

Improved Identification of Nonlinear Dynamic Systems using Artificial Immune System

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Abstract-Over the recent few years the area of Artificial Immune System (AIS) has drawn attention of many researchers due to its broad applicability to different fields. In this paper the AIS technique has been suitably applied to develop a new model for efficient identification of nonlinear dynamic system. Simulation study of few benchmark identification problems is carried out to show superior performance of the proposed model over the standard multilayer perceptron (MLP) approach in terms of response matching, number of training samples used and convergence speed achieved. Thus it is concluded that the AIS based model used is a preferred candidate for identification of nonlinear dynamic system.

I. INTRODUCTION

The biological immune system (BIS) is a multilayer protection system where each layer provides different types of defense mechanisms for detection, recognition and responses. It also resists infectious diseases and reacts to foreign substances. Following the BIS principle a new branch of computational intelligence known as artificial immune system (AIS) [1] has evolved which finds applications in optimization[5]-[6], computer security, data clustering, pattern recognition, fault tolerance etc. Like other evolutionary computing algorithms it also helps to develop efficient computational models. The four forms of AIS algorithm reported in the literature are immune network model, negative selection, clonal selection and danger theory. In 2002 [2] Charsto and Zuben has proposed the clonal selection principle for optimization.

Identification of nonlinear dynamic plants finds extensive application in control, communication, instrumentation, power system engineering and many other fields. For identifying such complex plants, the recent trend of research is to employ nonlinear structures and to train their parameters by evolutionary computing tools. Many research work on this topic have been reported but the first important one is using multilayer perceptron (MLP) by Narendra and Parthasarathy [3]. Later on in 1999 [4] 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 using low complexity FLANN structure is proposed for efficient identification of nonlinear dynamic systems.

The paper is organized as follow. In Section II we begin with a review of nonlinear dynamic system and their system

identification. The proposed model using FLANN structure learning by AIS algorithm is discussed in section III. The basic principle of cloning is dealt in section IV. The proposed algorithm is presented in section V. The simulation study of few benchmark dynamic systems using proposed method is presented in section VI. The comparison of identification performance obtained from simulation of MLP and the new method is presented in section VII. Finally section VIII presents the concluding remarks of the paper.

II. PRINCIPLE OF ADAPTIVE SYSTEM IDENTIFICATION

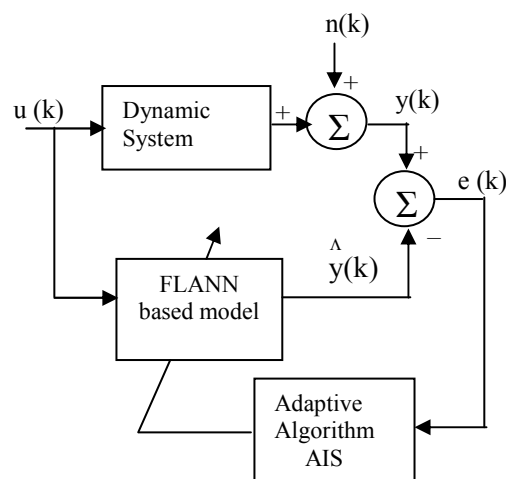


Figure1. Block diagram of dynamic system identification

The basic block diagram of adaptive system identification is shown in Fig.1 in which the plant is considered as nonlinear, dynamic in nature and is associated with noise $n(k)$. The proposed model is a nonlinear single layer functional link neural network (FLANN) with no hidden layer with its connecting weights $\hat{\lambda}$ trained by AIS based algorithm. The symbols $u(k)$, $y(k)$, $\hat{y}(k)$ and $e(k)$ represent the input, output of plant, the estimated output of the model and the error signal respectively. The objective of the identification task is to minimize the error $e(k)$ recursively such that $\hat{y}(k)$ approaches $y(k)$ when the same input $u(k)$ is applied to the plant and the model. In this paper the complex SISO plant is assumed to have one of the following three forms.

