GENETIC ALGORITHM AND ITS VARIANTS: THEORY AND APPLICATIONS

B.TECH FINAL YEAR

PROJECT REPORT

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CERTIFICATE:

This is to certify that the project report entitled "**Genetic Algorithm and its variants: Theory and Applications**" is a bonafide work done by BINEET MISHRA, Final year student of Electronics and Communication Engineering, Roll No.:10509033 and RAKESH KUMAR PATNAIK, Final year student of Electronics and Instrumentation Engineering, Roll No.:10507002 at NATIONAL INSTITUTE OF TECHNOLOGY, ROURKELA during their final year.

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ABSTRACT

The Genetic Algorithm is a popular optimization technique which is bio-inspired and is based on the concepts of natural genetics and natural selection theories proposed by Charles Darwin. The Algorithm functions on three basic genetic operators of selection, crossover and mutation. Based on the types of these operators GA has many variants like Real coded GA, Binary coded GA, Sawtooth GA, Micro GA, Improved GA, Differential Evolution GA. This paper discusses a few of the forms of GA and applies the techniques to the problem of Function optimization and System Identification. The paper makes a comparative analysis of the advantages and disadvantages of the different types of GA. The computer simulations illustrate the results. It also makes a comparison between the GA technique and Incremental LMS algorithm for System Identification.

Key terms: ***Genetic Algorithm, Crossover, Mutation, Selection, Real coded GA, Binary code GA, Sawtooth GA, Differential Evolution GA, Incremental LMS Algorithm, System Identification .***

CONTENTS:

CHAPTER 1

INTRODUCTION

1.1) GENETIC ALGORITHM:

God is the creator of the whole universe. Ever since its creation evolution has been a part and parcel of its functioning. New organisms have evolved from their ancestors; and this evolution is governed by a simple law which Charles Darwin named as –"*Survival of the Fittest*".

Genetic Algorithms are search algorithms based on natural selection and natural genetics. They combine survival of fittest among structures with structured yet randomized information exchange to form a search algorithm. Genetic Algorithm has been developed by John Holland and his co-workers in the University of Michigan in the early 60's. Genetic algorithms are theoretically and empirically proved to provide robust search in complex spaces. Its validity in – *Function Optimization* and *Control Applications* is well established.

Genetic Algorithms (GA) provide a general approach for searching for global minima or maxima within a bounded, quantized search space. Since GA only requires a way to evaluate the performance of its solution guesses without any apriori information, they can be applied generally to nearly any optimization problem. GA does not guarantee convergence nor that the optimal solution will be found, but do provide, on average, a "good" solution. GA is usually extensively modified to suit a particular application. As a result, it is hard to classify a "generic" or "traditional" GA, since there are so many variants. However, by studying the original ideas involved with the early GA and studying other variants, one can isolate the main operations and compose a "traditional" GA. An improvement to the "traditional" GA to provide faster and more efficient searches for GAS that does not rely on average chrornosome convergence (i.e. applications which are only interested in the best solution).

The "traditional" GA is composed of a fitness function, a selection technique, and crossover and mutation operators which are governed by fixed probabilities. These operations form a genetic loop as shown in Figure. Since the probabilities are constant, the average number of local and global searches in each generation is fixed. In this sense, the GA exhibits a fixed convergence rate and therefore will be referred to as the fixed-rate GA.

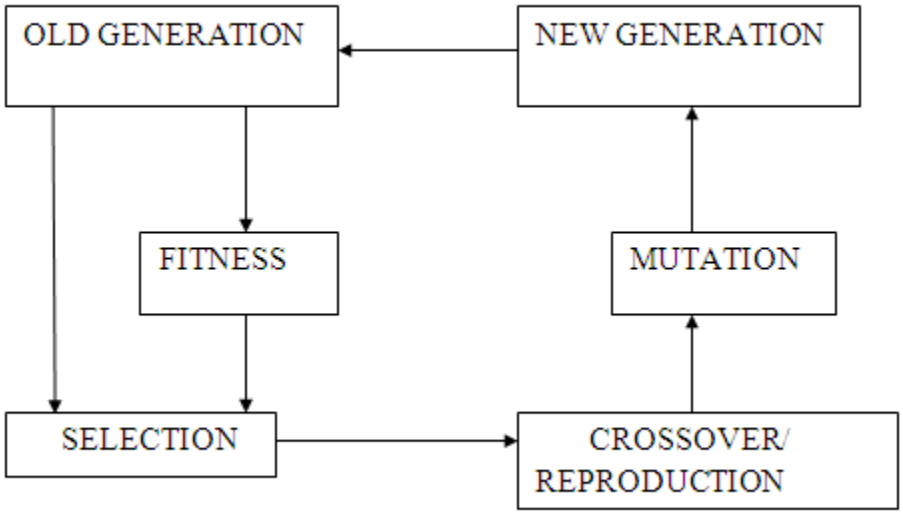


FIGURE: GENETIC LOOP

THE FIXED RATE GENETIC ALGORITHM:

