_{0}+h} [y(k) - \tilde{y}(k)]^{2}$$
 (11)

where, h is the width of identification, $\tilde{y}(k)$ are the estimated input of the model.

One can solve the minimum of Eq. 11 and get the θ of middle model using BCO algorithm. Suppose that the final gain of the linear subsystem of the model is 1, i.e., G(8) = 1. Thus, Eq. 12 can be obtained:

$$C^{T}B = C^{T}A \tag{12}$$

where, $C = (1,1,...,1)^T$, $A = (1a_1,...,a_n)^T$, $B = (b_0,b_1,...,b_m)^T$. So it follows from $\alpha_{ij} = r_ib_j$ that:

$$H = RB^{T}$$
 (13)

where, $R = (r_1, r_2, ..., r_p)^T$ and

$$H = \begin{pmatrix} \alpha_{10} & \alpha_{11} & \cdots & \alpha_{1m} \\ \alpha_{20} & \alpha_{21} & \cdots & \alpha_{2m} \\ \vdots & \vdots & \cdots & \vdots \\ \alpha_{p0} & \alpha_{p1} & \cdots & \alpha_{pm} \end{pmatrix}$$

Consequently, it follows from Eq. 13, $B^TC = C^TB$ and Eq. 12 that:

$$R = \frac{HC}{B^{T}C} = \frac{HC}{C^{T}B} = \frac{HC}{C^{T}A}$$
 (14)

Using $R^{T}C = C^{T}R$ and Eq. (14), it follows that:

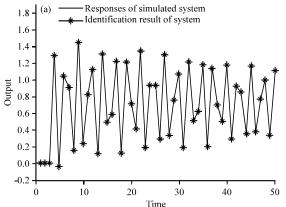
$$B = \frac{H^{T}C}{R^{T}C} = \frac{H^{T}C}{C^{T}R} = \frac{C^{T}AH^{T}C}{C^{T}HC}$$
(15)

Accordingly, the parameter assessments of Hammerstein model are achieved.

NUMERICAL SIMULATIONS

Now, suppose that the original system is described by the Hammerstein model with 2-order nonlinear subsystem and 3-order linear subsystem is considered. Its mathem- atical model is: $x(t)+0.8u^2(t)$:

$$G(z) = \frac{B(z^{-1})}{A(z^{-1})} = \frac{0.4 - 0.6z^{-1} + 0.9z^{-2}}{1 + z^{-1} + 0.2z^{-2} - 0.5z^{-3}}$$



Here, an impulse signal is adopted as an input signal, u(t). The training samples are formed based on the input and output response signal. In this study, the initial values of the simulated model are y(t) = 0, t = 1,2,3. The parameters of the algorithm are set as follows. h = 50, the number of bacteria is 20, the maximum iterative steps are 150 and system model parameters' initial values are all picked out randomly from [-0.7,1.1].

The parameter vector θ of the middle model can be obtained using the BCO algorithm:

$$\theta$$
 = (-0.9977.-0.1999, 0.5013, 0.40198,-0.6044, 0.9012, 0.3211,-0.4828, 0,7199)

Then, the parameter matrices H, A are formed using Eq. 13 and 12:

$$H = \begin{pmatrix} 0.4019 & -0.6044 & 0.9012 \\ 0.3211 & -0.4828 & 0.7199 \end{pmatrix}$$

$$A = (1 \ 0.99977 \ 0.1992 \ -0.5013)^{T}$$

So R can be obtained by Eq. 14:

$$R = (1.0021 \ 0.8005)^T$$

Finally, based on Eq. 15, it follows that:

$$B = (0.4011 - 0.6031 0.8993)^{T}$$

Accordingly, the identification of the Hammerstein model has been carried out via the proposed method. The outputs of the identification model are plotted against time in Fig. 2a. Note that Fig. 2a also includes the

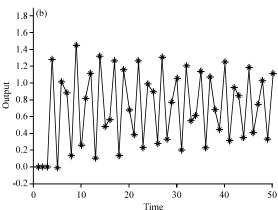


Fig. 2(a-b): Comparison of the response of simulated system with those for identification models, (a) Noiseless and (b) Noise

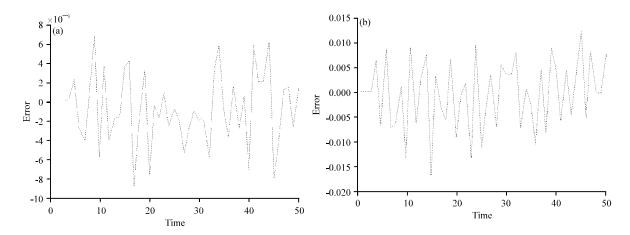


Fig. 3(a-b): Error curve between the response of simulated system and those for identification models, (a) Noiseless and (b) Noise

response of the simulated dynamic system. And the corresponding identification error curve is shown in Fig. 3a.

In order to further show the stability of the presented method, A Gaussian noise with zero mean and deviation, $\sigma^2 = 0.04$, is added to the response signal y(t) of the nonlinear dynamic system. Hammerstein model is identified using the same method and the identification results are obtained:

$$\theta = (-0.9889, -0.2021, 0.5018, 0.3979, -0.5987, \\ 0.8947, 0.3205, -0.4823, 0.7207)$$

$$H = \begin{pmatrix} 0.3979 & -0.5987 & 0.8947 \\ 0.3205 & -0.4823 & 0.7207 \end{pmatrix}$$

$$A = (1 \quad 0.9889 \quad 0.2021 \quad -0.5018)^{T}$$

$$R = (0.9888 \quad 0.7965)^{T}$$

and

$$b = (0.4021 -0.6055 0.9048)^{T}$$

The parameter values of Hammerstein model can still be well identified using the proposed approach. The outputs of the identification model are plotted against time in Fig. 2b. Note that Fig. 2b also includes the response of the simulated nonlinear dynamic system. And the corresponding identification error curve is shown in Fig. 3b.

From the above results, it can be seen that the presented identification method based on has a strong anti-disturbance ability.

CONCLUSION

This note presents an identification method for the nonlinear dynamic system, which is described by Hammerstein model. The model is changed to be a linear form via the function expansion. Then, the parameters of intermediate model are solved using BCO. The relationship of all the parameters is formulated to realize identification for nonlinear dynamic systems. The results of simulations have shown that the proposed method is robust in noise resistance.

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