Development of a New Optimization Algorithm Based on Artificial Immune System and Its Application

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Abstract

In resent years, research has taken an interest in design of approximation algorithms due to the requirement of these algorithms for solving many problems of science and engineering like system modeling, identification of plants, controller design, fault detection, computer security, prediction of data sets etc. The area of Artificial Immune System (AIS) is emerging as an active and attractive field involving models, techniques and applications of greater diversity. In this paper a new optimization algorithm based on AIS is developed. The proposed algorithm has been suitably applied to develop practical applications like design of a new model for efficient approximation of nonlinear functions and identification of nonlinear systems in noisy environments. Simulation study of few benchmark function approximation and system identification problems are carried out to show superior performance of the proposed model over the standard methods in terms of response matching, accuracy of identification and convergence speed achieved.

1. Introduction

The understanding of natural, more specifically biological immune system (BIS) has increased dramatically over the recent few years by several researchers and has provided a miraculous insight into how the body resists itself from infectious diseases. Through enhanced understanding and investigation, new algorithms inspired by BIS are developed which given rise to the development of a new branch of computational intelligence known as artificial immune system (AIS). Bersini (1990) first used immune algorithms to solve problems. D. Dasgupta in [1] has provided the details about the recent advances in theories and applications of AIS. Like other evolutionary computing algorithms AIS also helps to develop efficient models which are used for computer security, data mining, fault detection, fault tolerance of devices, optimization [2] etc. The four forms of AIS algorithm reported in the literature are immune network model, negative selection, clonal selection and danger theory. In this paper we focus on the optimization aspect of AIS.

2. Optimization Algorithm of AIS

Among the various principles and algorithms of AIS described in book [3] the clonal selection principle describes how the immune cells eliminate a foreign antigen and is simple but efficient approximation algorithm for achieving optimum solution.

When an antigen invades the organism; a number of immune cells or antibodies that recognize these pathogens survive. Among these cells some become effecter cells, while others are maintained as memory cells. The effecter cells secrete antibodies and memory cells having longer span of life so as to act faster or more effectively in future when the organism is exposed to same or similar pathogen. During the cellular reproduction, the somatic cells reproduce in an asexual form, i.e. there is no crossover of genetic material during cell mitosis. The new cells are copies of their parents as shown in Fig.1.During this process they under go a mutation mechanism which is known as somatic hypermutation as described in [2] and [3].

The affinity of every cell with each other is a measure of similarity between them. It is calculated by the distance between the two cells. The antibodies present in a memory response have on average a higher affinity than those of early primary response. This phenomenon is referred to as maturation of immune response. During the mutation process the fitness as well as the affinity of the antibodies gets changed. So in each iteration after cloning and mutation those antibodies which have higher fitness and higher

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affinity are allowed to enter the pool of memory cell .Those cells with low affinity or self-reactive receptors must be efficiently eliminated.