The population is defined to be the collection of all the chromosomes. A generation is the population after a specific number of iterations of the genetic loop. A chromosome is composed of genes, each of which reflects a parameter to be optimized. Therefore, each individual chromosome represents a possible solution to the optimization problem. The dimension of the GA refers to the dimension of the search space which equals the number of genes in each chromosome.

FITNESS:

The fitness function provides a way for the GA to analyze the performance of each chromosome in the population. Since the fitness function is the only relation between the GA and the application itself, the function must be chosen with care. The fitness function must reflect the application appropriately with respect to the way the parameters are to be minimized.

SELECTION:

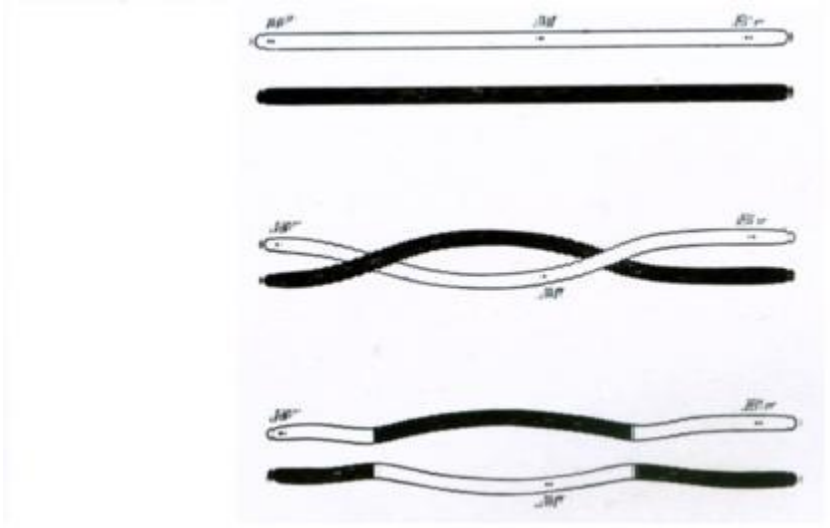
The selection operator selects chromosomes from the current generation to be parents for the next generation. The probability of each chromosomes selection is given by:

$$Ps(i)=f(i)/\sum_{J=1}^{N} f(j)$$

where *ps* ***(i)*** and *f (i)* are the probability of selection and fitness value for the ith chromosome respectively. Parents are selected in pairs. Once one chromosome is selected, the probabilities are renormalized without the selected chromosome, so that the parent is selected from the remaining chromosomes. Thus each pair is composed of two different chromosomes. It is possible for a chromosome to be in more than one pair.

CROSSOVER:

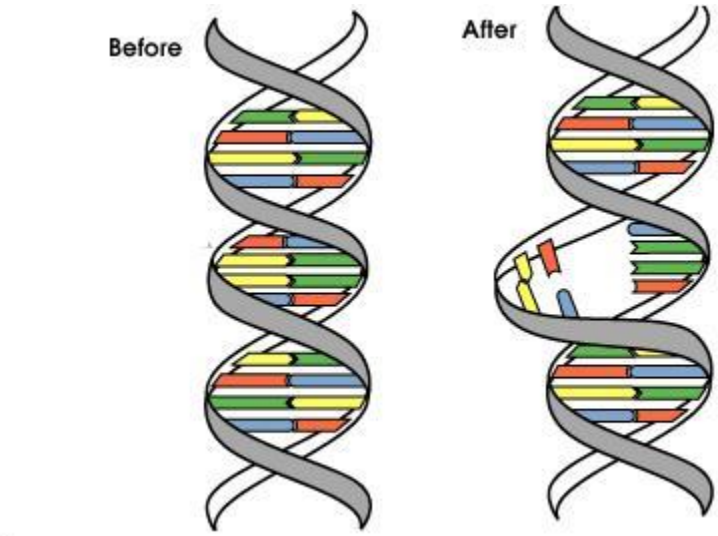
Crossover is the GA's primary local search routine. The crossover/reproduction operator computes two offspring for each parent pair given from the selection operator. These offspring, after mutation, make up the new generation. A probability of crossover is predetermined before the algorithm is started which governs whether each parent pair is crossed-over or reproduced. Reproduction results in the offspring pair being exactly equal to the parent pair. The crossover operation converts the parent pair to binary notation and swaps bits after a randomly selected crossover point to form the offspring pair.



