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Kinetic Parameters Identification of Double Pendulum Robot

Dan Yuanhong*[1], Li Zushu[2]
[1,2]Institute of Artificial Intelligence System, Chongqing University of Technology, Chongqing, China
[1,2]Institute of Intelligent Automation, Chongqing University, Chongqing, China
*Corresponding author, e-mail: cq.dan3@gmail.com

Abstract

The model structure of Double Pendulum Robot (DPR) has been built up with Lagrange equations. To reduce the difference between simulation control and real-time control, the kinetic parameters of Double pendulum robot (DPR) is accurately identified with proposed improved genetic algorithm (IGA) which integrated hybrid coding, hamming distance, orthogonal experiment, feedback mutation, and a specially designed fitness function. This improved genetic algorithm (IGA) overcome the shortcoming of traditional genetic algorithm, strengthen global and local searching capability, and get results more close to global optimal solution. Finally, the optimal results (kinetic parameter values) are applied to model, and make a contrast experiment of zero input response between searched optimal kinetic parameters and real kinetic parameters of DPR.

Keywords: *Double Pendulum Robot, model identification, improved genetic algorithm*

1. Introduction

The researches of underacutated articulated robot (such as pendulum robot and acrobat) attract an extensive interest [1], [2]. Because the complexity and difficult of motion control on double pendulum robot, it is very important for the real-time control of DPR to accurately identify kinetic parameters of DPR. There are two ways to get kinetic parameters: (1) direct measurement; (2) system identification. For parameters which can be conveniently detected (such as mass, length) are obtained by direct measurement method; while for parameters which are hard to measure (such centroid position, moment of inertia, coefficient of friction) usually are fixed by parameter identification method. The traditional parameter identification methods usually use least square method, some new parameter identification methods are developed for a certain problem. Mayeda. H,Koji.Yoshida [3] give a method to determine which is the basic kinetic parameter and figure out the number of basic kinetic parameter. From energy relation, M. Gautier and W. Khalil[4] deduced a method to get basic kinetic parameters of robot. All those methods need to precisely detect the real-time input torque of each axis on robot, this make the task of model identification hard to be achieved. From 1980s, a kind of “intelligent identification algorithm” is developed which introduced artificial intelligent, expert system, and neuronal networks [5], [6]. This paper propose a method to identify kinetic parameter by an improved genetic algorithm, such method don not need to detect the input torque of each joint, only make a contrast of zero response between simulation model and real system.

2. Problem Statements

2.1 Kinetic Model of Double Pendulum Robot

The kinetic model of double pendulum robot [7] is shown in equation (1):

$$\begin{bmatrix} 1 & 0 & 0 \\ M_1 & M_2 & M_3 \\ m_2 l_2 L_0 \cos\theta_2 & M_3 & J_2 + m_2 l_2^2 \end{bmatrix} \ddot{\Theta} + \begin{bmatrix} 0 & 0 & 0 \\ M_4 & c_1 + c_2 & M_5 \\ M_6 & M_7 & c_2 \end{bmatrix} \dot{\Theta} = \begin{bmatrix} u \\ M_8 \\ m_2 g \sin\theta_2 \end{bmatrix} \qquad (1)$$

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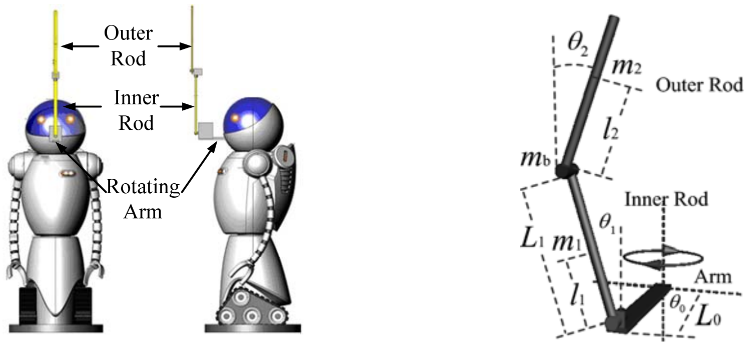
Where:

$$M_1 = (m_1 l_1 + m_2 L_1 + m_b L_1) L_0 \cos\theta_1, \quad M_2 = J_1 + m_1 l_1^2 + m_2 L_1^2 + m_b L_1^2,$$
$$M_3 = m_2 l_2 L_0 \cos(\theta_1 - \theta_2), \quad M_4 = (m_2 l_2 L_1 \sin\theta_2 - M_2 \sin\theta_1)\dot{\theta}_0 \cos\theta_1$$
$$M_5 = m_2 l_2 L_1 \dot{\theta}_2 \sin(\theta_1 - \theta_2) - c_2, \quad M_6 = (m_2 l_2 L_1 \sin\theta_1 - (J_2 + m_2 l_2^2)\sin\theta_2)\dot{\theta}_0 \cos\theta_2$$
$$M_7 = -m_2 l_2 L_1 \dot{\theta}_1 \sin(\theta_1 - \theta_2) - c_2, \quad M_8 = (m_1 l_1 + m_2 L_1 + m_b L_1) g \sin\theta_1$$