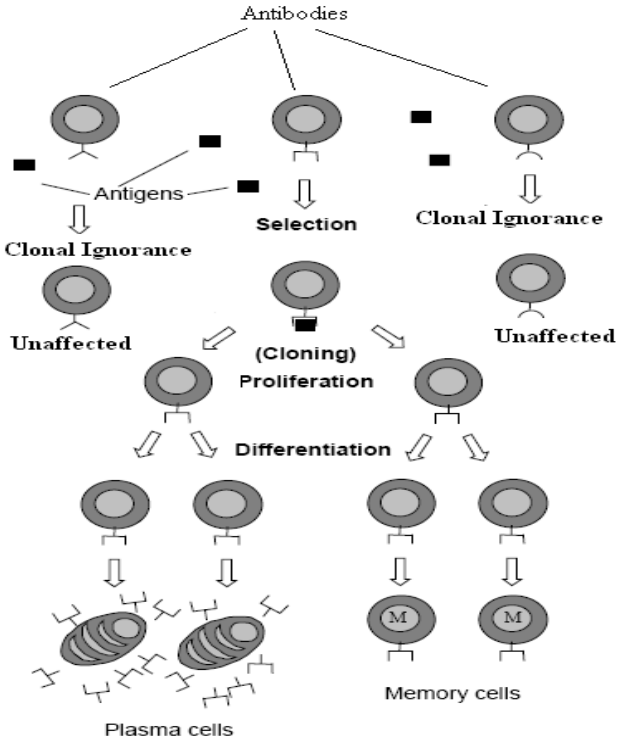

Fig.1 Clonal selection principle

3. Training of Structure

The steps involve in training the weights of any nonlinear structure using optimization algorithm of AIS is represented as follows.

1. Determination of output of plant: Let 'k' be the numbers of input samples taken which passed through the plant to produce plant output y(k).

2. Input samples passed through structure of model: Same input samples are passed through the model consisting of nonlinear structures like FLANN or FIR.

3. Initialization of a group of cells: Here a group of weight vector of the structure is taken which represent solutions. A weight vector consist of (M+2) no of elements if it is FLANN structure else M no of elements for FIR structure. Each element of weight vector is represented by a cell which is basically a binary string of definite length. So a set of binary strings is initialized to represent a weight vector and n number of such weight vectors is taken each of which represent probable solution.

4. Calculation of output of model: Initially weight vector is taken random value. The output of model is computed using the input samples x(k) and weight vector w(k) is given by

$$\hat{y}(k) = \sum_{i=1}^{Q-1} s_i(k) w_i(k) \quad (1)$$

$$s_i(k) = F(x(k)) \quad (2)$$

where weight vector **w**(k) having *Q* elements .

5. Fitness Evaluation: The output of the model $\hat{y}(k,n)$ due to k^{th} sample and n^{th} vector, is compared with the plant output to produce error signal given by

$$e(k,n) = y(k,n) - \hat{y}(k,n) \quad (3)$$

For each n^{th} weight vector the MSE is determined and is used as fitness function given by

$$MSE(n) = \frac{\sum_{k=1}^{K} e^2(k,n)}{K} \quad (4)$$

The objective is to minimize the fitness function of (4) by clonal selection principle.

6. Selection: To select the weight vector (corresponding cells) for which MSE is minimum.

7. Clone: The weight vector (corresponding cells) which yields best fitness value (minimum MSE) is duplicated.

8. Mutation: Mutation operation introduces variations into the immune cells. Probability of mutation P_m is a smaller value. Total number of bits to mutate is the product of total number of cells, number of bits in each cell and probability of mutation of each cell. Among the cloned cells the cell to be mutated is chosen randomly. A random position of the cell is chosen first and then its bit value is altered.

9. Stopping Criteria: The weight vector which provides the desired solution (minimum MSE) and corresponding cells are known as memory cells. Until a predefined MSE is obtained steps 4 -8 are repeated.

4. Applications

A. Nonlinear Function Approximations

The output of the system is a nonlinear function of input given by

$$y(k) = f[x(k)] \quad (5)$$

where the nonlinearity $f[.]$ is given by

$$f_1(x(k)) = x^3(k) + 0.3x^2(k) - 0.4x(k) \quad (6)$$

$$f_2(x(k)) = 0.6\sin(\pi x(k)) + 0.3\sin(3\pi x(k)) + 0.1\sin(5\pi x(k)) \quad (7)$$

For approximation of nonlinearity $f[.]$ in the model we consider FLANN structure shown in Fig.2. Pao originally proposed FLANN as a novel single layer ANN structure capable of forming arbitrarily complex decision regions by generating nonlinear decision

boundaries [4].Here input x(k) is a uniformly distributed random signal over the interval [-1, 1] which undergo trigonometric expansion given by

$$s_i(k) = \begin{cases} 1 & \text{for } i = 0 \\ x(k) & \text{for } i = 1 \\ \sin(i\pi x(k)) & \text{for } i = 2,4...M \\ \cos(i\pi x(k)) & \text{for } i = 3,5...M+1 \end{cases} \quad (8)$$