CROSSOVER OF TWO STRANDS OF CHROMOSOME.

MUTATION:

Mutations are global searches. A probability of mutation is again predetermined before the algorithm is started which is applied to each individual bit of each offspring chromosome to determine if it is to be inverted.

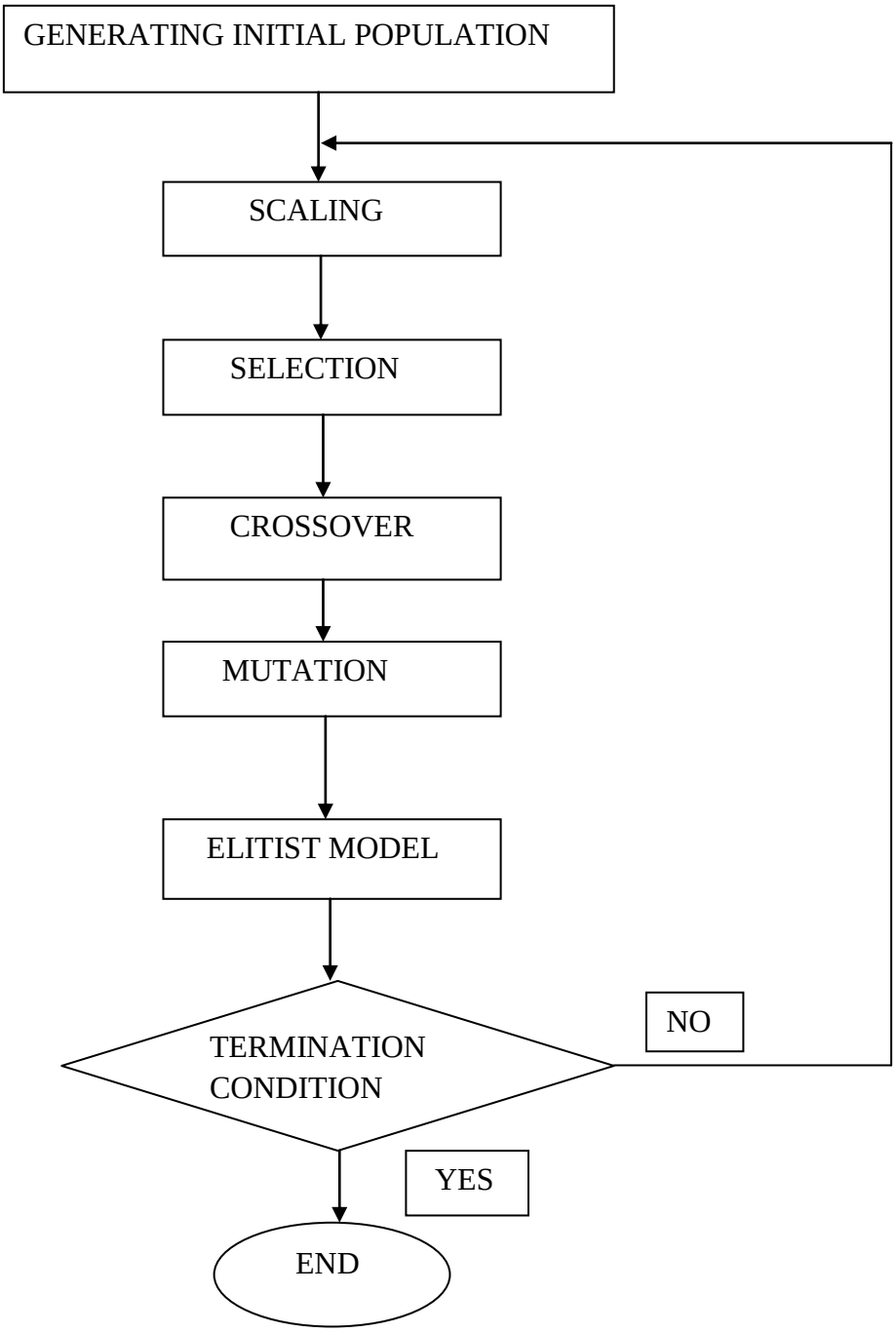


MUTATION OF A CHROMOSOME

ELITISM:

The elitist operator insures the GA will not get worse as it progresses. The elitist operator copies the best chromosome to the next generation bypassing the crossover and mutation operators. This guarantees the best chromosome will never decrease in fitness.

