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Structural parameter estimation combining domain decomposition techniques with immune algorithm

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Abstract. Structural system identification (SSI) is an inverse problem of difficult solution. Currently, difficulties lie in the development of algorithms which can cater to large size problems. In this paper, a parameter estimation technique based on evolutionary strategy is presented to overcome some of the difficulties encountered in using the traditional system identification methods in terms of convergence. In this paper, a non-traditional form of system identification technique employing evolutionary algorithms is proposed. In order to improve the convergence characteristics, it is proposed to employ immune algorithms which are proved to be built with superior diversification mechanism than the conventional evolutionary algorithms and are being used for several practical complex optimisation problems. In order to reduce the number of design variables, domain decomposition methods are used, where the identification process of the entire structure is carried out in multiple stages rather than in single step. The domain decomposition based methods also help in limiting the number of sensors to be employed during dynamic testing of the structure to be identified, as the process of system identification is carried out in multiple stages. A fifteen storey framed structure, truss bridge and 40 m tall microwave tower are considered as a numerical examples to demonstrate the effectiveness of the domain decomposition based structural system identification technique using immune algorithm.

Keywords: system identification; domain decomposition; evolutionary algorithm; immune algorithm; measurement noise; Nelder Mead algorithm.

1. Introduction

System identification (SI) is the process of constructing or updating the mathematical model of a dynamical system based on input and output (I/O) observations. Structural system identification is an important research topic and has greater significance for civil engineering applications. In addition to updating numerical models for better response prediction, system identification can be applied to health monitoring of structures and even detect damages based on changes in identified parameters. For active vibration control of structures, actual parameter values of the structure, rather than the assumed or design values, are required for effective control.

Due to rapid advances in computer and instrumentation capabilities, the use of structural identification methods has increasingly become a feasible option for nondestructive structural assessment. Research interest in this subject has been intense over the last two decades, and many different methods have been proposed (Ghanem and Shinozuka 1995). Even though, the structural

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*Corresponding Author, Dr., E-mail: arm2956@yahoo.com or arm@sercm.org identification methods can be classified under various categories, the main categorization is perhaps by means of the domain (frequency or time) in which structural identification is carried out. Frequency (or spectral) domain methods often deal with natural frequencies, mode shapes, transfer functions, mobilities etc. The major advantage of these frequency domain methods is that they give better insight in to the physical behavior gained in terms of contributions of various dynamic modes. Time domain methods, on the other hand, deal with the differential equations that describe the state of motion and solve the equations at discrete times over time intervals. The idea is to update the mathematical model with suitable parameters (to be identified) that can predict the next output based on observed input. In comparison with frequency domain methods, time domain methods are generally more capable of extracting detailed information by adjusting the system parameters so that they match as closely as possible with the time-evolving measured output, however at a higher computational cost. With their respective capabilities and limitations, frequency domain and time domain methods should be taken as complementary rather than competitive. The choice of a specific identification method depends on the nature of the physical problem, information available, and the purpose of structural identification. In this paper, the time domain approach is employed.

Currently, a wide range of analytical methods exists for linear or nonlinear system identification. Majority of earlier system identification methods comes under the purview of traditional methods, uses invariably least square methods. Some of the popular methods include recursive least square method (Tang *et al.* 2006, Yang *et al.* 2007, Zhang *et al.* 2007), the extended Kalman filter (Yang *et al.* 2005), instrumental variable, and maximum likelihood methods (Ghanem and Shinozuka 1995), H_α filter method (Sato and Qi 1998), particle filter method (Li *et al.* 2004, Tang and Sato 2005) etc. These methods often have certain traits in common that tend to limit their applicability and success due to the complexity of practical real world problems. Most of these methods require an initial guess so that the process can start. The problem can be very sensitive to the choice of these initial estimates, which makes them a poor choice if no prior knowledge is available. Further, these methods (Ghanem and Shinozuka 1995) in one way or another, search the optimal solution by exploiting the previous solution. As the system of unknowns grows in size, the numerical difficulty increases often to the extent that the convergence becomes extremely difficult, if not impossible. Hence, the challenge lies in developing system identification techniques to solve large and practical engineering problems. some reasonable successes have been achieved with various meta-heuristic algorithms such as genetic algorithms (GAs), evolution strategy (ES), simulated annealing (SA), and swarm intelligence techniques. These heuristic stochastic search techniques seem to be a promising alternative to traditional approaches In this paper, we present a formulation for system identification in time domain using an evolutionary strategy, which has several advantages over traditional system identification techniques. Nevertheless, if applied directly, this approach requires enormous computational time when dealing with structural systems large in both unknowns and degrees of freedom. Keeping this in view, a domain decomposition based approach is employed in order to identify the structural parameters in multiple stages rather than in single step. This reduces the number of variables for identification and also degrees of freedom, thereby considerably improves the computational efficiency and also robustness of the algorithm. The domain decomposition formulations discussed in this paper require only acceleration measurement at limited locations which can be measured much more accurately when compared to velocities and displacements.

In recent years, population based meta-heuristic algorithms like Genetic Algorithms (GA) (Goldberg 1989), immune algorithms (IA) (Luh and Chueh 2004), swarm intelligence techniques (Dorigo *et al.* 1996, Eberhart and Kennedy 1995) like ant colony optimisation (ACO), particle swarm optimization

(PSO) algorithms and also guided search algorithms like simulated annealing(SA) (Kirkpatrick Jr. *et al.* 1983), tabu search (TS) (Glover 1990) are being popularly employed for solving variety of engineering optimisation problems. Specific to structural system identification, Cunha *et al.* (1999) used GAs to identify the elastic constants of composite materials. Franco *et al.* (2004) used evolutionary strategies (ES) to identify multiple degree-of freedom (DOF) systems. Perry *et al.* (2006) used a modified GA to identify structural systems. Chou and Ghaboussi (2001) introduced GAs method to identify damage severity of trusses. Koh *et al.* (2000, 2000a, 2003) applied GAs method to solve the global system identification problem in shear-type building structures. Levin and Lieven (1998) applied SA method to optimize a finite element model for describing the dynamic behavior of structures.

However, it is a well known fact that every optimisation algorithm has its own advantages and disadvantages. This fact is also valid for these modern meta-heuristic algorithms, too. For instance, the performance of TS and SA usually depends on the starting point of the search since these two algorithms employ a form of neighbourhood search mechanism. The main features of ACO algorithm are distributed computation, positive feedback and constructive greedy search. Of these algorithms, GA and artificial IA are the approaches inspired from biological systems. GA is a stochastic optimisation algorithm employed for combinatorial and continuous optimisation problems. GA can efficiently search large solution spaces due to its parallel structure and the probabilistic transition rules employed in the operators. However, a basic GA has two main drawbacks: lack of good local search ability and premature convergence. The natural immune system (Farmer *et al.* 1986, Dipankar Dasgupta 1999) uses learning, memory, and associative retrieval to solve recognition and classification tasks. Specifically, it learns to recognize relevant patterns, remember patterns that have been seen previously, and use combinatorics to construct pattern detectors efficiently. The natural immune system is a great source of inspiration for developing intelligent problem solving techniques and however a few computational models have been developed. So, artificial immune systems emerged currently as a new computational research area (Farmer *et al.* 1986, Dipankar Dasgupta 1999, Cortes and Coello 2003, Hunt and Cooke 1996, Anoop Prakash *et al.* 2008, Naderi *et al.* 2009, Gong *et al.* 2008). An immune algorithm simulates a learning technique carried out by natural immune system. The following are some of merits of artificial immune algorithm (IA) over other popular probabilistic optimization algorithms such as genetic algorithms.

i. IA operates on the memory cell, which guarantees fast convergence towards the global optimum.
ii. IA has an affinity calculation feature to numerically simulate the diversity of the real immune system.
iii. The self-adjustment of the immune response can be numerically simulated to either encourage or suppress antibodies production.

In this paper a method based on immune algorithm is devised and employed for solving complex optimisation problem associated with structural system identification formulations. Application of immune algorithm for structural system identification has not been reported so far, in the literature.