$\Theta=[\theta_0, \theta_1, \theta_2]^T$ is generalized coordinates; m_1, m_2, m_b are respectively the mass of inner rod, outer rod, and encoder; L_0, L_1 are respectively the length of rotating arm and inner rod; J_1, J_2 are the moment of inertia of inner rod and outer rod; l_1, l_2 are the centroid position of inner rod and outer rod; c_1, c_2 are friction of arm-inner rod axis and inner rod-outer rod axis; u is the control variable.



(a) The physical device of DPR (b) Physical structure of DPR

Figure 1. Double Pendulum Robot

2.2 Solution Definition

The structure of kinetic model for DPR has been deduced out by Lagrange method (equation (1)); the key is to choose a set of kinetic parameter values, so that the simulation model is equivalent to physical device, and to make simulation experiment prepare for real-time control.

Take the zero response error sum of square between simulation model and physical device as evaluation index; the optimal problem can be defined as:

$$\begin{cases} \min E(Z), \quad Z \in [L,U] \\ E(Z) = \sum_{i=0}^{2} \sum_{k=1}^{n} [(\theta_i(k) - \hat{\theta}_i(k))^2 + (\dot{\theta}_i(k) - \hat{\dot{\theta}}_i(k))^2] \end{cases} \tag{2}$$

Where, Z =(m_1, m_2, m_b, J_1, J_2, l_1, l_2, c_1, c_2) are kinetic parameters need to be identified. $\theta_i(k)$, $\hat{\theta}_i(k)$, $\dot{\theta}_i(k)$, $\hat{\dot{\theta}}_i(k)$ are respectively the angle and angular velocity of the i^{th} axis at time k for actual device and simulation model. $[L,U]$ is the feasible solution space for kinetic parameters (Z).

3. Improved Genetic Algorithm

To overcome the defect of traditional genetic algorithm (such as premature convergence, inbreeding), we introduced an improved genetic algorithm which combined hybrid coding, hamming distance, orthogonal experiment, feedback mutation etc.

3.1. Hybrid Coding

In genetic algorithm, each solution vector is encoded to a chromosome in population, and each gene in a chromosome corresponding to a parameter in solution vector, and certain numbers of chromosome constitute a population. Hybrid coding has the both advantages of float encoding and binary encoding, which guarantee solution vectors (chromosomes) take a uniform distribution in solution space with a relative high precision. The hybrid encoding algorithm is shown as follow:

$$\begin{cases} x = \{x_1, \cdots, x_i, \cdots, x_N\} \\ x_i = l_i + \beta(u_i - l_i), \quad \beta \in \{0, 0.1, 0.2, \cdots, 1.0\} \end{cases} \tag{3}$$

where, x is a chromosome, x_i is the i^{th} gene of x, u_i and l_i are the upper limit and lower limit of the i^{th} gene, β is a random value from $\{0, 0.1, 0.2, \ldots, 1.0\}$.

3.2. Pairing Operation for Crossover

When the hamming distance of two chromosomes is less than 2, we can not get offspring chromosome with enough diversity if take those two chromosomes as parents, this problem is so-called “inbreeding”. In order to avoid inbreeding, only choose chromosomes with enough difference (hamming distance lager than 2) to perform crossover operation. The hamming distance of two chromosomes is defined as follow:

$$\begin{cases} D_{Ha\min g}(x, y) = \sum_{i=1}^{N} d_i \\ d_i = \begin{cases} 0, & x_i = y_i \\ 1, & x_i \neq y_i \end{cases} \end{cases} \tag{4}$$

where, x and y are two chromosomes selected to perform crossover operation, x_i and y_i are respectively the i^{th} gene of x and y.

When hamming distance of two chromosomes is less than 2, one chromosome will be replaced by a new generated chromosome with hybrid encoding. Pairing operation based on hamming distance can reduce the number of orthogonal experiment, especially at the late stage of genetic algorithm.