FLOW CHART OF GENETIC ALGORITHM:



Computing the probabilities of crossover and mutation as a function of fitness allow the probabilities to reflect the current state of the GA. Different probabilities of crossover are used for different parent pairs, while different mutation probabilities are used for each individual chromosome within the same generation. One can then isolate poor performing chromosomes with low relative fitness to be treated more as global searches by using a high probability of mutation. This allows the GA to concentrate on better performing chromosomes while using the other to search for new minima or maxima.

Genetic Algorithm overrides the already existing traditional methods like derivative method, enumerative method in the following ways:-

(1) It is not restricted to any local neighborhood and tends to achieve the global maxima.

(2) It is fundamentally not restricted by assumptions of search space like existence of derivatives, unimodality etc.

1.2) REAL CODED GENETIC ALGORITHM:

The concept of the genetic algorithm was first formalized by Holland and extended to functional optimization by DeJong .It imitates the mechanism of the natural selection and evolution and aims to solve an optimization problem with object function f(x) where x=[x1 x2 ……. xn] is the N-dimensional vector of optimization parameters. It has proved to be an effective and powerful global optimization algorithm forms any combinatorial optimization problems, especially for those problems with discrete optimization parameters, nondifferentiable and/or discontinuous object function. Genes and chromosomes are the basic building blocks of the binary GA. The conventional binary GA encodes the optimization parameters into binary code string. A gene in GA is a binary bit.

Real coded Genetic Algorithm (RCGA) possesses a lot of advantages than its binary coded counterpart when dealing with continuous search spaces with large dimensions and a great numerical precision is required. In RCGA, each gene represents a variable of the problem, and the size of the chromosome is kept the same as the length of the solution to the problem. Therefore, RCGA can deal with large domains without sacrificing precision as the binary implementation did (assuming a fixed length for the chromosomes). Furthermore, RCGA possesses the capacity for the local tuning of the solutions; it also allows integrating the domain knowledge so as to improve the performance of Genetic Algorithm (GA). But RCGA is still harassed by the requirement of population diversity and the frequent computation of fitness, and may become very time-consuming. As a result, its inherent parallelism is inhibited and its application field is restricted by the speed bottleneck as its binary implementation did.

The binary GA does not operate directly on the optimization parameters but on a discretised representation of them. Discretization error will inevitably be introduced when encoding a real number. The encoding and decoding operations also make the algorithm more computationally expensive for problems with real optimization parameters. It is therefore worth developing a novel GA which works directly on the real optimization parameters. The real-coded GA is

consequently developed. Both theoretical proof and practical experiences show that RGA usually works better than binary GA, especially for problems with real optimization parameters

The RCGA operates on a population of chromosomes (or individuals, creatures, etc.) simultaneously. It starts from an initial population, generated randomly within the search space. Once the initialization is completed, the population enters the main RCGA loop and performs a global optimization for searching the optimum solution of the problem. In a RCGA loop, preprocessing, three genetic operations, and postprocessing are carried out in turn. The RCGA loop continues until the termination conditions are fulfilled.

SCALING OPERATOR:

The scaling operator, a preprocessor, is usually used to scale the object function into an appropriate fitness function. It aims to prevent premature convergence in the early stages of the evolution process and to speed up the convergence in the more advanced stages of the process.

GENETIC OPERATORS:

The three genetic operations are selection (or reproduction), crossover, and mutation. They are the core of the algorithm.

The **selection** operator selects good chromosomes on the basis of their fitness values and produces a temporary population, namely, the mating pool. This can be achieved by many different schemes, but the most common methods are roulette wheel, ranking, and stochastic binary tournament selection. The selection operator is responsible for the convergence of the algorithm.

The **crossover** operator is the main search tool. It mates chromosomes in the mating pool by pairs and generates candidate offspring by crossing over the mated pairs with probability. Many variations of crossover have been developed, e.g., one-point crossover, two-point crossover, -point crossover, and random multipoint crossover.

After crossover, some of the genes in the candidate offspring are inverted with a probability . This is the **mutation** operation. The mutation operator is included to prevent premature convergence by ensuring the population diversity. A new population is therefore generated.