Model 1 :

$$y_p(k+1) = \sum_{i=0}^{n-1} \alpha_i y_p(k-i) + g[u(k), u(k-1), \dots, u(k-m+1)] \quad (1)$$

Model 2 :

$$y_p(k+1) = f[y_p(k), y_p(k-1), \dots, y_p(k-n+1)] + \sum_{i=0}^{m-1} \beta_i u(k-i) \quad (2)$$

Model 3 :

$$y_p(k+1) = f[y_p(k), y_p(k-1), \dots, y_p(k-n+1); u(k), u(k-1), \dots, u(k-m+1)] \quad (3)$$

where $[u(k), y(k)]$ represents the input, output pair of SISO plant at time instant k and $m \leq n$. The terms $f[\cdot]$ and $g[\cdot]$ denote nonlinear functions and α_i and β_i represent constant values.

III. THE FLANN STRUCTURE OF THE MODEL

Pao originally proposed FLANN as a novel single layer ANN structure capable of forming arbitrarily complex decision regions by generating nonlinear decision boundaries [9]. In this method the initial representation of a pattern is enhanced by using nonlinear function and thus the pattern dimension space is increased. The functional link acts on an element of a pattern or entire pattern itself by generating a set of linearly independent function and then evaluates these functions with the pattern as the argument. Hence separation of the patterns becomes possible in the enhanced space. The use of FLANN not only increases the learning rate but also has less computational complexity [9] and [10]. A FLANN structure with one input is shown in Fig.2.

The input signal $x(k)$ is functionally expanded to a number of nonlinear values to feed to an adaptive linear combiner whose weights are altered according to an iterative learning rule. Usually the least mean square (LMS) algorithm is used for training the weights. The types of expansion suggested in the literature are either power series or trigonometric expansion. But the later expansion has been recommended for most applications as it offers better performance. Therefore in the proposed model we select trigonometric based linear expansion matrix given by

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

Where $i = 1, 2, \dots, M/2$ and $X(k)$ represents the input at the k^{th} instant. Total expanded values including an unity bias input become $Q=M+2$. Let the corresponding weight vector is represented as $w(k)$ having Q elements. The estimated output of the model is then given as

$$\hat{y}(k) = \sum_{i=1}^{Q-1} s_i(k) w_i(k) \quad (5)$$

The weights are updated by clonal selection algorithm.

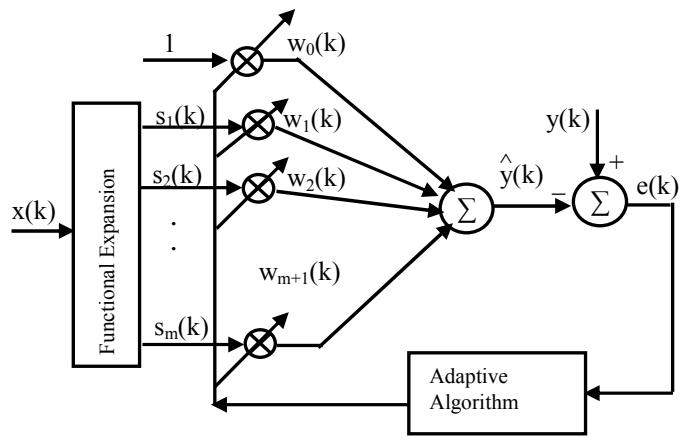


Figure2. Structure of FLANN model

IV. PRINCIPLE OF CLONAL SELECTION ALGORITHM

Immunity refers to a condition in which an organism can resist disease. The cells and molecules responsible for immunity constitute biological immune system (BIS). AIS is developed by following the principles of BIS. Bersini first used immune algorithms to solve problems. The books [11], [12] provide the details about the various principles and algorithms of AIS. The clonal selection principle of AIS describes how the immune cells react to pathogens (foreign cells also known as antigens) and is simple but efficient evolutionary computing tool for achieving optimum solution.