2. Formulation details

The governing equilibrium equation of structural dynamics can be expressed as

$$[\mathbf{M}]\{a\} + [\mathbf{C}]\{v\} + [\mathbf{K}]\{d\} = \{p(t)\} \tag{1}$$

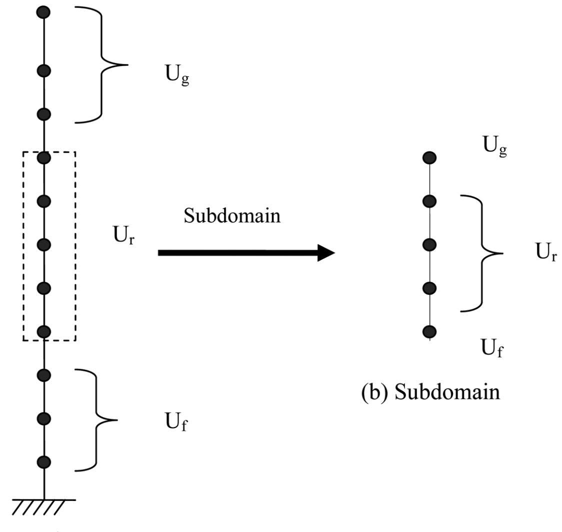
With $d(0) = d_0$ and $v(0) = v_0$

Where, **M** is the mass matrix, **C** is the damping matrix and **K** is the stiffness matrix. a, v and d are the acceleration, velocity and displacement vectors respectively. $p(t)$ is the time varying external excitation force. Solution of this initial value problem requires integration through time. Any one of the time integration procedures can be used for this purpose. In order to write the equations of motion for the subdomain as shown in Fig. 1(b), the equations of motion for the entire structure can be arranged as follows

$$\left(\begin{bmatrix} M_{uu} & M_{uf} & & & \\ M_{fu} & M_{ff} & M_{fr} & & \\ & M_{rf} & M_{rr} & M_{rg} & \\ & & M_{gr} & M_{gg} & M_{gd} \\ & & & M_{dg} & M_{dd} \end{bmatrix}\begin{Bmatrix} a_u \\ a_f \\ a_r \\ a_g \\ a_d \end{Bmatrix} + \begin{bmatrix} C_{uu} & C_{uf} & & & \\ C_{fu} & C_{ff} & C_{fr} & & \\ & C_{rf} & C_{rr} & C_{rg} & \\ & & C_{gr} & C_{gg} & C_{gd} \\ & & & C_{dg} & C_{dd} \end{bmatrix}\begin{Bmatrix} v_u \\ v_f \\ v_r \\ v_g \\ v_d \end{Bmatrix} + \begin{bmatrix} K_{uu} & K_{uf} & & & \\ K_{fu} & K_{ff} & K_{fr} & & \\ & K_{rf} & K_{rr} & K_{rg} & \\ & & K_{gr} & K_{gg} & K_{gd} \\ & & & K_{dg} & K_{dd} \end{bmatrix}\begin{Bmatrix} d_u \\ d_f \\ d_r \\ d_g \\ d_d \end{Bmatrix}\right) = \begin{Bmatrix} p_u \\ p_f \\ p_r \\ p_g \\ p_d \end{Bmatrix} \tag{2}$$

where subscript 'r' denotes internal degrees of freedom of the subdomain concerned, subscripts 'f'' and 'g' denotes interface degrees of freedom of the substructure with the remaining structure on the two sides 'f' and 'g', respectively as shown in Fig. 1(a), and the subscripts u and d represent degrees of freedom (DOFs) of the remaining structure. Let Subscript j denotes interface degrees of freedom (i.e., f and g included) for concise presentation. For the subdomain considered, the equations of motion may be extracted from the above system of equations as

$$[M_{rj}\ M_{rr}]\begin{Bmatrix} a_j(t) \\ a_r(t) \end{Bmatrix} + [C_{rj}\ C_{rr}]\begin{Bmatrix} v_j(t) \\ v_r(t) \end{Bmatrix} + [K_{rj}\ K_{rr}]\begin{Bmatrix} d_j(t) \\ d_r(t) \end{Bmatrix} = p_r(t) \tag{3}$$



(b) Subdomain

(a) Complete structure

Fig. 1 Schematic view of domain decomposition approach

The interaction effect at the interface is treated as 'input' and Eq. (3) can be rearranged as

$$M_{rr}a_r(t) + C_{rr}v_r(t) + K_{rr}d_r(t) = p_r(t) - M_{rj}a_j(t) - C_{rj}v_j(t) - K_{rj}d_j(t) \tag{4}$$

By representing damping with Rayleigh damping coefficients, Eq. (4) can be written as

$$M_{rr}a_r(t) + \alpha M_{rr}v_r(t) + \beta K_{rr}v_r(t) + K_{rr}d_r(t) = p_r(t) - M_{rj}a_j(t) - \alpha M_{rj}v_j(t) - \beta K_{rj}v_j(t) + K_{rj}d_j(t) \tag{5}$$

It is assumed that mass is known. Stiffness and damping parameters are unknown. Identification of the global structure parameters requires response measurements at interface degrees of freedom and some measurements at internal degrees of freedom. The point of application and magnitude of force is known *a priori.* Acceleration measurements at the interface degrees of freedom are measured. The velocity and displacement at the interface degrees of freedom can be obtained by integration. Since the R.H.S values in Eq. (4) i.e., displacements, velocities and accelerations at the interfaces are known, time integration can be performed with estimated parameters of stiffness and damping. Since the mass is known, the actual mass matrix can be used in the time integration. In the present work, Newmark's time marching scheme is employed for time integration.

The system identification is formulated as an optimization problem with element stiffness parameters and damping coefficients (α and β), as design variables. The objective function is formulated by comparing the actual acceleration responses obtained at some selected internal degrees of freedom with the responses obtained from time integration scheme with estimated stiffness and damping parameters. The fitness function can be defined in terms of the measured acceleration time history at selected internal degrees of freedom

$$f_e = \frac{\sum_{i=1}^{M}\sum_{n=1}^{NT} |a_m(i,n) - a_e(i,n)|^2}{M^*NT} \tag{6}$$

Where subscripts '*m*' and '*e*' denote measured and estimated quantities, respectively, *NT* is the number of time steps and *M* is the number of measurement sensors employed at internal degrees of freedom. The fitness function is alternatively referred to as objective function in this paper.

The complex nonlinear optimisation problem associated with the proposed domain decomposition system identification formulations is solved using evolutionary computing techniques. In this paper, an artificial immune algorithm has been employed for solving the optimisation problem.

3. Immune system

The natural immune system is a distributed adaptive novel pattern detection system with several functional components positioned in strategic locations through out the body to defend from foreign pathogens (bacteria or viruses). The immune system is able to categorize all cells (or molecules) within the body and identify these cells as self or non-self (Dasgupta 2002).

It has dramatic and complex mechanisms that recombine the gene to cope with the invading antigens, produce the antibodies and exclude the antigens (Mori *et al.* 1993). Pathogens are associated with specific proteins (antigens). The infection process involves invasion of a pathogen and its proliferation within the organism. The immune system contains cells that are capable of recognizing antigens and killing pathogens. These cells, further referred to as immune cells (antibodies), are randomly distributed throughout the immune system. In the relatively evolutionarily advanced animals, the immune system is capable of enhanced response to re-infection by an earlier encountered pathogen (adaptive immunity). Each individual immune cell involved in adaptive immunity is capable of recognizing only one type of antigen. Therefore, there is a huge diversity of immune cells in the organism waiting for many possible antigens. In case of infection only a small proportion of immune cells would react, i.e., those that are pre-programmed for this particular antigen. This interaction triggers fast multiplication of these particular cells (clonal proliferation). The number of immune cells capable of recognizing the specific antigens and killing the specific pathogen increases by many orders. Thus, the organism's immune system becomes tuned to fight not just random pathogens but specifically the one that actually invaded (Gutnikov and Melnikov 2003). The clonal selection and affinity maturation principles are used to explain how the immune system reacts to pathogens and how it improves its capability of recognizing and eliminating pathogens. Clonal selection states that when a pathogen invades the organism, a number of immune cells that recognize these pathogens will proliferate; some of them will become effector cells, while others will be maintained as memory cells. The effector cells secrete antibodies in large numbers, and the memory cells have long life spans so as to act faster and more effectively in future exposures to the same or a similar pathogen. During cellular reproduction, the cells suffer somatic mutations at high rates, together with a selective force; the cells with higher affinity to the invading pathogen differentiate into memory cells. This whole process of somatic mutation plus selection is known as affinity maturation (De Castro and Timmis 2002).