ELITIST MODEL:

The postprocessor is the elitist model. The worst chromosome in the newly generated population is replaced by the best chromosome in the old population if the best member in the newly generated population is worse than that in the old population. It is adopted to ensure the algorithm's convergence.

In the RGA, a gene is the optimization parameter itself and the *i*th chromosome in the *n*th population takes the form

$$chromosome^{n,i} = g^{n,i} = [g1^{n,i}\ \ g2^{n,i} \dots\dots\dots\dots\ gN^{n,i}]$$

Consequently, the crossover and mutation operators used in the RGA are quite different from those in the binary GA. The arithmetical one-point crossover and the random perturbation mutation are used and introduced.

A common form of real crossover involves an averaging of two parent genes. The child population is given by the formula

$$g_q^j(k+1) = g_q^j(k) + \alpha\, v_{qr}^j \omega_p \epsilon_q^j$$

$$g_r^j(k+1) = g_r^j(k) + \alpha\, v_{rq}^j \omega_p \epsilon_r^j$$

Where,

$g_q^j(k)$, $g_q^j(k)$ are the qth and rth individuals of the parent population set.

v_{qr}^{j} is the crossing vector given by the formula:

$$v_{rq} = g_r(k) - g_q(k)$$

ϵ is a normally distributed random number that determines the amount of gene crossing.

ω is the gene selection vector and the crossover takes place when the value is 1

α (0<α<=1) is the crossover range that defines the evolutionary step size and is equivalent to the step size in he LMS algorithm.

The real mutation operator takes the selected gene and adds a random value from within a specified mutation range. The child produced by mutation is given by

$$g_q^j(k+1)' = g_q^j(k+1) + \beta\Phi$$

Where,

β is the mutation range or step size.

Φ is the random value which decides the amount of mutation in the individual.

1.3) BINARY CODED GENETIC ALGORITHM:

The binary coded *genetic algorithm* is a probabilistic search algorithm that iteratively transforms a set (called a *population*) of mathematical objects (typically fixed-length binary character strings), each with an associated fitness value, into a new population of offspring objects using the Darwinian principle of natural selection and using operations that are patterned after naturally occurring genetic operations, such as crossover (sexual recombination) and mutation. Following the model of evolution, they establish a population of individuals, where each individual corresponds to a point in the search space. An objective function is applied to each individual to rate their fitness. Using well conceived operators, a next generation is formed based upon the survival of the fittest. Therefore, the evolution of individuals from generation to generation tends to result in fitter individuals, solutions, in the search space. Empirical studies have shown that genetic algorithms do converge on global optima for large class problems.

In binary coded genetic algorithms, a population is nothing but a collection of "chromosomes" representing possible solutions. These chromosomes are altered or modified using genetic operators through which a new generation is created. This process is repeated a predetermined number of times or until no improvement in the solution to the problem is found.

A. ENCODING SCHEMES:

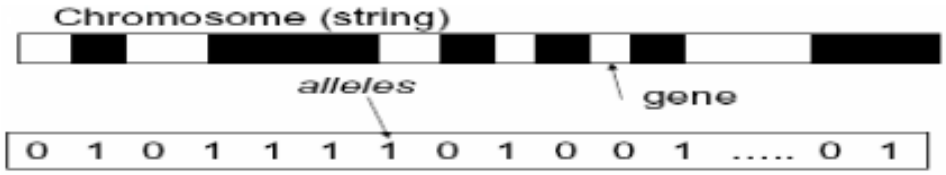
Originally, the chromosomes (or individuals) in the population were represented as strings of binary digits. However, bit string representations are still the most commonly used encoding techniques and have been used in many real-world applications of genetic algorithms. Such representations have several advantages: -

i) They are simple to create and manipulate,

ii) Many types of information can be easily encoded,

iii) The genetic operators are easy to apply.

REPRESENTATION OF CHROMOSOME:



Each chromosome represents a solution, often using strings of 0's and 1's.Each bit typically corresponds to a gene. This is Binary Encoding. The value for a given gene is called Alleles.

B. EVALUATION:

The evaluation of a chromosome is done to test its "fitness" as a solution and is achieved by making use of a mathematical formula known as an objective function. The objective function plays the role of the environment in natural evolution by rating individuals in terms of their fitness. Choosing and formulating an appropriate objective function is crucial to the efficient solution of any given genetic algorithm problem.

