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Surname Inherited Algorithm Research based on Artificial Immune System

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Abstract

To keep the diversity of antibodies in artificial immune system evolution process, this paper puts forward a kind of increase simulation surname inheritance algorithm based on the clonal selection algorithm, and identification and forecast the Vibration Data about CA6140 horizontal lathe machining slender shaft workpiece prone. The results show that the algorithm has the characteristics of flexible application, strong adaptability, an effective approach to improve efficiency of the algorithm, a good performance of global searching and broad application prospect.

Keywords: a*rtificial immune system, clone algorithm, inheritance algorithms*

1. Introduction

People never give up developing artificial intelligence in all ages [1]. They have proposed the artificial neural network model through studying and simulating the biological cranial neuroid network, and developed the model greatly.

In addition, the artificial immune system (called as AIS, too) proposed based on the immunological network theory proposed by Jerne [2-4] become a hot spot in the artificial intelligence field. Artificial immune system, as a new branch of computational intelligence, is a computational method inspired by the biology immune system. In 1986, Farmer, et al proposed the dynamic model of the immune system based on the immunologic network theory, and probed into the relationship between the immune system and other artificial intelligence methods, and started studying the artificial immune system. Later, the artificial immune system becomes more and more developed, which reflects mainly in the negative selection algorithm proposed by Forrest in 1996 for detecting computer viruses [5-6], the RLAIS algorithms proposed by Timmis in 2000 [4], the Clone Selection Algorithm proposed by De Castro in 2002 [7], the aiNet [8], etc. These algorithms were proposed by fully drawing lessons from the biological immune method of the immune cells, like B-cells and T-cells in the immune system [9], lay a foundation for the artificial immune system, and have born many application fruits especially in computer virus prevention field, etc. However, as for the Smart Diagnosis of the mechanical equipment, the study target is more complex, and the requirement for AIS system is different.

At present, the study and application of AIS focuses on data clustering, but Nowadays, the productivity, reliability and safety of industrial mechanisms are more and more important. A permanent condition monitoring system to the critical devices is proved to be necessary, whose status of state not only affects the operation of itself but also the follow-up of productions. And bearing faults, as most common faults, have been concerned by researchers for a long time, especially using the artificial intelligence. Traditional intelligent algorithms, like the BP algorithm of the artificial neural network, are often subjected to local extremum, which can be relieved by AIS. Considering the above, the paper presents the study on how to keep the diversity of antibodies during AIS development, and presents a method that enriches algorithms and effectively avoids premature constriction and repetitive computation by setting family identifications and simulating surname inheritance based on the traditional Clone Selection Algorithm. This method speeds up the computation.

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2. Research Method

As the study goes on, the Clone Selection Algorithm also undergoes continuous development. The flow of the Clone Selection Algorithm [10] proposed by De Castro is shown as below:

1) Generate a candidate scheme set S(P), which is the sum of the subset of memory cells (M) and residual groups (P_r), ($P = P_r + M$);
2) Determine n best individuals P_n in the group P based on the affinity extent;
3) Clone (copy) the N best individuals to generate a clone group C;
4) Put the clone group C under mutation operation with the mutation probability in inverse proportion to the affinity of the antibodies. Then generate a mature antibody group C^*;
5) Reselect improved individuals from the group C^* to form a memory cell set, and some of the members of the set P may be replaced by the improved ones of the group C^*;
6) Replace d low-affinity antibodies in the group to maintain the diversity of antibodies.

Similar to the classical genetic algorithm proved by Rbdolph, it can be proved that the algorithm constriction is based on probability if the best individual of every population does not participate in the hybridization and mutation. So, when the Clone Selection Algorithm is employed, the best antibodies are always reserved. In order to reserve the diversity of antibodies, a mutation operator is employed for the temporary clone group C that is put under mutation operation, and a crossover operator is always employed for the gene interchange of the individuals of the temporary clone group C. The Figure 1 shows the flow of the Clonal Selection Algorithm.