4. Artificial immune algorithm

Inspired by the above clonal selection and affinity maturation principles, an artificial immune algorithm is proposed for structural system identification. The objective function and constraints are represented as antigen inputs. Initial antibodies are randomly generated on a feasible space. The exploration of new antibodies is generally implemented by crossover and mutation. The Gaussian mutation operator could be viewed as a heuristic mutation operator and is employed in artificial immune algorithm. Clones of each antibody are mutated proportional to the objective function value of their parent antibody, which is inversely proportional to the affinity between the antigen and antibody. This embodies affinity maturation. An affinity calculation between antibodies is also embedded within the algorithm to suppress similar antibodies. Through immune algorithm computations, an antibody that most fits the antigen is considered as the solution to system identification problem. Details of the proposed immune algorithm is discussed below:

1. **Recognize antigen**: formulate the objective function
2. **Generation of initial group of antibodies**: Initial group of antibodies is randomly formed.
3. **Calculation of affinities of each antibody**: Calculate the objective function and the affinity between antigen and antibodies and normalize the vector of the objective function. It is corresponding with the effectiveness of counter measures of the antibody. Moreover, the affinity between two antibodies is calculated. It is corresponding with the resemblance of two antibodies.
4. **Clonal Proliferation and hyper-mutation**: in biological immune systems, only antibodies

stimulated by antigens enter the germinal center for clonal proliferation. In proposed immune algorithm, the best antibody determined based on the affinity values are chosen for hyper-mutation during the clonal proliferation process, with a user-defined *hyper-mutation rate and proliferation number*.

5. **Renewal of memory cell**: The antibody having high affinity with the antigen is added into the memory cell. New antibody is placed in memory cell by replacing the already existing antibody with close resemblance.
6. **Selection of antibodies for reproduction**: The antibodies reproduced into the group in next generation are selected by tournament selection method.
7. **Crossover and mutation**: Several pairs of antibodies perform a crossover to produce new antibodies. This process is akin to exchanging their information. Moreover, mutation is applied to each element of antibody with the assumed probability. Thus, a new group of antibodies is formed. Since the optimization process in the proposed system identification formulations involves continuous search spaces, it is proposed to use float encoded design variables. To suit this formulation, the SBX crossover (Kalyanmoy Deb and Agarwal 1996) and parameter based mutation operators (Kalyanmoy Deb and Goyal 1996) are used for crossover and mutation respectively.
8. **Judgment of convergence conditio**n: The above process is repeated until the specified convergence criterion is met.

4.1 Recognition of antigen

In the proposed immune algorithm, the antigen pattern is represented in real coding. Compared with binary coding, neither encoding nor decoding is performed and the computation time is shorter. Using artificial immune algorithm for SSI, the measurement data including representations of the objective function and constraints are regarded as antigen.

4.2 Generation of initial antibody

The design variables in the proposed system identification formulations are the stiffness and damping parameters. Since the proposed optimization involves searching continuous design spaces, float encoded design variables are employed and accordingly the initial antibodies are randomly generated in the feasible space.

4.3 Affinity computation

There are two kinds of affinities in immune algorithms. One is the affinity $(aff_g)_i$ between the antigen and an antibody i, which represents the combination intensity between antigen and antibody i. For the proposed system identification problem, the smaller the objective function, the higher the affinity aff_g and the better the antibody. In Immune algorithm, the affinity $(aff_g)_i$ is calculated by

$$(aff_g)_i = \frac{1}{(1+f_i)} \tag{7}$$

where f_i is the objective function of antibody i.

The other is the affinity $(aff_b)_{jk}$ between antibody j and antibody k, which measures how similar these two antibodies are. It is calculated by

$$(aff_b)_{jk} = \frac{1}{(1 + dis_{jk})} \tag{8}$$

where dis_{jk} is the Euclidean distance between antibody j and antibody k. The shorter the distance dis_{jk} is the larger the affinity $(aff_b)_{jk}$. In otherwords, it can also be inferred that if the affinity is larger, the similarity between antibodies j and k is higher.

4.4 Antibody clones

Generate n_c clones for each antibody, where n_c is the number of clones. The clones and their parent antibody are viewed as a family.

4.5 Self-adaptive mutation

The clones are self-adaptively mutated. The mutated clones and their parent antibody are viewed as a new family. In each new family, only one best antibody can survive and enter the next generation.

Self-adaptive mutation plays the key role in immune algorithm. In order to avoid trapping in a local optimal solution and to ensure the searching capability of near global optimal solution, the better antibody suffers a smaller mutation, whereas the worse one undergoes a larger mutation.

The self-adaptive mutation is performed according to the following expression

$$X_{ji}^{n} = x_{ji}^{o} + \gamma_j N_{ji}(0, 1) \tag{9}$$

where N_{ji} (0,1) is a Gaussian random variable of mean zero and standard deviation $\sigma = 1$ when re-sampling each variable x_{ji} of antibody j, $j = 1, 2, \ldots$ *popsize*, $i = 1, 2, \ldots,$ *numvar*, where *popsize* is the number of antibodies and *numvar* is the number of design variables in the antibody.

γ_j is the mutation step length of antibody j and is expressed as

$$\gamma_j = \zeta \tilde{f}_j + \psi \tag{10}$$

where $\tilde{f}_j$ is the objective function value of antibody j normalized in the interval [0,1], and ψ is a parameter that controls the mutation step length of the best antibody in every generation of evolution. ψ is set to different values in different evolution phases. In proposed algorithm, the evolution process towards minimising the objective function is divided into two phases. In the first phase, the primary objective is to find the approximate solution and to reduce the search space. Therefore, ψ is set larger. In the second phase, the main aim is to tune the solution in order to find the best solution, so ψ is set a bit smaller. ζ is also a parameter that controls the mutation intensity and is usually set to 1. The values of ψ is experimentally decided based on detailed parametric studies using the standard test functions and also current application. In our experiment, based on the parametric studies, ψ is set to 0.00115 and 0.000085 in two phases, respectively.

4.6 Suppress similar antibodies

If the Euclidean distance between two antibodies is less than the suppression threshold ε_s, these two antibodies are called similar ones. In order to maintain diversity, the similar antibody whose objective function value is larger is suppressed and a new antibody is generated randomly. During evolutionary process in immune algorithm, all the antibodies in each generation must be evaluated and the best one among them substitutes for the worst one.

4.7 Selection of immune algorithm control parameters

Based on detailed parametric studies on some well known bench mark test functions like DE Jong's Sphere function, Schaffer2 function, Rosenbrock and Ackley function etc., which are being popularly used for the evaluation of meta-heuristic algorithms and also the current system identification problems, the control parameters of the proposed immune algorithm are tuned for optimal performance. The details of these studies are deliberately omitted in the paper as they are very elaborate and are of least consequence. Based on these studies, the following control parameters are used in the numerical investigations carried out in this paper.

Diversification rate = 0.10
Crossover = 0.85
Maximum number of generations = 500

The antibody size and clone size are set to 20 and 30 respectively. Suppression threshold is set to 0.05. The proliferation number is taken as 5 and mutation rate is set as 0.004. The solution is assumed to have converged if there is no improvement in the last 20 evolutions.

5. Numerical studies

In order to evaluate the performance of the domain decomposition based SSI techniques three numerical examples of increased complexities are considered. The numerical examples considered in this paper are a fifteen storey framed structure, truss bridge and a 40 m tall microwave tower. The experiment is numerically simulated using the known models. The data of all DOFs of the numerical model is first calculated in terms of displacement, velocity and acceleration using Newmark's time integration method.

One of the main issues related to structural system identification techniques, when applied to real situations, is their sensitivity to noise. In view of this, It is decided to add white Gaussian noise to the acceleration time history response generated by the finite element code. The white Gaussian noise is added to the acceleration time history before they were processed. The white Gaussian noise is added in the form of 'snr' (signal-to-noise ratio) that defines the 'amplitude' of the noise with respect to that of the clean signal. When the noise level is given by a particular value of 'snr' it means that a noisy signal with such an 'snr' has been added to the time series of each node. Moreover the noisy sequences affecting different nodes are uncorrelated, in this way severe experimental conditions are simulated. The velocity and displacement responses at each DOF are obtained by integrating the acceleration response.