C. GENETIC OPERATORS

Genetic operators are used to alter the composition of chromosomes. The fundamental genetic operators such as selection, crossover, and mutation are used to create children (or individuals in the next generation) that differ from their parents (or individuals in the previous generation).

Selection Operator:

Individual chromosomes are selected according to their fitness, which is evaluated using an objective function. This means that a chromosome with a higher fitness value will have a higher probability of contributing one or more chromosomes in the next generation. There are many ways this operator can be implemented. A basic method calls for using a weighted **roulette wheel** with slots sized according to fitness .Thus, on the roulette wheel the individual with the highest fitness will have a larger slot than the other individuals in the population. Consequently, when the wheel is spun, the best individual will have a higher chance of being selected to

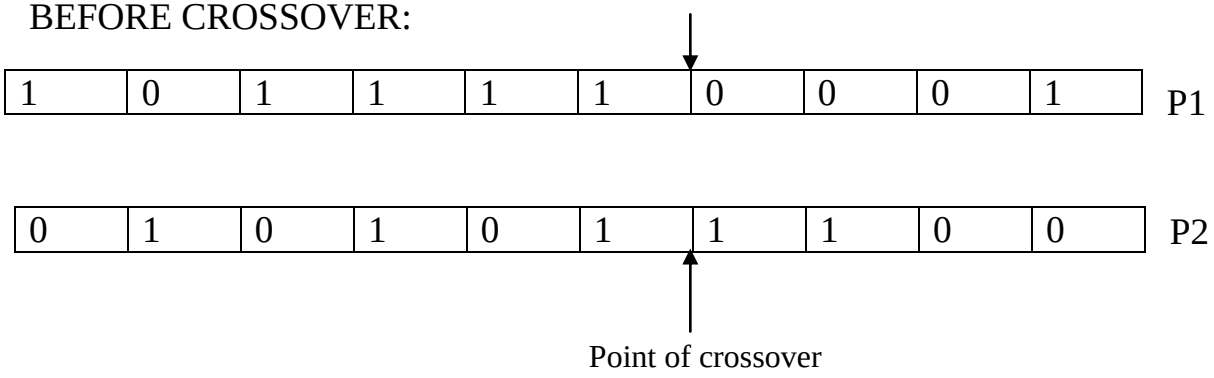
contribute to the next generation. Individuals thus selected are further operated on with other genetic operators such as crossover and mutation.

Crossover Operator:

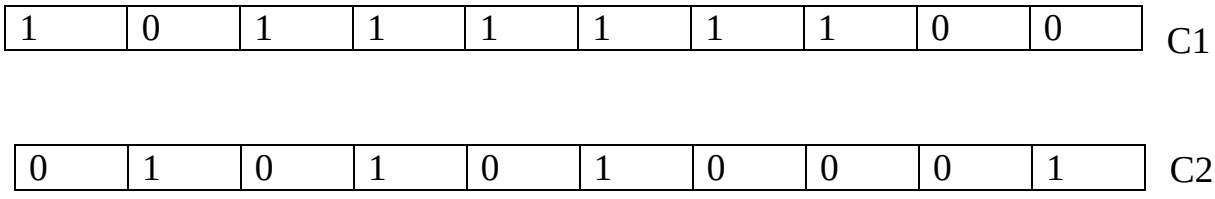
The purpose of the crossover operator is to produce new chromosomes that are distinctly different from their parents, yet retain some of their parent characteristics. There are two important crossover techniques called one-point crossover and two-point crossover.

In ***one-point crossover***, two parent chromosomes are interchanged at a randomly selected point thus creating two children.

BEFORE CROSSOVER:

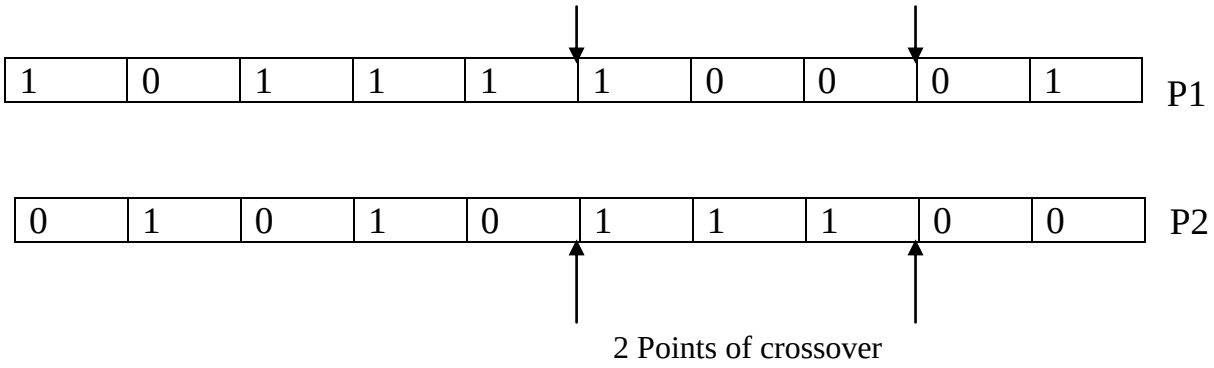


AFTER CROSSOVER:

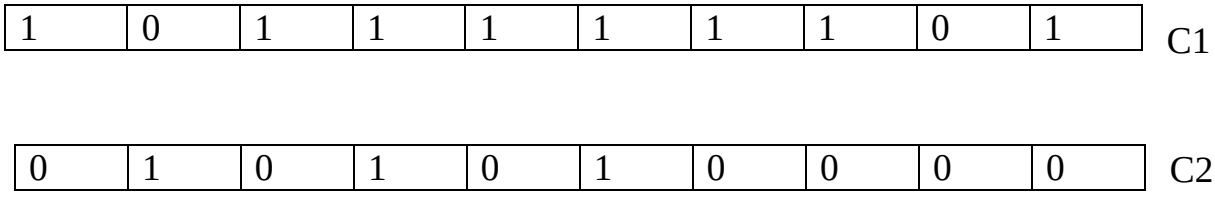


In ***two point crossover***, two crossover points are selected instead of just one crossover point. The part of the chromosome string between these two points is then swapped to generate two children. Empirical studies have shown that two point crossover usually provides better randomization than one-point crossover.

BEFORE CROSSOVER:



AFTER CROSSOVER:



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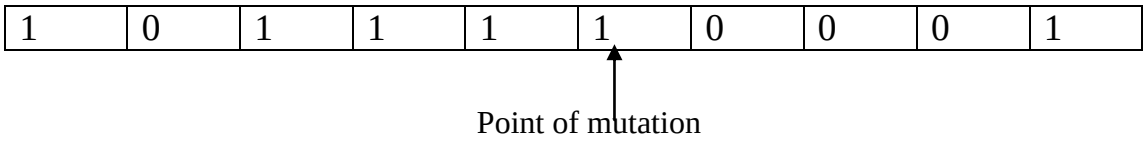
Mutation Operator:

Some of the individuals in the new generation produced by selection and crossover are mutated using the mutation operator. The most common form of mutation is to take a bit from a chromosome and alter (i.e., flip) it with some predetermined probability. As mutation rates are very small in natural evolution, the probability with which the mutation operator is applied is set to a very low value and is generally experimented with before this value is fixed.

BEFORE MUTATION:



AFTER MUTATION:

1	0	1	1	1	0	0	0	0	1

An ***elitist policy***, the fittest individual in the previous generation conditionally replaces the weakest individual in the current generation is used.It forces binary GA to retain some number of the best individuals at each generation. It has been found that elitism significantly improves performance.

Starting with an initial population and the corresponding fitness values the algorithm iterates through several generations and finally converges to optimal solution.

ADVANTAGES:

1) Binary GA always gives an answer and answer get better with time.
2) Binary GA is a good algorithm for noisy environment.
3) Binary GA is inherently parallel and is easily distributed.

The main issue concerning Binary GA is slow convergence because conversion of a number from real value to its corresponding binary value or the conversion of binary value to its real value takes a lot of computational time.

1.4) SAWTOOTH GA

A number of methods have been developed to improve the robustness and computational efficiency of GAs. A simple GA uses a population of constant size and guides the evolution of a set of randomly selected individuals through a number of generations that are subject to successive selection, crossover, and mutation, based on the statistics of the generation (standard GA). Population size is one of the main parameters that affect the robustness and computational efficiency of the GAs. Small population sizes may result in premature convergence to nonoptimal solutions, whereas large population sizes give a considerable increase of computational effort. Several methods have been proposed in the literature that attempt to increase the diversity of the population and avoid premature convergence.

In the method adopted here a variable population size with periodic reinitialization is used that follows a saw-tooth scheme with a specific amplitude and period of variation (saw-tooth GA). In each period, the population size decreases linearly and at the beginning of the next period randomly generated individuals are appended to the population.