L.N.de Castro and F. J. Von Zuben have dealt the clonal selection in [2]. When a pathogen invades the organism; a number of immune cells that recognize these pathogens survives. Among these cells some become effector cells, while others are maintained as memory cells. The effector 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.3. During this process they undergo a mutation mechanism which is known as somatic hypermutation as described in [2] and [6].

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

The clonal selection algorithm has several interesting features such as population size is dynamically adjustable, exploration of the search space, location of multiple optima, capability of maintaining local optima solutions and defined stopping criteria.

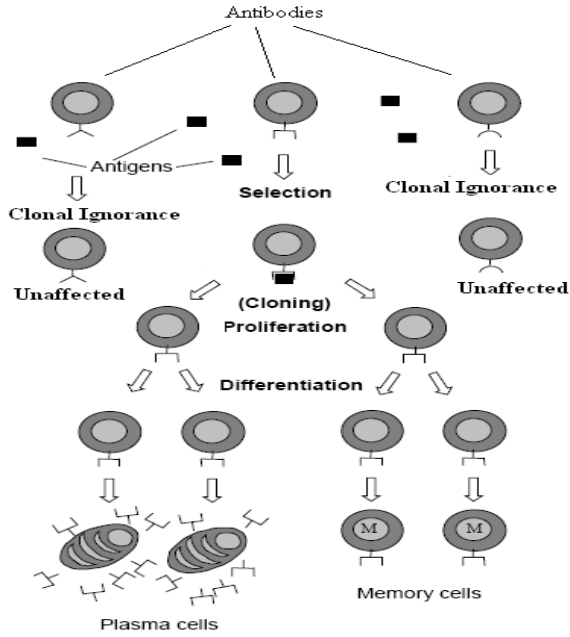


Figure3. The Clonal Selection Principle

V. WEIGHT UPDATE OF FLANN STRUCTURE USING CLONAL SELECTION ALGORITHM

1. Determination of output of plant:

The input is a random signal drawn from a uniform distribution in the interval $[-1, 1]$. Let 'k' be the numbers of input samples taken. The input sample is then passed through the plant to produce plant output $y(k)$.

2. Functional expansion of input:

Same input samples are passed through the model consisting FLANN structure. Each input sample under go trigonometric expansion as represented in (4).

3. Initialization of a group of cells:

As it is an evolutionary algorithm we begin with a group of solutions. Here a group of weight vector of FLANN is taken. A weight vector consist of $(M+2)$ no of elements. 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 expanded values of $u(k)$ and weight vector as described in (5). This is repeated for n times.

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

$$e(k, n) = y(k, n) - \hat{y}(k, n) \quad (6)$$

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

$$\text{MSE}(n) = \frac{\sum_{k=1}^K e^2(k, n)}{K} \quad (7)$$

The objective is to minimize the fitness function of (7) 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 which indicates that the operation occurs occasionally. 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.

VI. SYSTEM SIMULATION

In this study the dynamic plants are represented in form of difference equation described in (2). The input to the system is a uniformly distributed random signal over the interval $[-1, 1]$. The testing is carried out by the sinusoidal input given by

$$u(n) = \begin{cases} \sin\left(\frac{2\pi n}{250}\right) & \text{for } n \leq 250 \\ 0.8\sin\left(\frac{2\pi n}{250}\right) + 0.2\sin\left(\frac{2\pi n}{25}\right) & \text{for } n > 250 \end{cases} \quad (8)$$

To validate the performance of the proposed method simulation study using MATLAB is carried out using some standard dynamic plants. Different examples simulated are **Example 1:**

This dynamic system is assumed to be of second order and is given by the difference equation

$$y_p(k+1) = 0.3 y_p(k) + 0.6 y_p(k-1) + g[u(k)] \quad (9)$$

where function g is given by

$$g(u) = 0.5 \sin^3(\pi u) - \frac{2}{u^3 + 2} - 0.1 \cos(4\pi u) + 1.125 \quad (10)$$

For identification of the plant the model used is of the form

$$\hat{y}_p(k+1) = 0.3 \hat{y}_p(k) + 0.6 \hat{y}_p(k-1) + N[u(k)] \quad (11)$$

where $N[u(k)]$ represents either the proposed model or the MLP structure $\{1_20_10_1\}$. For MLP both convergence factor and momentum term is taken as 0.1. The number of iteration and input sample for training used are 50000. The FLANN-AIS based structure in Fig.4 is used. In FLANN structure each input value is expanded to 5 trigonometric terms. Initial population of cell is taken as 20. The weights are trained for 200 iterations.