3.3. Variable Precision Crossover Operation

Part idea of variable precision crossover comes from Convex Set Theory in Management which performs single-point crossover operation. Take two chromosomes x and y to perform crossover operation at the i^{th} gene, offspring can be generated by following algorithm:

$$\begin{aligned} & x' = \{x_1, \cdots, x_{i-1}, x_i^{'}, y_{i+1}, \cdots, y_N\} \\ & y' = \{y_1, \cdots, y_{i-1}, y_i^{'}, x_{i+1}, \cdots, x_N\} \\ & x_i^{'} = x_i + \beta(y_i - x_i), \quad y_i^{'} = l_i + \beta(u_i - l_i) \end{aligned} \tag{5}$$

where, $x^{'}$ and $y^{'}$ are the offspring chromosomes, x_i and y_i are the i^{th} gene of x and y, $x_i^{'}$ and $y_i^{'}$ are the new generated gene at crossover point. If the i^{th} gene is repeatedly selected as crossover point, the precision of the i^{th} gene will be enhanced, and eventually improve the precision of optimal solution.

3.4. Orthogonal Experiment

Orthogonal experiment is applied after crossover operation; the purpose is to make an optimal combination of genes from two selected parents’ chromosome with fewer numbers of experiments (less computation). To access detail information about orthogonal experiment, please see literature [8], [9] or Statistics related books.

3.5. Hybrid Mutation

Hybrid mutation means the combination of single-point mutation and multi-point mutation, the purpose is to improve the genetic diversity of population. Whether single-point mutation or multi-point mutation, this is randomly online determined.

3.6. Feedback Mutation

Dynamic Encoding means dynamically change the solution space of parameters (genes), and gradually reduce search range. This will enhance the local search ability of GA, but it's also probably leads to premature convergence and fall into a local optimal solution. Feedback mutation using randomly generated new chromosome replace the similar chromosome in the population, this will maintain the diversity of the population [10]. So, the combination of dynamic encoding and feedback mutation can overcome the defect of premature convergence and make the search result closer to global optimal solution. Whether or not take dynamic encoding and feedback mutation, depends on the relation between population fitness and best individual fitness. The population fitness is calculated by:

$$f_{population} = \frac{\sum_{i=1}^{n} f_i}{M \times f_{optimal}} \tag{6}$$

where, $f_{optimal}$ is best individual fitness, f_i is the fitness of the i^{th} chromosome in population, M is population size.

New chromosome is generated by dynamic encoding with following method.

$$y_i = \mu x_i + \beta v x_i \tag{7}$$

where, y_i is the i^{th} gene of the new chromosome, x_i is the i^{th} gene of the optimal chromosome in population, μ, β, v are constants less than 1.

3.7. Fitness Function

Fitness function is very important for genetic algorithm, detailed analysis on E(Z) should be made before choose a fitness function. As we can see from the experiment data shown in table 1, E(Z) is obviously a multimodal function and function values changed rapidly with different Z (kinetic parameters). If directly take E(Z) as fitness function, chromosomes which have not so good fitness may "die" with out any genetic manipulation. Reference the concept of signal-to-noise ratio in signal processing, fitness function is constructed as follow:

$$f(Z) = 10\log\frac{1}{E(Z)} = -10\log E(Z) \tag{8}$$

Table 1. The values of E(Z) for different kinetic parameters on the same initial condition

	l_1	l_2	m_1	m_2	m_b	c_1	c_2	J_1	J_2	$E(Z)$
1	0.2	0.2	0.1	0.1	0.208	0.001	0.001	0.00133	0.00133	0
2	0.176	0.208	0.084	0.088	0.176	0.0009	0.00109	0.00117	0.00138	78.73
3	0.223	0.207	0.104	0.104	0.224	0.0011	0.0110	0.00143	0.00128	0.149
4	0.223	0.208	0.106	0.104	0.224	0.0012	0.00106	0.00143	0.00128	17.45
5	0.196	0.200	0.106	0.108	0.225	0.0010	0.00108	0.00146	0.00141	52.07
6	0.216	0.200	0.103	0.104	0.212	0.0010	0.00101	0.00136	0.00138	4.69
7	0.208	0.195	0.102	0.110	0.229	0.0009	0.00102	0.00136	0.00144	37.35

Given three initial conditions of Double Pendulum Robot: $X_1=[0, \pi, 0.1, 0, 0, 0]^T$, $X_2=[0, 0.1, 0.1, 0, 0, 0]^T$, $X_3=[0, 0.1, \pi, 0, 0, 0]^T$; and three groups of kinetic parameters in table 1: first group, fourth group, sixth group. Table 2 shows the fitness values of those three groups' kinetic parameters on different initial conditions.