In order to demonstrate the performance of the proposed artificial immune algorithm, the system identification is also attempted using genetic algorithm with the proposed domain decomposition based approach. Since proposed system identification formulation leads to a continuous parameter optimisation, float-encoded GAs are employed in the present work with tournament selection. SBX crossover with 0.85 as probability and parameter based mutation operator with 0.004 are employed.

A modified version of genetic algorithm usually known in the literature as a memetic algorithm

(Moscato 1999) is also employed for solving the optimization problem associated with the proposed domain decomposition based system identification technique. Basically, they are genetic algorithms that apply a separate neighbourhood search process to refine individuals. It is usually being applied after crossover and mutation and before the selection. One big difference between memes and genes is that memes are processed and possibly improved by the people that hold them - something that cannot happen to genes. Experimental results show that the memetic algorithms have better results over simple genetic or evolutionary algorithms (Moscato 1999). The memetic algorithm employed here is devised by introducing a neighborhood search algorithm to improve the intensification mechanism of the algorithm by way of searching around a good solution and adopting a better solution, if found.

Nelder-Mead algorithm (Nelder and Mead 1965) is one of the most popular derivative-free nonlinear optimization algorithms. Instead of using the derivative information of the function to be minimized, the Nelder-Mead algorithm maintains at each iteration a non-degenerate simplex, a geometric figure in n dimensions of nonzero volume that is the convex hull of $n+1$ vertices, x_1; x_2; ...; x_{n+1}, and their respective function values. In each iteration, new points are computed, along with their function values, to form a new simplex. Four scalar parameters must be specified to define a complete Nelder-Mead algorithm; coefficients of reflection (ρ), expansion (χ), contraction (γ), and shrinkage (σ): These parameters are chosen to satisfy: $\rho > 0$, $\chi > 1$, $0 < r < 1$ and $0 < \sigma < 1$. The Nelder-Mead algorithm is given in Fig. 2. The implementation of Nelder-Mead algorithm in the float encoded GA algorithm is as follows:

1. *Order. Order and re-label the n + 1 vertices as* x_1, x_2, ……., x_{n+1} *so that* $f(x_1) \geq f(x_2) \geq \ldots \geq f(x_{n+1})$. *Since we want to maximise f, we refer to* x_1 *as the best vertex or point, to* x_{n+1} *as the worst point.*

2. *Reflect. Compute the reflection point* x_r *by*

   $$x_r = \bar{x} + \rho(\bar{x} - x_{n+1}),$$

   where $\bar{x}$ *is the centroid of the n best points, i.e.,* $\bar{x} = \sum_{i=1}^{n} x_i / n$. *Evaluate* $f(x_r)$.

   if $f(x_1) \geq f(x_r) > f(x_n)$, *replace* x_{n+1} *with the reflected point* x_r *and go to step 6*

3. *Expand. If* $f(x_r) > f(x_1)$, *compute the expansion point* x_e *by* $x_e = \bar{x} + \chi(x_r - \bar{x})$, *Evaluate* $f(x_e)$. *If* $f(x_e) > f(x_r)$ *replace* x_{n+1} *with* x_e *and go to step 6; otherwise replace* x_{n+1} *with* x_r *and go to step 6.*

4. *Contract. If* $f(x_r) \leq f(x_n)$, *perform a contraction between x and the better of* x_{n+1} *and* x_r.
   1. *Outside. If* $f(x_n) > f(x_r) > f(x_{n+1})$ *(i.e.,* x_r *is strictly better than* x_{n+1}*), perform an outside contraction: Calculate* $x_{oc} = \bar{x} + \gamma(\bar{x} - x_r)$. *Evaluate* $f(x_{oc})$. *If* $f(x_{oc}) \geq f(x_r)$, *replace* x_{n+1} *with* x_{oc} *and go to step 6; otherwise, go to step 5.*
   2. *Inside. If* $f(x_r) \leq f(x_{n+1})$, *perform an inside contraction: Calculate* $x_{ic} = \bar{x} + \gamma(\bar{x} - x_{n+1})$. *Evaluate* $f(x_{ic})$. *If* $f(x_{ic}) \geq f(x_{n+1})$, *replace* x_{n+1} *with* x_{ic} *and go to step 6; otherwise, go to step 5.*

5. *Shrink. Evaluate f at the n new vertices* $x'_i = x_1 + \sigma(x_i - x_1), i = 2, \ldots\ldots, n+1$. *Replace the vertices* x_2, ……, x_{n+1} *with the new vertices* $x'_2, \ldots\ldots, x'_{n+1}$.

6. *Stopping Condition. Order and re-label the vertices of the new simplex as* x_1, x_2, …….x_{n+1} *such that* $f(x_1) \geq f(x_2) \geq \ldots\ldots\ldots f(x_{n+1})$. *If* $(f(x_1) - f(x_{n+1})) < \varepsilon$, *then stop, where* $\varepsilon > 0$ *is a small predetermined tolerance. Otherwise go to step 2.*

Fig. 2 Nelder-Mead algorithm

i After every user specified number of generations, the population is sorted according to their fitness values and the best twenty percent of the total number of population is chosen for refinement using neighbourhood search algorithm.

ii. After several years of studying and applying the Nelder-Mead method, McKinnon (1999) shows that the Nelder-Mead algorithm can stagnate and converge to a non-optimal point even for very simple problems. However, Kelley (1999, 1999a) proposes a test for sufficient decrease which, if passed for all iterations, will guarantee convergence of the Nelder-Mead iteration to a stationary point under some appropriate conditions. The Kelley's modification (Kelley 1999, Tang *et al*. 2006) of the Nelder-Mead method is employed in the final stage of our method i.e., at the end of the search, the best solution is refined using the Kelly's modification of Nelder-Mead algorithm.

The resulting memetic algorithm is termed in this paper as hybrid genetic algorithm. Both the float encoded GA and hybrid GA discussed above are used in the proposed system identification formulations. Numerical studies have been carried out using GA and hybrid GA to compare and evaluate the performance of the proposed immune algorithm for structural system identification problems.

5.1 Example 1: 15-story building frame

The proposed domain decomposition based technique is employed to identify the structural parameters of a 15-story-high building shown in Fig. 3. The actual parameters are given in Table 1. The first four natural frequencies of the structure are 0.62 Hz, 1.84 Hz, 3.05 Hz, 4.23 Hz respectively. The two damping coefficients of the Rayleigh damping model are computed assuming 5% damping ratio for the first two modes of vibration. Accordingly the Rayleigh coefficients α and β are taken as 0.2963 and 0.0064 respectively. The structure is assumed to be excited by an earthquake load and

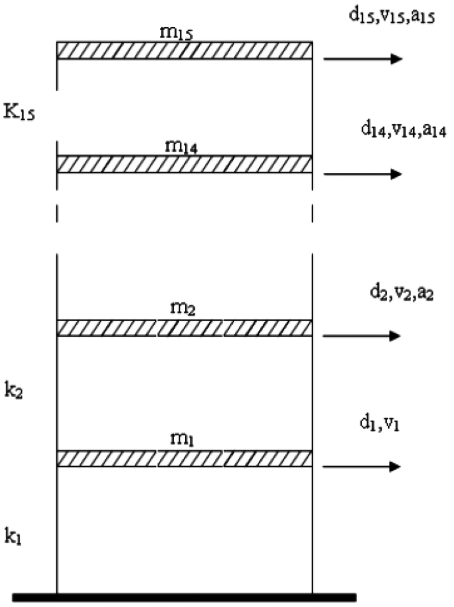


Fig. 3 15 storey framed Structure

Table 1 Actual system properties of shear building model

Element number	Stiffness kN/m	Mass 10^3 Kg.
1	4.3051	30.0000
2	4.2776	28.8960
3	4.2761	28.8960
4	4.2536	28.8960
5	4.2496	28.8960
6	4.2422	28.8960
7	4.2398	28.8960
8	4.2372	28.8960
9	4.2291	28.8960
10	4.2172	28.8960
11	4.2114	28.8960
12	4.2093	28.8960
13	4.1898	28.8960
14	4.1649	28.8960
15	4.1464	27.7410

Bhuj earth quake acceleration data is used for this purpose. The dynamic responses are computed for 10 seconds with a time step of 0.001s.

