

Identification of Hammerstein Model Based on Quantum Genetic Algorithm

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Abstract

Nonlinear system identification is a main topic of modern identification. A new method for nonlinear system identification is presented by using Quantum Genetic Algorithm (QGA). The problems of nonlinear system identification are cast as function optimization over parameter space, and the Quantum Genetic Algorithm is adopted to solve the optimization problem. Simulation experiments show that: compared with the genetic algorithm, quantum genetic algorithm is an effective swarm intelligence algorithm, its salient features of the algorithm parameters, small population size, and the use of Quantum gate update populations, greatly improving the recognition in the optimization of speed and accuracy. Simulation results show the effectiveness of the proposed method.

Keywords: system identification, Hammerstein model, Quantum Genetic Algorithm, genetic algorithm, Parameter estimation

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1. Introduction

With the development and progress of society, more and more non-linear systems had aroused extensive attention. Nonlinearity system has combined with linear dynamic model and static nonlinear function of sub-models, with a little calculation, it can reflect the characteristics of features better, which is suitable for process control model to use. According to specific forms, such non-linear model can be divided into [1]: Hammerstein, Wiener, Hammerstein-Wiener, Wiener-Hammerstein model. Among them, Narendra and Gellman were introduced Hammerstein model in 1966, the model consisted of a non-linear block and then a linear structure into a dynamic module in series [2]. Relatively linear model, the overall dynamic characteristics of the Hammerstein model will more fully describe the system in the work area [3], while the corresponding control problem doesn't require the introduction of non-linear optimization, so as to avoid problems of NLP (nonlinear programming).

Quantum Genetic Algorithm (QGA) [4] is probability of a novel evolutionary algorithm; it introduces the theory of quantum computing to evolution of the field. QGA was expressed in terms of probabilities quantum bit basic bits of information were encoded, realization of populations with variation of quantum-inspired evolutionary, guided quantum mutation process with the optimal solution, can be effective in overcoming the early linear evolution, faster than the traditional evolutionary convergence, global optimization capability updates. It can be used to solve nonlinear, non-differentiable and multimodal complex issues, in order to solve complex nonlinear systems identification issue came up a way possible. In this paper, QGA was used to identify the Hammerstein model, simulation results showed that received quite satisfactory results, illustrated the effectiveness and feasibility of the method.

2. Quantum Genetic Algorithm

Quantum Genetic Algorithm (QGA) is built on the basis of the quantum state vector, based on quantum bit encoding to represent chromosomes, used quantum revolving doors to achieve adjustments of the chromosomal gene. QGA is in the superposition of a chromosome which can express more than one state, while traditional encoding can only indicate a specific state, so the QGA is easier than traditional genetic algorithms to maintain the diversity of the population, the solution to the target problem is more optimized [5][6].

2.1. Quantum Chromosome

Information carrier of quantum information theory is the superposition of the two-state qubits, preferred value of qubit state is 0 or 1, status is described as [7]: $|\varphi\rangle = \alpha|0\rangle + \beta|1\rangle$, $|\alpha|^2 + |\beta|^2 = 1$. Where, $|\varphi\rangle, |0\rangle, |1\rangle$ represent the state of qubit, α, β represent two complex numbers of the probability of occurrence of the corresponding status, $|0\rangle$ and $|1\rangle$ respectively represent the self-rotating downwardly and upwardly from the rotating state. $|\alpha|^2, |\beta|^2$ Denote the qubit, the probability of 0 and 1, normalized condition is met. QGA uses qubits to encode. M-qubit system can be described as:

$$\begin{bmatrix} \alpha_1 & \alpha_2 & \dots & \alpha_m \\ \beta_1 & \beta_2 & \dots & \beta_m \end{bmatrix} \quad (1)$$

where, $|\alpha_i|^2 + |\beta_i|^2 = 1, 2, \dots, m$.

2.2. Quantum encoded converts into binary-coded

In quantum space, a quantum state is represented as $\alpha|0\rangle + \beta|1\rangle$, it's not to be observed, with different probability in the basic state, once the measurement on the probability of $|\alpha|^2$ or $|\beta|^2$ collapse to 0 or 1, this is known as quantum measurement principle of collapse [8]. In quantum-inspired evolutionary algorithm uses the principle to achieve binary quantum superposition into the traditional evolutionary algorithms, determines the configuration of the transformation, as describes in the type m-bit quantum chromosomes, corresponding binary code is m, every probability of $|\alpha|^2$ or $|\beta|^2$ take 0 or 1. Method of converting it is to create a $[0, 1]$ random number $Randi$ of uniform distribution, if $Randi \leq |\alpha_i|^2$, then 0 is taken, otherwise, take 1.