Table 2. E(Z) values of kinetic parameters on different initial condition

	X_1	X_2	X_3
1	0	0	0
4	0.149	164.45	139.46
6	4.69	53.195	64.470

As we can see from table 2, E(Z) values of the same kinetic parameters are different on different initial condition, this means it fall into a local optimal solution. in order to evaluate certain group of kinetic parameter more objectively, we finally construct fitness function as follow:

$$H(Z)=\begin{cases}\sum_{i=1}^{3} E_i(Z,X_i), & H(Z)\le M\\ M, & H(Z)>M\end{cases} \tag{9}$$

$$f(Z)=\delta-10\log H(Z),\quad \delta>10\log M \tag{10}$$

Considering the values of H(Z) are generally big, it is not suitable directly adopted to judge certain group of kinetic parameter. M is a relative big positive real constant which define a limiting chances of survival, while the positive real constant δ is a regulatory factors which determines the survival chance of individuals with bad fitness. Then, the problem of kinetic parameter identification can be denoted as:

$$\max f(Z),\quad L<Z<U \tag{11}$$

3.8. Algorithm description

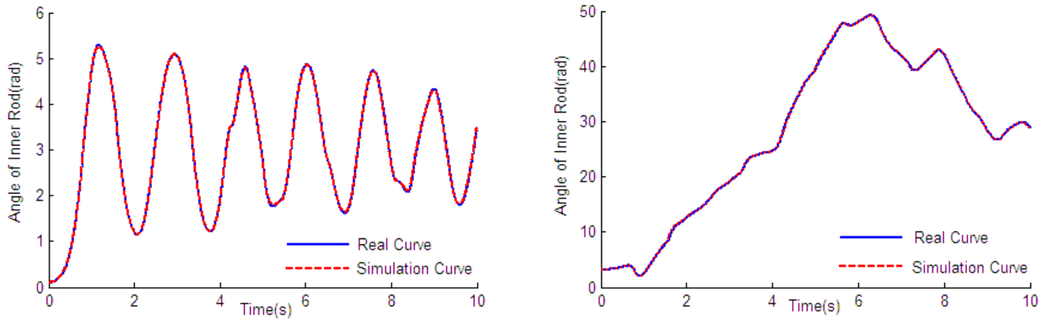
(1) Initialize population with hybrid encoding
(2) Calculate fitness of each individuals in population, and sorted in descending order
(3) Calculate the fitness of population $f_{population}$
(4) If $f_{population}>\alpha$, and $f_{optimal}>\sigma$ then perform dynamic encoding and feedback mutation; otherwise, perform traditional mutation
(5) Crossover operation: select two parent chromosomes based on hamming distance, and perform variable precision crossover operation.
(6) Perform orthogonal experiment on previous new chromosomes to produce an optimal offspring
(7) Hybrid mutation
(8) Repeat (5)~(7), until M.Pc/2 new chromosomes are produced
(9) Combine parent population and offspring population, and sort in descending order
(10) Select the first M chromosomes as the population of next generation
If meet the termination condition, then stop; otherwise, reapet (3)~(10)

4. Numerical simulation and analysis

4.1. Experiment results

Experiment condition: population size M=200, crossover rate $P_c=0.8$, mutation rate $P_m=0.1$, max generation 1000, α=0.999, σ=5, δ=35, μ=0.95, ν=0.1, simulation duration 10s, simulation interval 0.005s, numerical algorithm is four order Runge-Kutta algorithm. The actual kinetic parameter value of double pendulum robot is Z={0.2, 0.2, 0.1, 0.1, 0.208, 0.001, 0.001, 0.00133, 0.00133}, the upper limit of genet value is 1.2Z, and lower limit of gene value is 0.8Z, the initial condition of double pendulum robot is X_1, X_2, X_3.

Table 3 shows some experiment data of parameter identification, figure 2 shows the zero input response curves of real kinetic parameter and optimal kinetic parameter at the same initial condition. Figure 3 shows the difference of zero input response between real kinetic parameter and optimal kinetic parameter. While the evolutionary process of optimal individual in each generation is shown in figure 4.