The numerical simulated response is used to identify the stiffness parameters and input time history of the full structure and substructure. The full structure is divided into three subdomains, as shown in Fig. 4. The forces shown at the ends A and B of the subdomain are forces due to interface

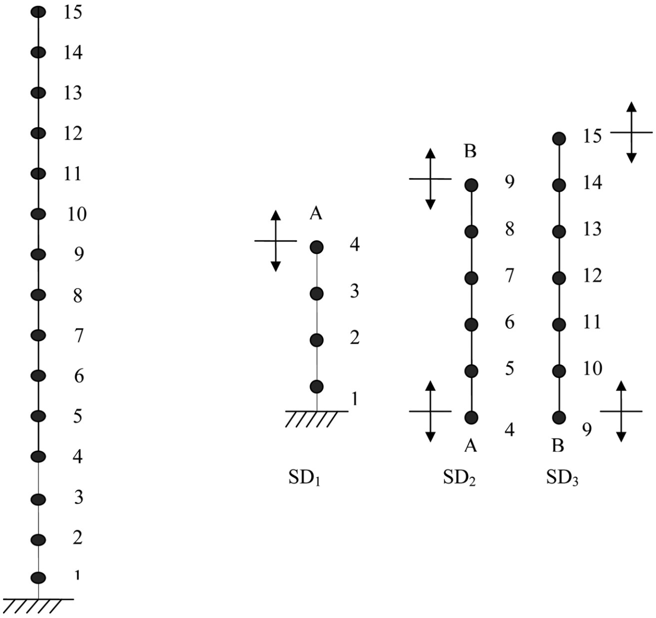


Fig. 4 Details of the three subdomains of the framed structure considered in the proposed system identification

Table 2 Details of identified stiffness and damping parameters for framed structure using the proposed system identification formulation with immune algorithm

Element number	Actual stiffness kN/m	Without noise		With noise SNR=40		With noise SNR=50		With noise SNR=60	
		Identified stiffness kN/m	% error	Identified stiffness kN/m	% error	Identified stiffness kN/m	% error	Identified stiffness kN/m	% error
1	4.3051	4.3102	0.11846415	4.2734	0.73633597	4.2724	0.75956424	4.2865	0.43204571
2	4.2776	4.2696	0.18702076	4.2943	0.39040584	4.2653	0.28754442	4.2821	0.10519918
3	4.2761	4.2701	0.14031477	4.2982	0.51682608	4.2867	0.24788943	4.2791	0.07015739
4	4.2536	4.2489	0.11049464	4.2677	0.33148392	4.2642	0.24920068	4.2544	0.0188076
5	4.2496	4.2456	0.09412651	4.2686	0.4471009	4.2364	0.31061747	4.2511	0.03529744
6	4.2422	4.2501	0.18622413	4.2261	0.37952006	4.2359	0.14850785	4.2404	0.04243081
7	4.2398	4.2432	0.08019246	4.2584	0.43869994	4.2375	0.05424784	4.2402	0.00943441
8	4.2372	4.2488	0.27376569	4.2566	0.45784952	4.2453	0.19116398	4.2308	0.0094402
9	4.2291	4.2308	0.04019768	4.2049	0.57222577	4.2354	0.14896787	4.2205	0.15105828
10	4.2172	4.2193	0.04979607	4.2312	0.33197382	4.2242	0.16598691	4.2088	0.19918429
11	4.2114	4.2198	0.19945861	4.2444	0.78358741	4.2336	0.52714062	4.2042	0.17096452
12	4.2093	4.2003	0.21381227	4.2234	0.33497256	4.2429	0.79823249	4.2154	0.14491721
13	4.1898	4.1844	0.12888443	4.2432	1.27452384	4.2127	0.54656547	4.1944	0.10979044
14	4.1649	4.1602	0.11284785	4.1231	1.00362554	4.1554	0.22809671	4.1405	0.58584479
15	4.1464	4.1497	0.07958711	4.1114	0.84410573	4.1312	0.36658306	4.1406	0.13988038
α	0.2963	0.296108	0.06479919	0.284082	4.12352346	0.306912	3.58150523	0.302524	2.10057374
β	0.0064	0.006482	1.28125	0.006964	8.8125	0.006704	4.75	0.006623	3.484375

reactions (they are shown by arrows in Fig. 4). The first subdomain consists of the stiffnesses of the first four levels from the base; the unknown parameters here are these four stiffnesses and two Rayleigh damping coefficients. The rest of the structure is divided into two subdomains with five and six stiffnesses (levels), respectively. Table 2 gives the identified parameters of the full structure and subdomain for the noise free case. The 15 stiffness values and 2 damping parameters are identified using three subdomains. To investigate the effectiveness of the proposed parameter identification technique with noisy measurements, SNR values of 40, 50 and 60 are considered. Table 2 also shows the identified stiffness parameters and damping coefficients with various SNR values. A close look at the results presented in Table 2, clearly indicates that the proposed system identification algorithm performs rather well even with noisy measurements. The damping parameters are also identified with reasonable accuracy. In order to study the convergence characteristics of immune algorithm, the system identification of the framed structure given in Fig. 3 is carried out using GA and also hybrid GA with the proposed domain decomposition formulations. In order to have a fair comparison, the control parameters and convergence criteria are set identical for all the three algorithms. The convergence characteristics of all the three algorithms are shown in Fig. 5. The comparative performances of the three algorithms i.e., proposed immune algorithm, hybrid GA and genetic algorithm are shown in Table 3. A close look at Fig. 5 and also the results furnished in Table 3, clearly indicates that the proposed immune algorithm converges faster and also the solutions obtained are optimal.

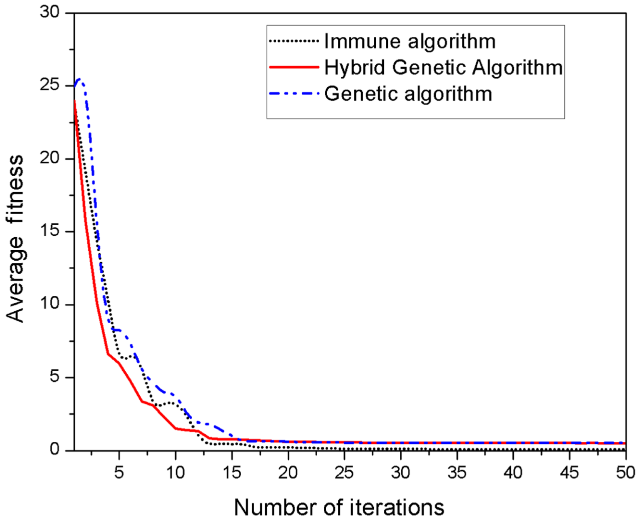


Fig. 5 Convergence characteristics of immune algorithm for system identification of a framed structure for subdomain SD_2

Table 3 Performance of the proposed structural system identification algorithm for building frame

Details	Proposed immune algorithm	Hybrid GA	GA
	without noise		
Minimum error(%)	0.0402	0.0823	0.1018
Maximum error(%)	0.2738	0.6071	0.8419
Absolute mean error(%)	0.1343	0.2358	0.2908
	With noise-SNR=60		
Minimum error(%)	0.0094	0.0120	0.0104
Maximum error(%)	0.5858	0.6731	0.6412
Absolute mean error(%)	0.1612	0.2574	0.3276
	With noise-SNR=50		
Minimum error(%)	0.0542	0.0413	0.0827
Maximum error(%)	0.7982	0.8822	0.8946
Absolute mean error(%)	0.3354	0.3973	0.4134
	With noise-SNR=40		
Minimum error(%)	0.3315	0.3876	0.3031
Maximum error(%)	1.2745	1.1945	1.6621
Absolute mean error(%)	0.5895	0.6912	0.7849

5.2 Example 2: Truss bridge

The model of the truss bridge with 55 elements, 24 nodes and 44 DOFs is taken as the second numerical example. The detailed geometrical configuration of the truss bridge is shown in Fig. 6. The structure is subjected to vertical harmonic excitation at F_1 and F_2. It is considered here for the identification of axial rigidity of the substructure members and the two Rayleigh damping coefficients.