2.3. Quantum Evolution Mechanism

QGA is a population-based evolutionary algorithm, the advantages are: ① by selecting allow individuals increased with higher fitness, and according to the principle of quantum collapse, random observation methods used to generate new individuals, and continuously explore new spaces; ② representation of the quantum chromosome, chromosome itself carries more status information in a quantum, brings a wealth of species, maintains the Group's diversity, overcoming the premature phenomenon in the GA; ③ absorbs the advantages of evolutionary Particle Swarm Optimization algorithm used historical optimal information "smart" guides evolution of current population, can effectively overcome the blindness of GA variation in operation, avoids random perturbation of the evolutionary process, improving the convergence rate; ④ chromosome is a quantum probability, equivalent to the crossover and mutation of GA operations.

QGA doesn't use genetic algorithm of selection, crossover and mutation and other operators to change the state of chromosomes, but using quantum gates for each superposition method respectively. The offspring generation probability amplitude decides depends on the best individual of its parents and its state. Genetic manipulation of the QGA is mainly constructed of quantum gates which operate on the ground state of quantum superposition [9], so that occurs mutual interference, phase change, thereby changes the ground state probability amplitude. According to calculation of the QGA features and choose quantum revolving door is relatively appropriate. Adjustment of quantum gate operation for [10]:

$$\begin{bmatrix} \alpha_i \\ \beta_i \end{bmatrix} = \begin{bmatrix} \cos \theta_i & -\sin \theta_i \\ \sin \theta_i & \cos \theta_i \end{bmatrix} \begin{bmatrix} \alpha_i \\ \beta_i \end{bmatrix} \quad (2)$$

Where, (α_i, β_i) is the i-th chromosome qubit, θ is the angle of rotation, its symbol determines the direction of convergence of the algorithm, the magnitude determines speed of convergence and efficiency.

$P(t)$ represents the observed value of $Q(t)$; $Q(t)$ represents populations of the time t .
QGA algorithm processes:

Procedure QGA

Begin

$t \leftarrow 0$

Initialize $Q(t)$

Make $p(t)$ by observing $Q(t)$ states

Evaluate $p(t)$

Store the best solution among $p(t)$

While (not termination-condition)do

Begin

$t \leftarrow t + 1$;

Make $p(t)$ by observing $Q(t)$ states

Evaluate $p(t)$

Update $Q(t)$ using quantum gates $U(t)$

Store the best solution among $p(t)$

End

End

3. Identification of Nonlinear System Based On the QGA

Identification of nonlinear system includes structure identification and parameter estimation of two parts. Solving identification of nonlinear systems problems, first describes the problem you want to solve the nonlinear system. In this article to Hammerstein model identification of nonlinear system model most commonly used as an example for discussion.

3.1. Single-input Single-output Hammerstein Model

Like the global search technique, Genetic Algorithms, Particle Swarm Optimization Algorithm, QGA simultaneously evaluate points in the parameter space, so it is more likely converge toward the global solution. Moreover the studies by Kristinsson [11] have shown that genetic algorithms can be effectively applied for system identification of both continuous and discrete time systems and be able to directly identify physical parameters or poles and zeros. So the problems of nonlinear system identification can be viewed as optimization problems with the estimated parameters as the optimized variables in search space. And then the QGA is applied to obtain the optimal solution to the minimization problem (i.e. the optimal estimation of Hammerstein model parameters) by searching in the whole parameter space in parallel.

Hammerstein model is in series by the nonlinear static and dynamic linear pulse transfer function, connects it as shown in Figure 1 [12][13]:

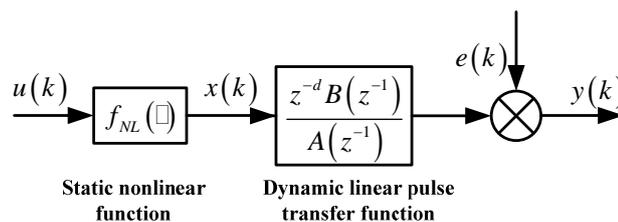


Figure 1. Hammerstein model structure diagram

A static nonlinear function is:

$$x(k) = f_{NL}[u(k)] = r_0 + r_1 u(k) + r_2 u^2(k) + \dots + r_p u^p(k) \quad (3)$$

Where, $r_i (i = 0, 1, \dots, p)$ is the coefficient of static nonlinearity.