(a) Angle of inner rod (b) Angle of outer rod

Figure 2. Contrast response curve between real kinetic parameter and optimal parameter

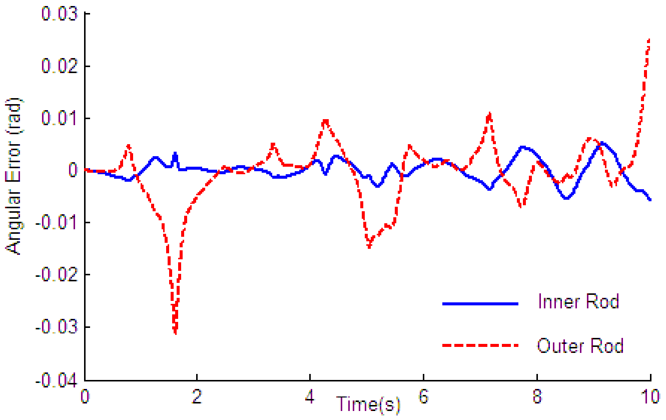


Figure 3. Angular error of inner / outer rod between real curve and simulation curve

Table 3. Some optimal search results of kinetic parameter identification

	l_1	l_2	m_1	m_2	m_b	c_1	c_2	J_1	J_2	$H(Z)$
1	0.21200	0.20000	0.09071	0.10000	0.24000	0.00104	0.00104	0.0010640	0.0013300	56.8910
2	0.20240	0.19200	0.11600	0.10557	0.19093	0.00104	0.00092	0.0013548	0.0014896	43.2663
3	0.20800	0.19513	0.10200	0.11000	0.22880	0.00092	0.00110	0.0013566	0.0014364	37.3511
4	0.21316	0.19200	0.09400	0.09800	0.19552	0.00108	0.00096	0.0013592	0.0013566	20.4388
5	0.19000	0.19480	0.09254	0.09400	0.19136	0.00106	0.00092	0.0013257	0.0013310	12.1238
6	0.19600	0.20000	0.10600	0.10800	0.22464	0.00980	0.00108	0.0014500	0.0014364	7.16146
7	0.21600	0.20000	0.10319	0.10400	0.21216	0.00104	0.00104	0.0013566	0.0013832	4.69242
8	0.19874	0.20000	0.09200	0.09800	0.20800	0.00100	0.00099	0.0013598	0.0013182	1.21646
9	0.19874	0.20000	0.09420	0.09800	0.20800	0.00100	0.00099	0.0013465	0.0013162	0.86943
10	0.19970	0.20000	0.1010	0.0995	0.2080	0.00101	0.00099	0.0013399	0.0013281	0.07534

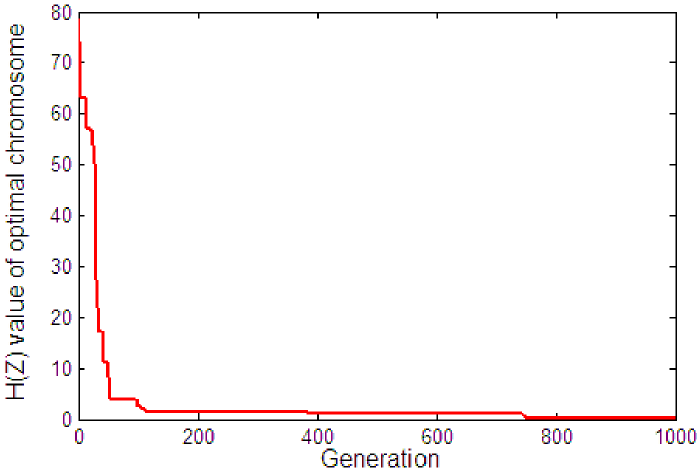


Figure 4. Evolutionary process of best chromosome in each generation

4.2. Analysis of experiment result

The last row of table 3 is the best chromosome (kinetic parameters) obtained by proposed improved genetic algorithm, and the percentage errors corresponding to real kinetic parameters respective are: 0.15%, 0.00%, 1.00%, 0.50%, 0.00%, 1.00%, 1.00%, 0.74%, and 0.14%. The response curves of optimal kinetic parameters and real kinetic parameter are almost overlapped as we can see from figure 2. All this indicate that IGA successfully found the global optimal solution with a high precession. In figure 4, thanks to orthogonal experiment, optimal chromosome has a fast convergence at beginning stage (before generation 100); after that, feedback mutation is activated, this slow down convergence speed but guaranteed global optimal solution; finally, dynamic encoding and variable precession crossover enhanced the accuracy of optimal solution.

5. Conclusion

This paper proposed an improved genetic algorithm, which introduced hybrid encoding, variable precession crossover, orthogonal experiment, and feedback mutation. Numerical experiment shows that proposed IGA can efficiently solve the kinetic parameter identification problem of double pendulum robot; this testified the validity of IGA.

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