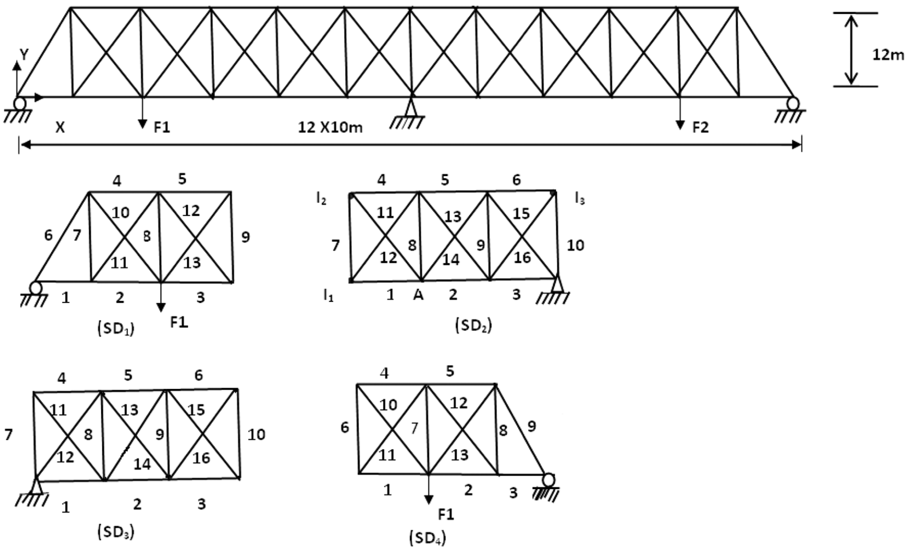


Fig. 6 Truss-bridge bridge-system identification using domain decomposition techniques

The elastic modulus *E*, cross-sectional area *A* and mass density of all the elements are 210 GPa, 0.03 m^2 and 8000 kg/m^3, respectively. The two damping coefficients α and β are chosen as 2.177 and 0.0011, respectively, resulting in a 5% damping ratio for the first two modes. The first two natural frequencies of the structure are 5.9 Hz and 8.3 Hz. Identification of full structural parameters (i.e., all 55 axial elemental rigidities and two damping parameters) needs response measurements at all 44 DOFs, which would be impractical because of limitations on the number of sensors. Thus, the global identification is not attempted here. For identification, purposes, the truss is divided into four subdomains (SD-1 to SD-4), as shown in Fig. 6. The subdomain SD-2 is used for identification here. The elemental axial rigidity (*EA*) for each element and the two Rayleigh damping coefficients are assumed to be unknown. Identification results for the entire structure are presented here. The identified parameters for the first two subdomains are shown in Table 4 for the noise-free condition as well as with measurement noise considering SNR as 40, 50 and 60. A close look at the results indicates that the proposed system identification technique with immune algorithm performs rather well even for noisy measurements. The damping parameters are also identified with reasonable accuracy. The velocity time history response obtained with the identified structure at node 5 is shown in Fig. 7 and it has been compared with the original structural response. It can be easily verified from the response time history given in Fig. 7 that the proposed identification strategy is effective. The comparative performances of the three algorithms i.e., proposed immune algorithm, hybrid GA and genetic algorithm for system identification of truss bridge are shown in Table 5. Finally, the convergence characteristics of the proposed Immune algorithm with float encoded genetic algorithm and hybrid GA for the second subdomain is shown in Fig. 8. It can be clearly observed from Fig. 8 and also the details furnished in Table 5 for various levels of measurement noise, that the proposed immune algorithm exhibits better convergence characteristics than hybrid GA and also the genetic algorithms.

Table 4 Details of identified axial rigidity and damping parameters of truss bridge using the proposed system identification formulation with immune algorithm

Element number	Actual axial rigidity (AE)×10^6 kN	Without noise		With noise SNR=40		With noise SNR = 50		With noise SNR = 60	
		Identified axial rigidity (AE)×10^6 kN	% error	Identified axial rigidity (AE)×10^6 kN	% error	Identified axial rigidity (AE)×10^6 kN	% error	Identified axial rigidity (AE)×10^6 kN	% error
Subdomain-1 (SD_1)									
1	6.3	6.2932	0.10793	6.3323	0.5126	6.3188	0.29841	6.2949	0.080952
2	6.3	6.2974	0.04126	6.3488	0.7746	6.3167	0.26507	6.3062	0.098412
3	6.3	6.3127	0.20158	6.3367	0.5825	6.3127	0.20158	6.2907	0.147653
4	6.3	6.2964	0.05714	6.2732	0.4253	6.2804	0.31111	6.2901	0.157131
5	6.3	6.2908	0.14603	6.3204	0.3238	6.2888	0.17777	6.3008	0.127936
6	6.3	6.2932	0.10793	6.2654	0.5492	6.2832	0.26666	6.2905	0.150820
7	6.3	6.2874	0.2	6.2667	0.5285	6.2884	0.18412	6.2931	0.109523
8	6.3	6.3047	0.07460	6.3475	0.7539	6.3167	0.26507	6.3098	0.155609
9	6.3	6.3052	0.08253	6.3396	0.6285	6.3142	0.22539	6.3078	0.123890
10	6.3	6.3067	0.10634	6.3276	0.4380	6.3107	0.16984	6.3074	0.117522
11	6.3	6.2912	0.13968	6.3345	0.5476	6.3142	0.22539	6.2802	0.314317
12	6.3	6.3044	0.06984	6.3498	0.7904	6.3044	0.06984	6.3012	0.019047
13	6.3	6.3066	0.10476	6.3401	0.6365	6.2908	0.14603	6.3004	0.006349
α	0.2963	0.296108	0.06479	0.284082	4.1235	0.306512	3.4465	0.306512	3.44650
β	0.0064	0.006432	0.5	0.006964	8.8125	0.006704	4.75	0.006704	4.75
Subdomain-2 (SD_2)									
1	6.3	6.3057	0.09047	6.3278	0.4412	6.3224	0.35555	6.2852	0.226984
2	6.3	6.3064	0.10158	6.3323	0.5126	6.3223	0.35396	6.2933	0.057142
3	6.3	6.2973	0.04285	6.2636	0.5777	6.3146	0.23174	6.2767	0.360317
4	6.3	6.2952	0.07619	6.2727	0.4333	6.284	0.25396	6.3126	0.241269
5	6.3	6.2904	0.15238	6.3318	0.5047	6.2723	0.43968	6.3119	0.165079
6	6.3	6.3087	0.13809	6.2709	0.4619	6.3268	0.42539	6.2882	0.179365
7	6.3	6.3092	0.14603	6.3312	0.4952	6.3121	0.19206	6.2987	0.012698
8	6.3	6.3017	0.02698	6.3437	0.6936	6.3267	0.42380	6.3219	0.344444
9	6.3	6.2963	0.05873	6.2721	0.4428	6.3235	0.37301	6.3056	0.100024
10	6.3	6.3187	0.29682	6.3367	0.5853	6.2979	0.03333	6.2904	0.020634
12	6.3	6.3154	0.24444	6.3501	0.7952	6.2841	0.25238	6.3281	0.403174
13	6.3	6.2993	0.01111	6.2795	0.3253	6.2697	0.48095	6.3383	0.623809
14	6.3	6.3126	0.20001	6.2688	0.4952	6.3304	0.48253	6.3155	0.204582
15	6.3	6.2944	0.08888	6.3428	0.6793	6.3356	0.56507	6.3244	0.387301
16	6.3	6.3021	0.03333	6.2797	0.3222	6.3267	0.42380	6.3021	0.033333

5.3 Example 3: Microwave tower

The third numerical example considered is a 40 m high microwave tower shown in Fig. 9. It has 360 members with 164 nodes. The young's modulus is taken as 205 GPa. The mass is taken as