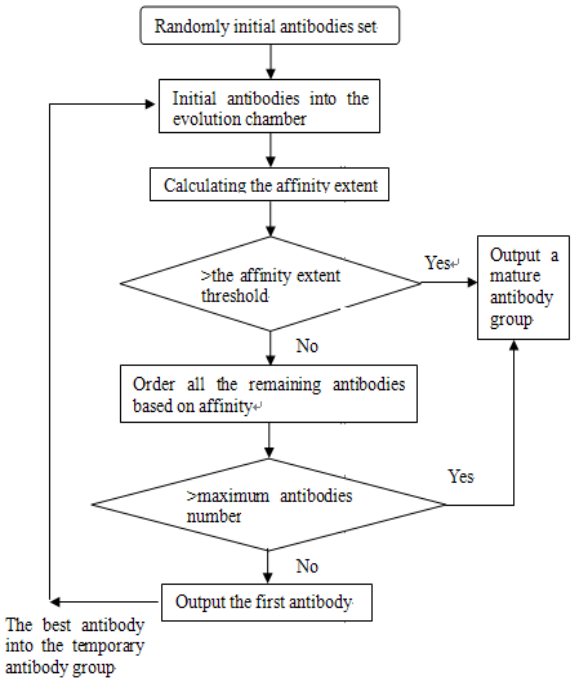

Figure 1. Clonal Selection Algorithm Flowchart

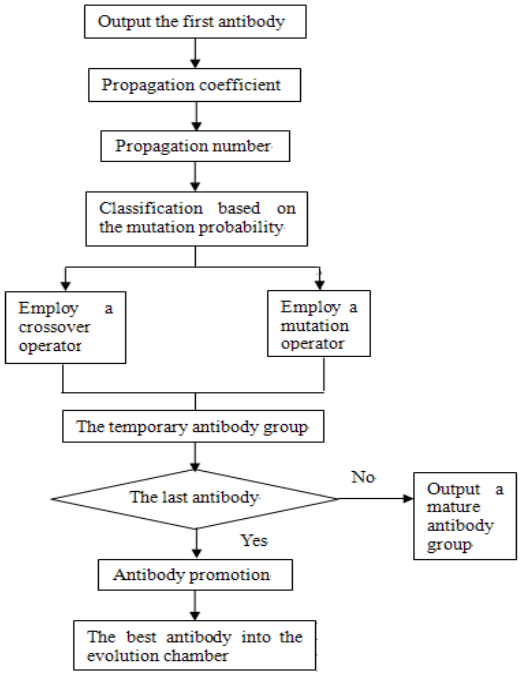

Figure 2. Clonal Selection Algorithm Flowchart (continued)

In this paper, the improvement for the Clone Selection Algorithm is to further raise antibody diversity by adding genetic marker bits to the temporary antibody group during the evolution for the purpose of raise algorithm global search and efficiency. The details of this are shown as below:

1) Provide family identifications as per generation order when generating an initial antibody group;
2) When employ a mutation operator, the antibody family marker is used for newly generated antibodies;
3) When employ a crossover operator, all the family markers of the actively employed antibodies are succeeded to newly generated antibodies;
4) Order the members of each family based on affinity as per family identifications at first when ordering temporary antibody groups;
5) Put the best antibodies from each family into the temporary antibody group (namely the evolution chamber), and discard surplus temporary antibodies as per the set maximum concentration;
6) After removal, order all the remaining antibodies based on affinity, and then inject them into the evolution chamber.

Mainly through setting marker bits, this method is to raise ergodicity and algorithm efficiency by avoiding the large amount of useless computation caused by the premature constriction of antibodies at local extremum point. The concentration is defined as the ratio of a whole family to the temporary antibody group. In order to verify the algorithm, this paper develops the analysis according to the training process of the vibration data during the machining course of CA6140 horizontal lathe.

3. Fault Diagnosis System

The rolling bearing fault diagnosis system consists of three processes: feature extraction, antibody training and online diagnosis.

Feature extraction. This process is the essential step. Assume the discrete data of signal $x(t)$ is $x_1, x_2, \cdots, x_n$ with certain sampling frequency, the time-domain features are extracted as follows:

Skewness:

$$\alpha = \frac{1}{N}\sum_{i=1}^{N} x_i^3 \tag{1}$$

Waveform index:

$$S_f = \frac{X_{rms}}{|\overline{X}|} = N \times X_{rms} / \sum_{i=1}^{N} |x_i| \tag{2}$$

Kurtosis index:

$$K = \frac{\beta}{X_{rms}^4} = \frac{1}{N}\sum_{i=1}^{N} x_i^4 / X_{rms}^4 \tag{3}$$

Autocorrelation coefficient:

$$\rho_x(n\Delta t) = R_x(n\Delta t) / R_x(0) \tag{4}$$

where $X_{\max}$ is the max amplitude of signal, X_{rms} is the root mean square amplitude, N is the length of discrete data and.

$$R_x(n\Delta t) = \frac{1}{N-n}\sum_{n=1}^{N-n} x(r)x(r+n) \tag{5}$$

Then add peak values and the peak frequencies in the specific frequency intervals as the frequency-domain features after STFT procedure. Each interval corresponds to a theoretic frequency of a typical fault.