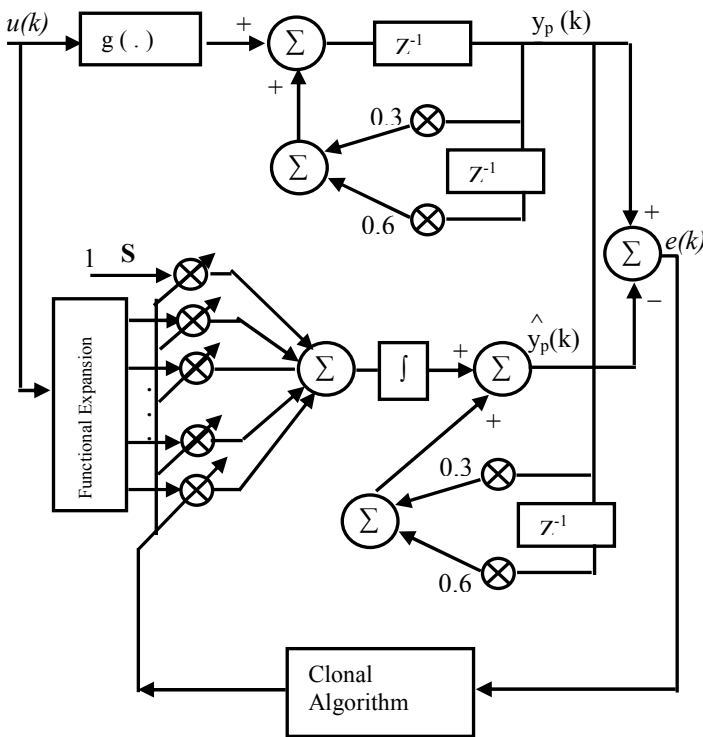


Figure4. Proposed FLANN-AIS based structure for identification of dynamic system of Example1

Example 2:

The dynamic system to be identified is described by the difference equation of Model 2. The second order difference

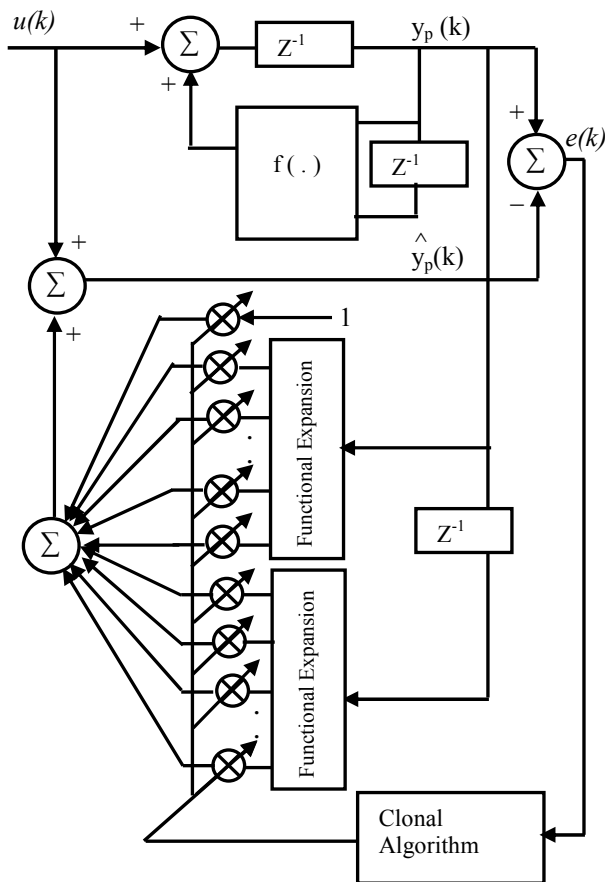


Figure5. Proposed FLANN-AIS based structure for identification of dynamic system of Example2