Dynamic linear pulse transfer is:

$$\frac{y(z)}{x(z)} = \frac{z^{-d}B(z^{-1})}{A(z^{-1})} \quad (4)$$

Where, $A(z^{-1}) = 1 + a_1z^{-1} + \dots + a_{n_a}z^{-n_a}$,
 $B(z^{-1}) = 1 + b_1z^{-1} + \dots + b_{n_b}z^{-n_b}$

Hammerstein model output/input expression:

$$y(k) = \frac{z^{-d}B(z^{-1})}{A(z^{-1})} [r_0 + r_1u(k) + \dots + r_pu^p(k)] \quad (5)$$

Hammerstein model expresses as a difference equation:

$$\begin{cases} A(q^{-1})y(k) = B(q^{-1})x(k-1) + C(q^{-1})e(k) \\ x(k) = f(u(k)) = r_0 + r_1u(k) + r_2u^2(k) + \dots + r_pu^p(k) \\ A(q^{-1}) = 1 + a_1q^{-1} + \dots + a_nq^{-n} \\ B(q^{-1}) = b_1q^{-1} + \dots + b_rq^{-r} \\ C(q^{-1}) = 1 + c_1q^{-1} + \dots + c_mq^{-m} \end{cases} \quad (6)$$

Where, $u(k)$ and $y(k)$ are the inputs and outputs of the system, $x(k)$ is intermediate signal which can't be measured, is memory less nonlinear gain output, $e(k)$ is measurable noise. q^{-1} is operator of lag, $A(q^{-1})$, $B(q^{-1})$ and $C(q^{-1})$ are the lag operator polynomial. $f(\square)$ is memory less nonlinear gain; $e(k)$ is the value for 0, and variance the σ^2 is white Gaussian noise sequence. $e(k)$ and $u(k)$ are independent of each other.

At this point, the question is to identify parameters of non-linear system, $\{a_i\}$ 、 $\{b_j\}$ and $\{c_k\}$. The parameter vector is $\tilde{\theta} = (a_1, a_2, \dots, a_n, b_1, b_2, \dots, b_m, c_1, c_2, \dots, c_r, r_1, r_2, \dots, r_p)^T$; because traditional methods of identification of nonlinear gain links is not easy to identify, identification of low precision, ineffective, slow and so on. QGA is used by nonlinear system parameter variables expressed in a set of vectors to identify Hammerstein model, improved the recognition accuracy, recognition speed and results, and solved the problem of nonlinear gain links was not easy to identify.

3.2. QGA Identifies the Hammerstein Model

Hammerstein model identification of the objective function is the actual model and output and the squares of the differences of the parameters of model output, also known as the fitness function. That is:

$$f(\theta) = 1 / \left(1 + \left(\sum_{i=1}^s [y(k-i) - \tilde{y}(k-i)]^2 \right) \right) \quad (7)$$

where, s is the window of identification, and $\tilde{y}(k)$ is the output of the estimated parameter model. Selection of objective function is to determine a standard of individual QGA, targets to transmit the smaller the number, the better performance of the individual, but worse.

Application of QGA for Hammerstein model identification, its nature is to every discerning parameter as a quantum bit; these quantum bits are in a superposition, in parameter space regards as solution space, $f(\theta)$ regards as an estimated function. For best individual satisfies the conditions as the loop-termination criteria, conducts the optimization of parameters. The process was:

- (1) Initialized population, the 2mn probability amplitude of all n chromosomes were initialized to $1/\sqrt{2}$, possible solutions in the probability of Hammerstein model parameters that appeared the same.
- (2) Collapsed the initialized of each individual to determine the various solutions.
- (3) Fitness assessment to determine solutions (each qubit in the utilization of evaluation function for Hammerstein model parameters evaluation);
- (4) Recorded the best individual and the corresponding fitness (For best individual as the next-generation evolution of target; According to $f(\theta) = 1 / \left(1 + \left(\sum_{i=1}^s [y(k-i) - \hat{y}(k-i)]^2 \right) \right)$);
- (5) The judgment whether the parameter was an optimal solution, if they meted the optimal solution was to quit or continued to run;
- (6) Did not meet the optimal solution value, continued to be implemented on population measurement, the various solutions identified;
- (7) Conducted fitness assessments to determine solutions;
- (8) Quantum revolving door updated Hammerstein model parameters of chromosome species;
- (9) Recorded the best individual and the corresponding fitness
- (10) Number of iterations t plus 1, returned to step (5);

4. Experimental Results and Analysis

Now consider the following system identification: systems as Hammerstein model of differential equations is described in section 3.1, where the mean value of the noise $e(k)$ is 0, variance of $\sigma^2 = 0.01$; Input signal $u(k)$ is zero mean Gaussian white noise sequences, variance is b, then

$$\begin{cases} A(q^{-1})y(k) = B(q^{-1})x(k-1) + C(q^{-1})e(k) \\ x(k) = u(k) + 0.5u(k)^2 \\ A(q^{-1}) = 1 + 1.5q^{-1} + 0.7q^2 \\ B(q^{-1}) = q^{-1} + 0.8q^{-2} + 0.3q^{-3} + 0.1q^{-4} \\ C(q^{-1}) = 1 + q^{-1} + 0.6q^{-2} + 0.3q^{-3} + 0.1q^{-4} \end{cases} \quad (8)$$