4. Results and Analysis

During the experiment, AIS system was used to identify and forecast the flutter fault occurring frequently when the lathe machines a workpiece with a slim shaft, and the vibration signals of the lathe in the x, y and z directions were acquired respectively, and the signal energy in each frequency domain was normalized to act as eigenvalue. The following Figure 3 shows the constriction results of the training of the antibodies with family markers and those without family markers respectively based on evolutionary generation.

When use the abscissa to represent the evolutionary generation, adopting the surname inheritance algorithm can delay the constriction of antibodies, which is caused by keeping antibody diversity. However, because some over concentrated antibodies are discarded, the algorithm' speed becomes much higher. In the following table, the maximum affinity and training duration (set 50 families) figured out by using the surname inheritance algorithm under various concentrations, the same specimens and the same other parameters.

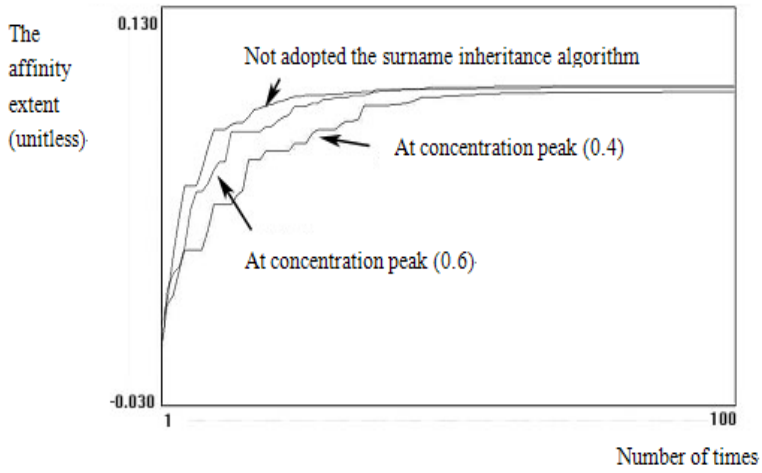

Figure 3. Convergence Results of the Antibodies with Family Markers and those without Family Markers Respectively

Table 1. The Maximum Affinity and Training Duration (set 50 families) by Adopted/Not Adopted the Surname Inheritance Algorithm

	1st	2nd	3rd
Not adopted / the affinity extent	0.090323	0.090340	0.090346
Not adopted / time(s)	5.484	6.438	6.86
at concentration (0.8) / the affinity extent	0.090332	0.090334	0.090338
at concentration (0.8)/ time(s)	5.688	6.141	6.156
at concentration (0.6)/ the affinity extent	0.090343	0.090316	0.090271
at concentration (0.6)/ time(s)	5.25	6.14	4.828
at concentration (0.4) the affinity extent	0.090313	0.090308	0.090323
at concentration (0.4)/ time(s)	5.047	3.484	4.672
at concentration (0.2)/ the affinity extent	0.090318	0.090327	0.090249
at concentration (0.2)/ time(s)	3.031	3.563	3.156
at concentration (0.1)/ the affinity extent	0.090336	0.090331	0.090328
at concentration (0.1)/ time(s)	3.078	2.921	2.89

Table 2. The Maximum Affinity and Training Duration (set 50 families) by Adopted/Not Adopted the Surname Inheritance Algorithm (continued)

	4th	5th	6th
Not adopted / the affinity extent	0.090323	0.090340	0.090346
Not adopted / time(s)	5.484	6.438	6.86
at concentration (0.8) / the affinity extent	0.090345	0.090343	0.090339
at concentration (0.8)/ time(s)	6.188	6.64	5.187
at concentration (0.6)/ the affinity extent	0.090335	0.090314	0.090312
at concentration (0.6)/ time(s)	6.109	5.453	5.578
at concentration (0.4) the affinity extent	0.090336	0.090336	0.090338
at concentration (0.4)/ time(s)	3.656	5.39	4.86
at concentration (0.2)/ the affinity extent	0.090340	0.090291	0.090336
at concentration (0.2)/ time(s)	3.594	3.579	3.063
at concentration (0.1)/ the affinity extent	0.090309	0.090323	0.090311
at concentration (0.1)/ time(s)	2.75	3.328	2.984