equation which represents the system is given by

$$y_p(k+1) = f[y_p(k), y_p(k-1)] + u(k) \quad (12)$$

The function f is given by

$$f(y_1, y_2) = \frac{y_1 y_2 (y_1 + 2.5)(y_1 - 1.0)}{1.0 + y_1^2 + y_2^2} \quad (13)$$

The model used for identification task is represented by

$$\hat{y}_p(k+1) = N[y_p(k), y_p(k-1)] + u(k) \quad (14)$$

Here N represents the structure of either MLP {2_20_10_1} or the new model structure of Fig.5. For MLP the convergence factor is taken as 0.05 and momentum term is 0.1. The no of iteration and input sample for training is taken 50000. In FLANN structure the inputs are expanded to 8 terms (each input 4 terms). Weights are trained for 20 iterations. Initial population of cells is taken as 60.

Example 3:

The example of the plant taken here is described by the difference equation of Model 3 is represented by

$$y_p(k+1) = f[y(k), y(k-1), y(k-2), u(k), u(k-1)] \quad (15)$$

where the functions f is given by

$$f(a_1, a_2, a_3, a_4, a_5) = \frac{a_1 a_2 a_3 a_4 (a_5 - 1.0) + a_4}{1.0 + a_2^2 + a_3^2} \quad (16)$$

The model for identification of plant is of the form

$$\hat{y}_p(k+1) = N[y_p(k), y_p(k-1), y_p(k-2), u(k), u(k-1)] \quad (17)$$

For MLP structure of $N[.]$ is taken as {5_20_10_1}. The convergence factor and momentum term each is taken as 0.1. No of iteration and input sample for training is taken 50000. The FLANN-AIS based identification structure used is shown in Fig.6. In FLANN for $N[.]$ the inputs are expanded to 20 terms (each input 4 terms). The number of input sample taken is 60. Weights are trained for 150 iterations. Initial population of cells is taken as 20.

VII. RESULTS

The performance of MLP structure trained by BP algorithm and FLANN structure trained by clonal algorithm is compared in terms of estimated output and the error plot as shown in Figures 7-9. Table1 also reveals that the proposed models offer smaller CPU time, lesser input samples and minimum sum squared errors compared to its MLP counter part.