From above differential equation, total of 11 parameters needed to estimate the model, namely:

$$\theta = [a_1, a_2, b_1, b_2, b_3, b_4, c_1, c_2, c_3, c_4, r_2]^T = [1.5 \ 0.7 \ 1 \ 0.8 \ 0.3 \ 0.1 \ 1 \ 0.6 \ 0.3 \ 0.1 \ 0.5]^T \quad (9)$$

Table 1. Hammerstein model runs 30 statistical results

P	T	GA		PSO		QGA	
		Mean	St.dev	Mean	St.dev	Mean	St.dev
a_1	1.5	1.4765	0.0145	1.4895	0.0065	1.4986	0.0013
a_2	0.7	0.6876	0.0231	0.6932	0.0016	0.6997	0.0011
b_1	1	0.9532	0.0201	0.9753	0.0025	0.9987	0.0016
b_2	0.8	0.7698	0.0189	0.7923	0.0017	0.7998	0.0011
b_3	0.3	0.3065	0.0146	0.3025	0.0012	0.3011	0.0005
b_4	0.1	0.1036	0.0256	0.1025	0.0023	0.1002	0.0002
c_1	1	0.8978	0.0431	0.9234	0.0023	1.0162	0.0017
c_2	0.6	0.6189	0.0536	0.6043	0.0032	0.6012	0.0003
c_3	0.3	0.3096	0.0148	0.3025	0.0012	0.3004	0.0002
c_4	0.1	0.0912	0.0234	0.0946	0.0026	0.0998	0.0020
r_2	0.5	0.5067	0.0212	0.5032	0.0165	0.5011	0.0100
Average T		36'45"		29'32"		16'35"	

The parameter of QGA setted:the window width was 50,binary length of quantum bit was 20,this measure used the QGA evaluation function to optimize, population size was 40,and evolving Algebra was 300.Used MATLAB simulation software for simulation, Table 1 listed the respectively used QGA,PSO and GA for stochastic simulation experiments of 30 times' results.

From the results showed in table 1, quantum genetic algorithm converged to the actual parameter values more precisely than the PSO and GA, identification of the parameter accuracy has improved significantly. Average time to run from the three algorithms, QGA's search speed was faster than the PSO and GA, showed the efficiency and viability of the QGA. With the increase of the evolution algebra, each generation of the best fitness value as shown in Figure 2.

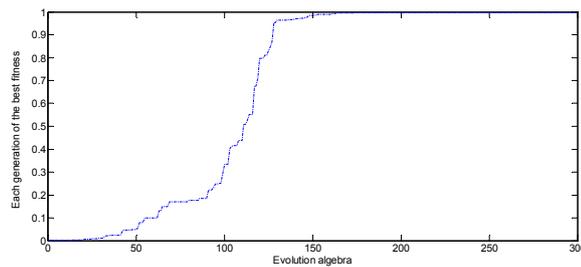
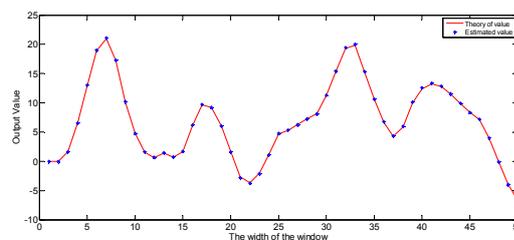


Figure 2. Adapt to changes in the value

As shown in Figure 2, with increasing evolutionary algebra, the fitness value is gradually changed to 1, indicating that the identification parameter reaches the minimum square sum of the error, fitness is the best.

With the evolutionary generation increases, when the identification window width is reached, QGA identification of the corresponding estimated parameters and the actual parameters of the fitting shown in Figure 3.



Notes: “—” was Theory of value,“*” was Estimated value
Figure 3. QGA identification parameters fitting curve

As can see from Figure 3,theoretical output curve and an estimate of the value of the output curve were basically the same, identification with good effect, and thus verify effectiveness of the QGA parameter estimation of non-linear models, also provided an effective method for nonlinear system identification.

5. Conclusion

In this article used QGA to identify for nonlinear Hammerstein model. Quantum chromosome ensured that the diversity of the individual stocks, quantum population increased stocks of revolving door update-optimizing speed. Quantum rotation angle of the revolving door symbol decided convergence of algorithm in the derection, amplitude decided speed the

convergence and efficiency. Simulation results showed that using quantum genetic algorithm for Hammerstein model identification accuracy and speed were satisfactory, showed the feasibility and effectiveness of this method.

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