Table 3. The Maximum Affinity And Training Duration (set 50 families) By Adopted/Not Adopted the Surname Inheritance Algorithm (continued)

	7th	8th	9th	10 times
Not adopted / the affinity extent	0.090347	0.090345	0.090324	0.090319
Not adopted / time(s)	5.938	6.047	5.922	5.25
at concentration (0.8) / the affinity extent	0.090345	0.090335	0.090343	0.090317
at concentration (0.8)/ time(s)	6.5	7.125	5.407	6.11
at concentration (0.6)/ the affinity extent	0.090329	0.090337	0.090345	0.090341
at concentration (0.6)/ time(s)	5.938	5.484	5.188	5
at concentration (0.4) the affinity extent	0.090319	0.090303	0.090334	0.090339
at concentration (0.4)/ time(s)	4.375	4.5	4.781	4.953
at concentration (0.2)/ the affinity extent	0.090341	0.090316	0.090261	0.090191
at concentration (0.2)/ time(s)	4.094	3.75	3.344	3.546
at concentration (0.1)/ the affinity extent	0.090301	0.090326	0.090288	0.090336
at concentration (0.1)/ time(s)	2.812	3.015	2.719	3.36

According to the above table, although the maximum becomes a little lower after adopting the surname inheritance algorithm, the falling amplitude may be neglected. However, when the surname inheritance algorithm is not adopted, the average duration is 6.11s, and the duration at concentration peak (0.4) is 5.49s; after the surname inheritance algorithm is adopted, the duration at the concentration peak (0.1) sharply cuts down to 3.47s. Similarly, according to the distribution of the 50 evolutionary antibodies in the temporary antibody chamber, we can see that such algorithm raises antibody diversity.

The evolutional antibodies gotten by using such algorithm can correctly recognize the lathe fault.

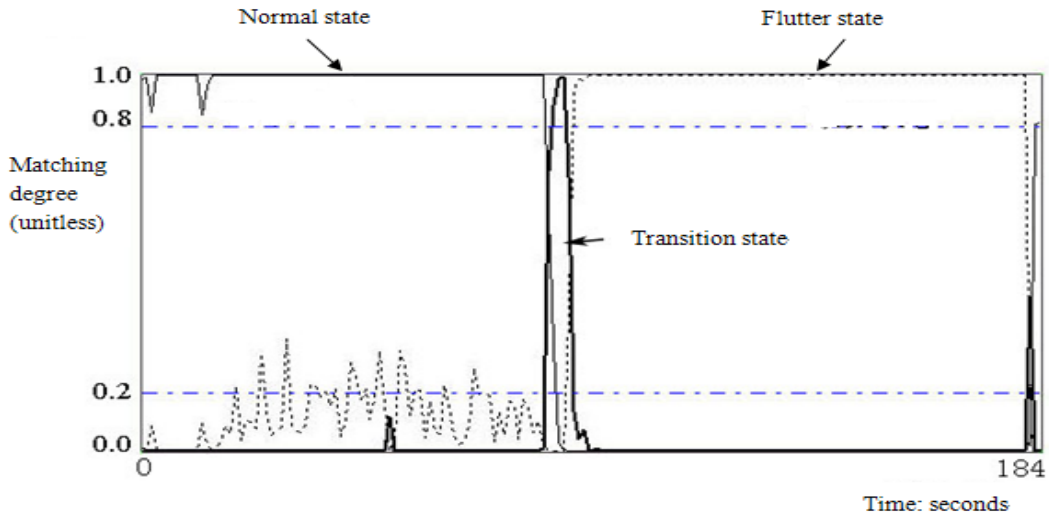

Figure 4. Recognized the CA6140 Lathe Fault

5. Conclusion

The paper presents a surname inheritance algorithm based on the Clone Selection Algorithm. Using such algorithm can effectively raise algorithm diversity, avoid the repetitive computation caused by the premature constriction of antibodies during evolution, and accordingly raise algorithm efficiency. As an auxiliary algorithm for the evolution of the artificial immune system, this algorithm can bring obvious effects when the evolution chamber size is limited or the optimal value needs not to be very accurate.

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