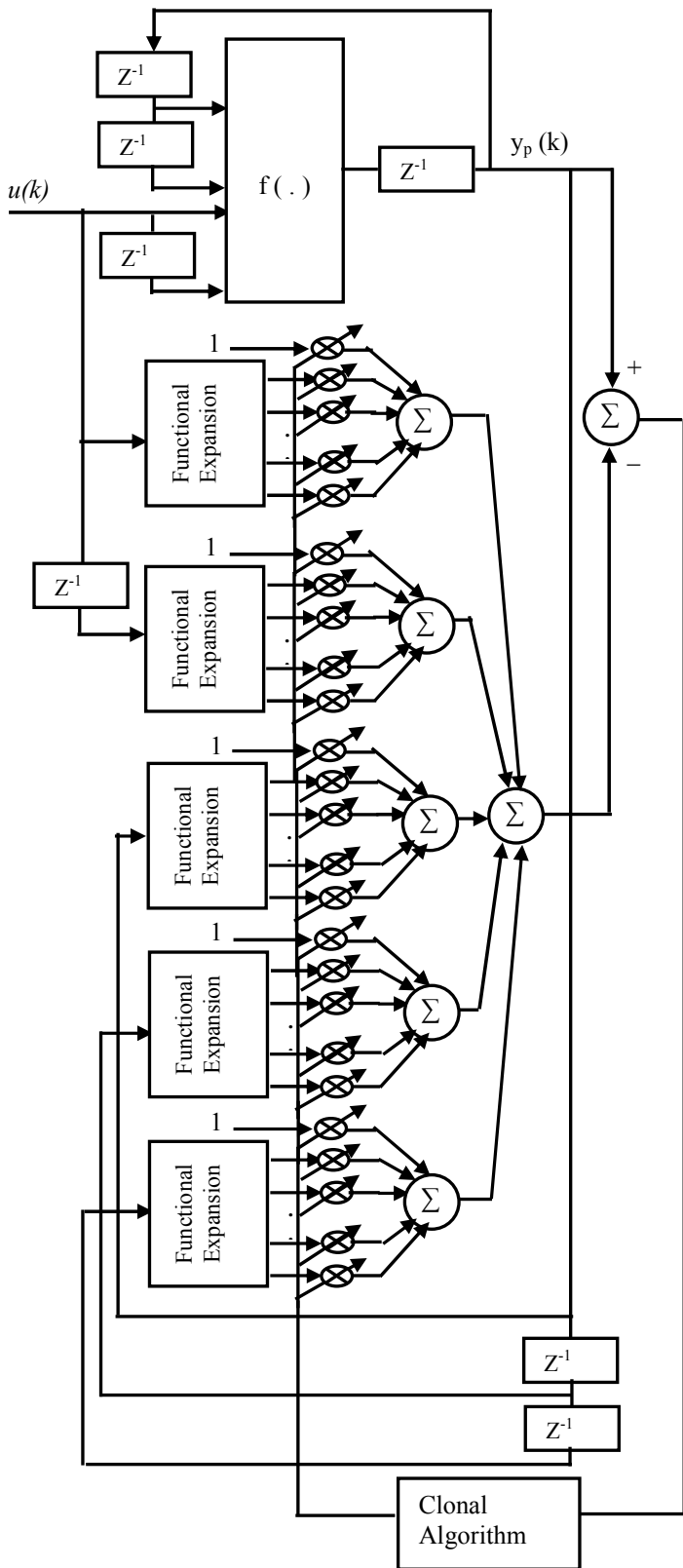


Figure6. Proposed FLANN-AIS based structure for identification of dynamic system of Example3

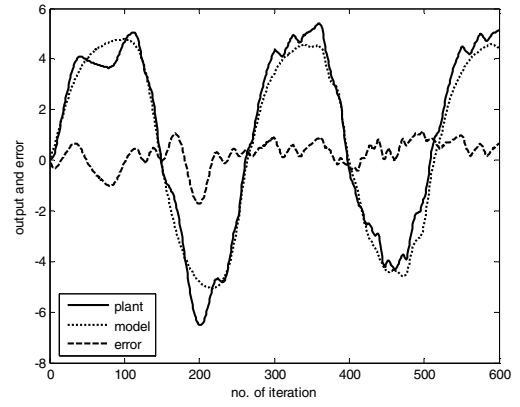


Figure7.(a)

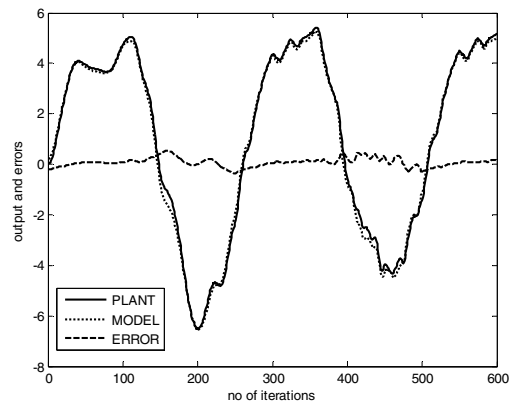


Figure7.(b)