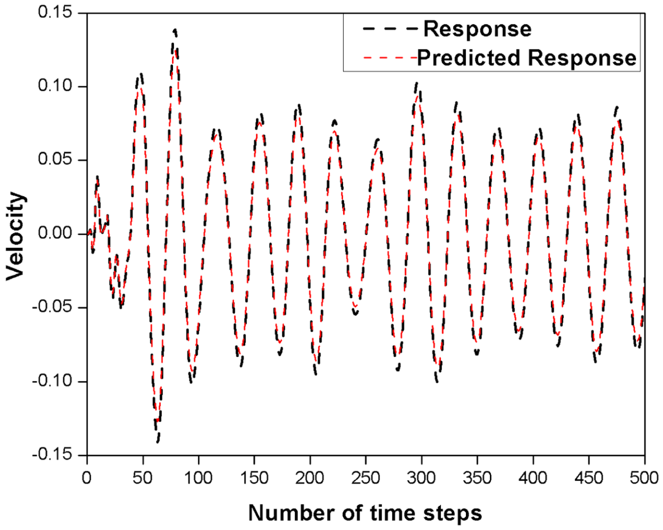


Fig. 7 Velocity time history response of the identified system

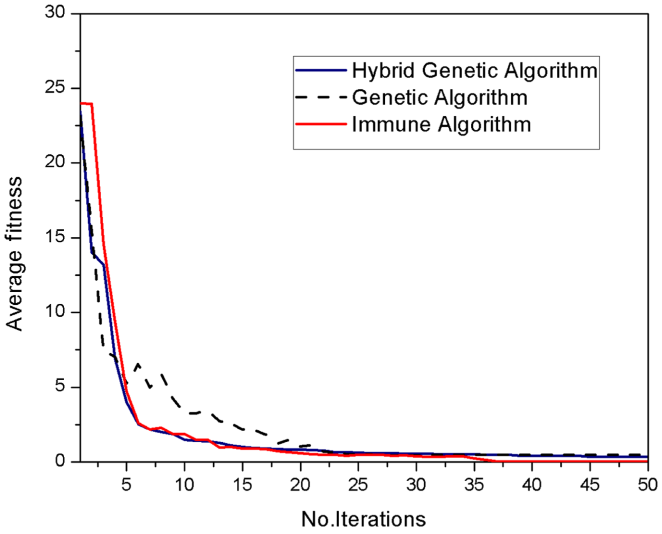


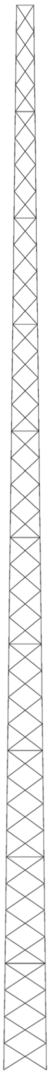
Fig. 8 Convergence characteristics of Immune algorithm for system identification of a truss bridge

7850 Kg/m^3. The two damping coefficients α and β are chosen as 0.977 and 0.0081, respectively, resulting in a 5% damping ratio for the first two modes. Identification of full structural parameters (i.e., all 360 axial elemental rigidities and two damping parameters) needs response measurements at all 480 DOFs, which would be impractical. Hence, the global identification is not a feasible option for parametric identification. For identification purposes, the tower model is decomposed into 10 subdomains. The elemental rigidities of all leg members at each level are considered constant and similarly the bracings at each level are considered constant. It may be observed that at each

Table 5 Performance of the proposed structural system identification algorithm for truss bridge

Details	Proposed immune algorithm	Hybrid GA	GA
SD-1 with no measurement noise			
Minimum error (%)	0.0413	0.0823	0.0912
Maximum error(%)	0.2016	0.6071	0.5417
Absolute mean error(%)	0.1107	0.2358	0.3498
SD-2 with no measurement noise			
Minimum error (%)	0.0111	0.0312	0.0287
Maximum error(%)	0.2968	0.4201	0.5417
Absolute mean error(%)	0.1139	0.2512	0.3017
SD-1 with noise SNR=60			
Minimum error(%)	0.0063	0.0023	0.0087
Maximum error(%)	0.3143	0.5122	0.6732
Absolute mean error(%)	0.1149	0.2746	0.3898
SD-2 with noise SNR=60			
Minimum error (%)	0.0206	0.0312	0.0410
Maximum error(%)	0.6079	0.5932	0.7123
Absolute mean error(%)	0.2412	0.2976	0.3376
SD-1 with noise SNR=50			
Minimum error(%)	0.0698	0.0712	0.0703
Maximum error(%)	0.3111	0.3818	0.4563
Absolute mean error(%)	0.2159	0.2612	0.2973
SD-2 with noise SNR=50			
Minimum error (%)	0.0333	0.0727	0.0867
Maximum error(%)	0.5651	0.6418	0.8761
Absolute mean error(%)	0.3525	0.3957	0.4314
SD-1 with noise SNR=40			
Minimum error(%)	0.3238	0.4658	0.4043
Maximum error(%)	0.7905	0.8842	0.9512
Absolute mean error(%)	0.5763	0.7752	0.8817
SD-2 with noise SNR=40			
Minimum error (%)	0.3222	0.2891	0.5621
Maximum error(%)	0.7952	0.8729	0.8892
Absolute mean error(%)	0.5176	0.7891	0.8917

level, the number of leg members is 4 and bracing members are 8. With this, the total number of design variables including the Rayleigh damping coefficients, for each subdomain identification reduces to 10. The stiffness ratio of the identified element stiffness to the actual element stiffness is evaluated. The stiffness ratios of the microwave tower obtained from the proposed domain decomposition based formulation discussed in this paper using the proposed immune algorithm, hybrid GA and GA are shown in Fig. 10. Similarly the results obtained with measurement noise

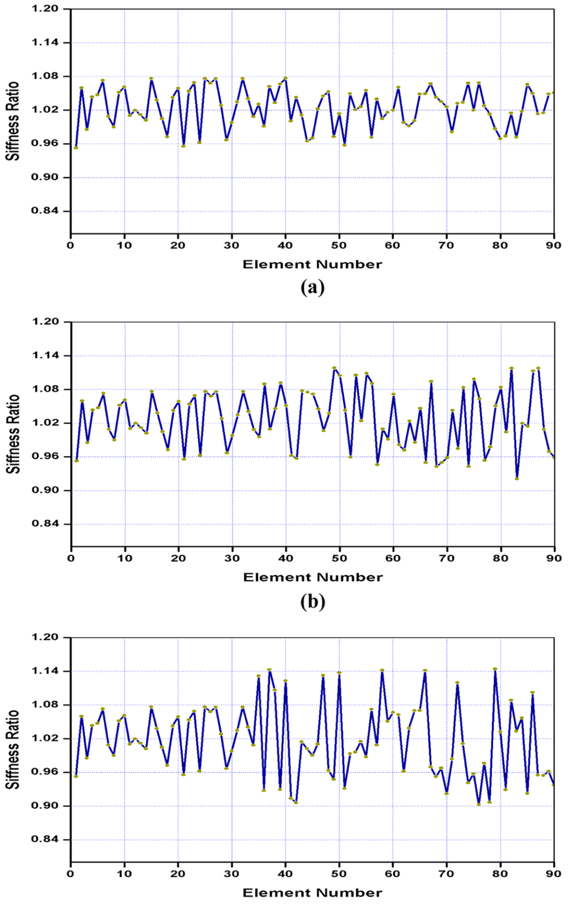


Height of tower: 40 m
Elastic modulus: 205 GPa
Poisson's ratio: 0.33
Number of active nodes: 40

Area No	Area (cm^2)
1	45.65
2	34.77
3	25.12
4	15.39
5	13.79
6	8.66
7	6.25
8	4.79
Leg Area	
Bays	Area #
1 to 8	1
9 to 16	2
17 to 24	3
25 to 32	4
33 to 40	5
Braces Area	
Bays	Area #
1 to 8	6
9-24,33,34	7
25 to 32	8
35 to 40	8

Fig. 9 40 m microwave tower

(i.e., with SNR=40, SNR=50 and SNR=60) are shown in Figs. 11 to 13. The comparative performances of the three meta-heuristic algorithms are also shown in Table 6. A close look at the Figs. 10 to 13 and also the details furnished in Table 6 clearly indicates that the proposed system identification with immune algorithm gives fairly accurate stiffness parameters even with noisy measurements. The performance of Hybrid GA follows immune algorithm, while GA stands last. The three numerical experiments conducted in this paper and comparisons made with other popular GA based algorithms clearly establish that the domain decomposition formulations together with artificial immune algorithms are effective in identifying the structure with reasonable accuracy.