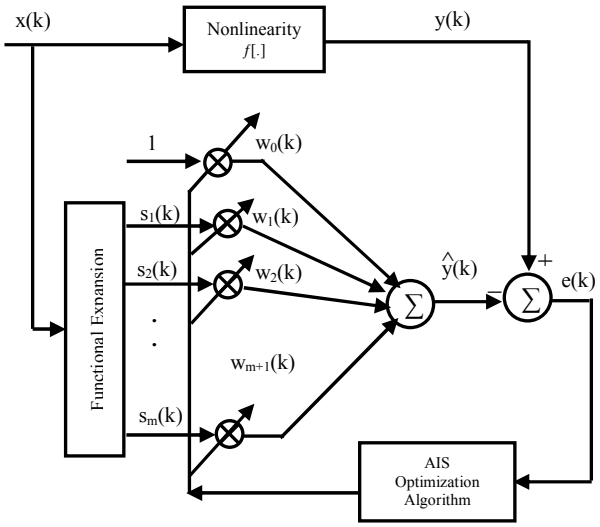

Fig.2 Proposed FLANN-AIS Model for Nonlinear Function Approximation

The output of FLANN structure is feed to an adaptive linear combiner whose weights are altered according to clonal selection algorithm. Simulation study is also carried out for the above functions using MLP structure trained by back propagation algorithms as presented in our paper [6].

The number of input samples used for training and testing is represented in Table I. In the proposed model the initial population of cells is taken as 78. For f_1,f_2 the number of trigonometric expansions are 5and 11 respectively. The weights are trained for 150, 300 iterations respectively for f_1, f_2. For simulation using MLP, the structure is taken as {1_20_10_1}.The nonlinearity used at the node is hyperbolic tan function. In back propagation training both the convergence parameter and momentum term is set to 0.1. The weights of MLP are trained for 50000 iterations. The testing is carried out by a uniformly distributed random signal over the interval [-1, 1]. The performance of both the algorithms is compared in terms of estimated output and the error plot as shown in Figs. 3-4.

TABLE I
RESULTS OF NONLINEAR FUNCTION APPROXIMATION

Fun. Apx.	CPU Time During training (in Sec.)		Sum of Square Errors (SSE)			No of input sample used in training	
	MLP	AIS	Samples For testing	MLP	AIS	MLP	AIS
f_1	105.5	10.5	50	0.017	0.010	50000	90
f_2	100.0	18.0	50	0.916	0.029	50000	60

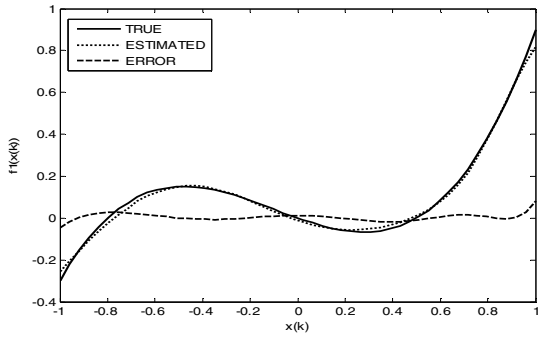

Fig. 3(a)

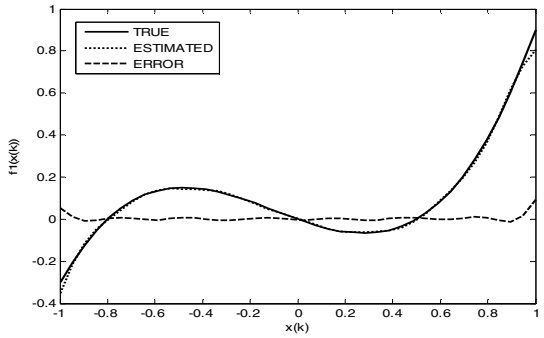

Fig. 3(b)

Fig.3 Function Approximation of f_1(x(k)): (a) using MLP (b) using proposed FLANN-AIS