Figure7. Identification of Example 1, (a) using MLP (b) using proposed FLANN-AIS

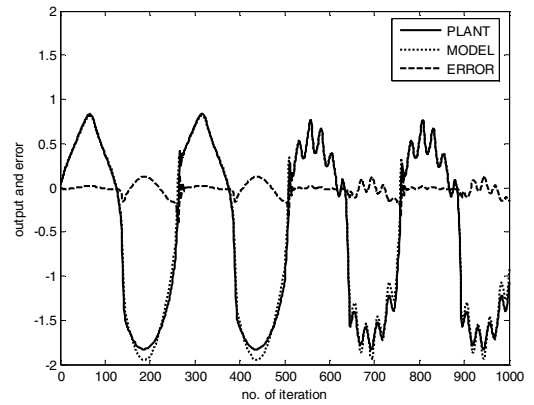


Figure8.(a)

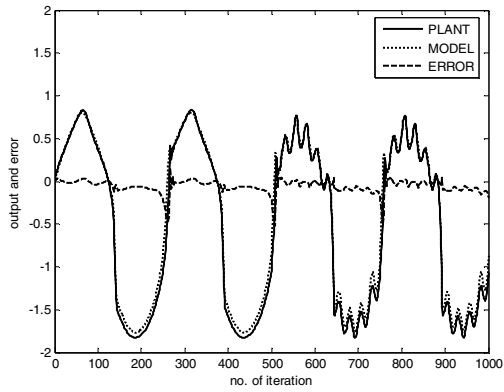


Figure8.(b)

Figure8. Identification of Example 2. (a) using MLP (b) using proposed FLANN-AIS

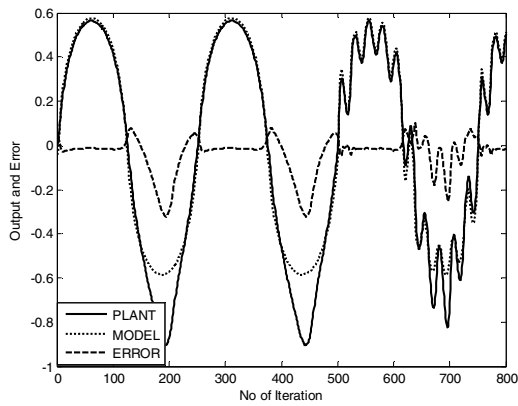


Figure9.(a)

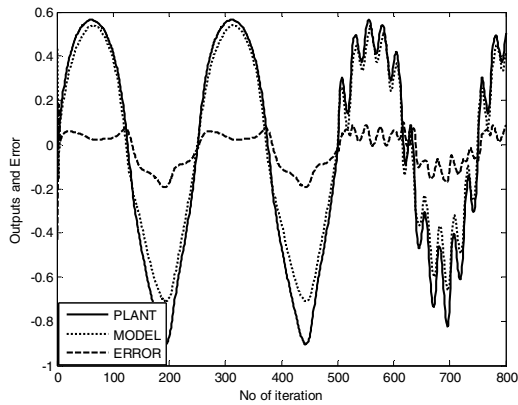


Figure9.(b)

Figure9. Identification of Example 3. (a) using MLP (b) using proposed FLANN-AIS

TABLE I
COMPARATIVE RESULTS OF DYNAMIC SYSTEMS OBTAINED THROUGH SIMULATION STUDY

System	CPU Time During training (in Sec.)		Sum of Square Errors (SSE)		No of input sample used in training		
	MLP	FLANN - AIS	No of Sample For testing	MLP	FLANN - AIS	MLP	FLANN - AIS
Ex1	131.5	2.3	600	220.5	37.3	50000	100
Ex2	114.8	8.8	1000	9.08	5.6	50000	150
Ex3	90.0	20.0	800	7.4	5.8	50000	150

VIII. CONCLUSION

The present paper proposes a novel application of the AIS to identification of nonlinear dynamic 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 based methods in terms of CPU time required for training of structure, sum of square errors and number of input samples required for training. The close agreement of output response of the plants and the model exhibit that the AIS is a potential learning tool for accurate identification of complex dynamic nonlinear systems.

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