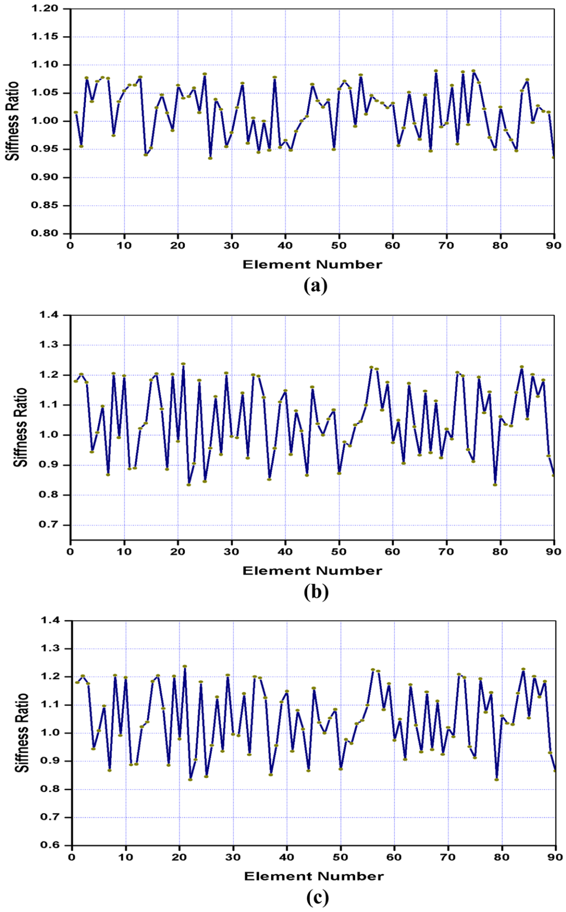


(a)

(b)

(c)

Fig. 10 System identification of the microwave tower using the proposed algorithm with (a) Immune algorithm, (b) hybrid genetic algorithm and (c) genetic algorithm with noise free measurements



(a)

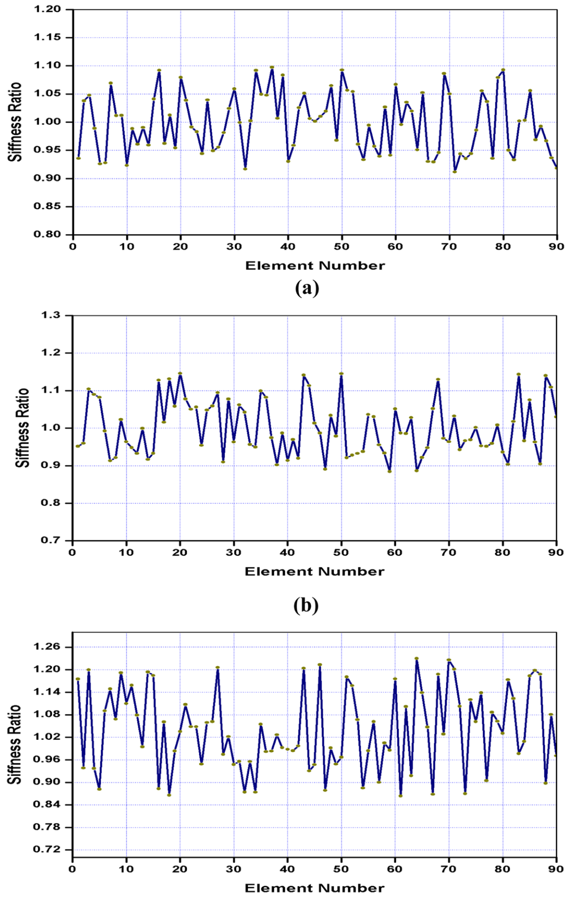
(b)

(c)

Fig. 11 System identification of the microwave tower using the proposed algorithm with (a) Immune algorithm, (b) hybrid genetic algorithm and (c) genetic algorithm noise (SNR=40)

6. Conclusions

In this paper, an artificial immune algorithm (IA) is presented for the problem of structural system identification. Immune algorithms are build with an effective diversification mechanism and are therefore extremely competitive for solving complex optimization problems associated with parametric identification of structural engineering problems. In order to minimize the number of sensors for measurement and also reduce the number of design variables, it is proposed to use domain decomposition approach. In this approach, the large structure is decomposed in to several convenient number of subdomains and each subdomain is identified independently. The number of sensors required will be limited to interface degrees of freedom and at selected location at the internal degrees of freedom. Numerical experiments are conducted by solving three problems in the

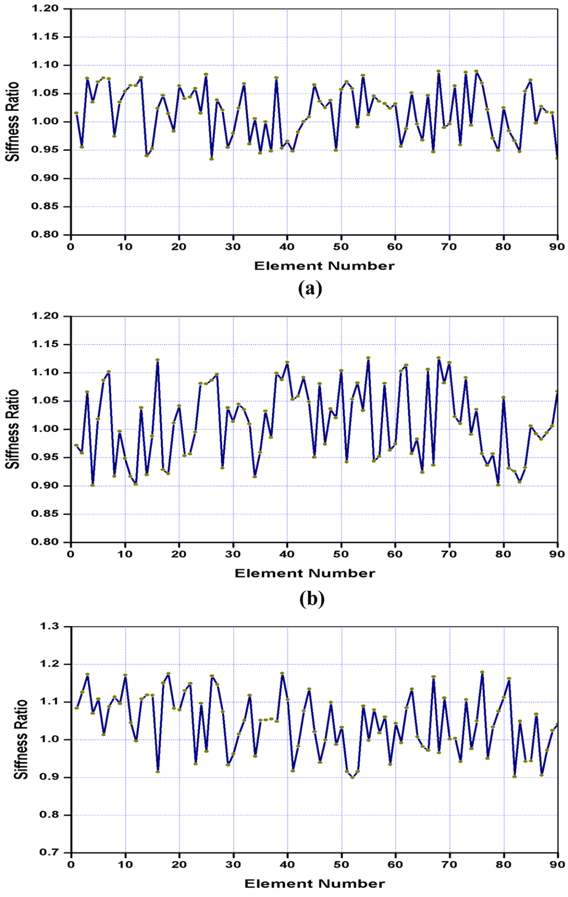


(a)

(b)

(c)

Fig. 12 System identification of the microwave tower using the proposed algorithm with (a) Immune algorithm, (b) hybrid genetic algorithm and (c) genetic algorithm noise (SNR=50)



(a)

(b)

(c)

Fig. 13 System identification of the microwave tower using the proposed algorithm with (a) Immune algorithm, (b) hybrid genetic algorithm and (c) genetic algorithm noise (SNR=60)

order of increasing complexity. To simulate the experimental measurements, measurement noise is included in the form of signal to noise ratio.

Numerical studies carried out in this paper clearly demonstrate that the proposed immune algorithm is clearly superior to GA and also hybrid genetic algorithm especially while solving large size problems. The proposed immune algorithm based technique is a promising tool for structural parameter estimation of structural systems in the sense that it is an optimal method requiring no prior knowledge of the structure. The domain decomposition features built in to the proposed formulations enable to solve large size problems with limited number of sensors placed on the structures.

Table 6 Performance of the proposed structural system identification algorithm for Microwave tower

Details	Proposed immune algorithm	Hybrid GA	GA
Minimum error (%)	0.0393	0.2319	0.1278
Maximum error(%)	7.668	11.9277	14.9489
Absolute mean error(%)	3.57	5.4358	6.49
SNR=60			
Minimum error(%)	0.0134	0.3576	0.2253
Maximum error(%)	8.9509	12.68	18.1763
Absolute mean error(%)	4.1948	5.8384	8.3679
SNR=50			
Minimum error(%)	0.0782	0.0701	0.3018
Maximum error(%)	9.7366	14.5729	19.9970
Absolute mean error(%)	4.5489	6.2224	9.5252
SNR=40			
Minimum error(%)	0.0263	0.1605	0.0099
Maximum error(%)	14.5697	17.7260	20.7521
Absolute mean error(%)	5.8571	8.4250	10.9692

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