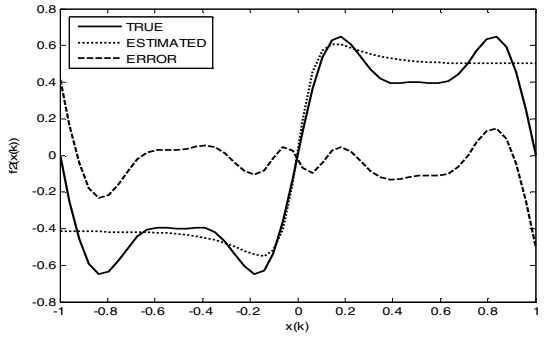

Fig. 4(a)

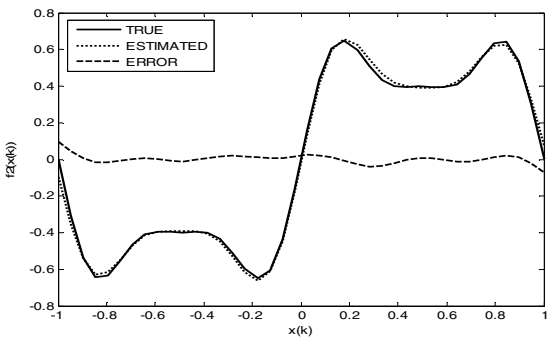

Fig. 4(b)

Fig.4 Function Approximation of f_2(x(k)): (a) using MLP (b) using proposed FLANN-AIS

B. Identification of Static Nonlinear SISO Plant in Noisy Environment

Many research works on identification have been reported in control, communication but the first important one is using multilayer perceptron (MLP) [5]. Later on in 1999 [6] we had proposed a new approach to identify such systems providing identical or even better performance but employing a low complexity FLANN structure. However, the major disadvantage of these methods is that they employ derivative based learning rule to update their weights which at times leads to local minima and thus incorrect estimate of the parameters. To alleviate this problem in this paper a new AIS based derivative free method is proposed. The SISO plant considered here is an all zero FIR filter given by

$$y(k) = h[0.2600\,x(k) + 0.9300\,x(k-1) + 0.2600x(k-2)] + n(k) \quad (9)$$

where nonlinearity h[.] is given by

$$h = u + 0.2u^2 - 0.1u^3 \quad (10)$$

where u is the output of the FIR filter. n(k) is white Gaussian noise associated with plant of SNR 30dB. For identification the model considered is a 3tap FIR filter whose weights are trained by optimization algorithm of AIS. Simulation study is also carried out using GA based algorithm as presented in our paper [7].

The number of input samples used for training and testing is 600 and 20 respectively. The input is a random signal taken over the interval [-0.5, 0.5]. In the proposed model the initial population of immune cells is taken as 30.Each immune cell is represented by a binary string of length 10bits. The weights are trained for 80 iterations. The probability of mutation is taken value 0.1. In GA based algorithm initial population of chromosome is 30. Each chromosome is represented by a binary string of 10bits.The weights are trained for 30 iterations. The probability of crossover and mutation are taken values 0.8 and 0.1 respectively. Table II represents the proposed model offers smaller CPU time, lesser MSE and minimum sum squared errors compared to Genetic algorithm.

TABLE II
RESULTS OF NONLINEAR SISO PLANT IDENTIFICATION

System Identification	Training		Testing
Algorithm	MSE	CPU time (in Sec.)	SSE
AIS	-24.06	66.62	0.0110
GA	-23.80	108.18	0.0114

5. Conclusion

The paper proposes a new optimization algorithm based on AIS. It suitably represents novel application of proposed algorithm to nonlinear function approximation and identification of nonlinear static system. The simulation study of the proposed model is carried out using standard examples to demonstrate its performance. The computed results show its superior performance compared to the MLP and GA. So AIS is a potential learning tool for accurate approximation of nonlinear functions and improved identification of static SISO plants.

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