VARIABLE POPULATION SIZE:

Varying the population size between two successive generations affects only the selection operator of the GA. Let n_t and n_{t+1} denote the population size of the current and the subsequent generation, respectively. The selection of the individuals can be considered as a repetitive process of n_{t+1} selection operations, with p_j being the probability of selection of the jth individual. For most of the selection operators, such as fitness proportionate selection and tournament selection with replacement, the selection probability remains constant for the selection operations. A GA with decreasing population size has bigger initial population size and smaller final population size, as compared to a constant population size GA with the same computing cost (i.e., equal average population size). This is expected to be beneficial, because a bigger population size at the beginning provides a better initial signal for the GA evolution

process; whereas, a smaller population size is adequate at the end of the run, where the GA converges to the optimum.

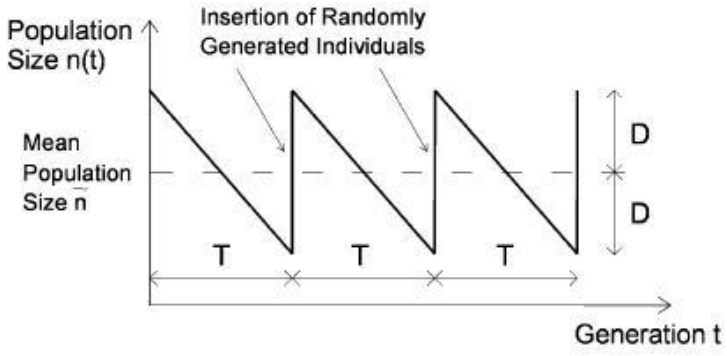


FIGURE: VARIABLE POPULATION IN SAWTOOTH GA

1.5) DIFFERENTIAL EVOLUTION

Differential evolution (DE) seeks to replace the classical crossover and mutation schemes of the genetic algorithm (GA) by alternative differential operators. The DE algorithm has recently become quite popular in the machine intelligence and cybernetics community. In many cases, it has outperformed the GA or the particle swarm optimization (PSO). As in other evolutionary algorithms, two fundamental processes drive the evolution of a DE population: the *variation* process, which enables exploring the different regions of the search space, and the *selection* process, which ensures exploitation of the acquired knowledge about the fitness landscape.

DE does suffer from the problem of premature convergence to some suboptimal region of the search space. In addition, like other stochastic optimization techniques, the performance of classical DE deteriorates with the increase of dimensionality of the search space.

Differential Evolution has proven to be a promising candidate for optimizing real-valued multi-modal objective functions. Besides its good convergence properties DE is very simple to understand and to implement. DE is also particularly easy to work with, having only a few control variables which remain fixed throughout the entire optimization procedure.

DE is a parallel direct search method which utilizes NP D-dimensional parameter vectors:
Xi,G, for i = **0,** 1 , 2, ... , NP-1, as a population for each generation G, i.e. for each iteration of the optimization. NP doesn't change during the minimization process. The initial population is chosen randomly and should try to cover the entire parameter space uniformly. As a rule, we will assume a uniform probability distribution for all random decisions unless otherwise stated. The crucial idea behind DE is a scheme for generating trial parameter vectors, by adding the weighted difference between two population vectors to a third vector. If the resulting vector yields a lower objective function value than a predetermined population member, the newly generated vector will replace the vector with which it was compared in the following generation; otherwise, the old vector is retained. This basic principle, however, is extended when it comes to the practical variants of DE. For example an existing vector can be perturbed by adding more than one weighted difference vector to it. In most cases, it is also worthwhile to mix the

parameters of the old vector with those of the perturbed one. The performance of the resulting vector is then compared to that of the old vector. For each vector **X**i,g, for i = 0,1,2, ..., NP-1, a perturbed vector **V**i **,**g+1 is generated according with $\mathbf{r_1}, \mathbf{r_2}, \mathbf{r_3} \in [0, \mathrm{NP} - 1]$, integer and mutually different, and F > 0. The integers $\mathbf{r_1}, \mathbf{r_2}, \mathbf{r_3}$ are chosen randomly from the interval [0, NP-1] and are different from the running index i. F is a real and constant factor ϵ [0, **21** which controls the amplification of the differential variation $(\mathrm{X_{r2,g}} - \mathrm{X_{r3,g}})$**.** Note that the vector X_{r1g} which is perturbed to yield $\mathrm{V_{i,g+1}}$ has no relation to $\mathrm{X_{i,g}}$, but is a randomly chosen population member. The perturbed vector is given by:

$$\mathrm{V_{i,g+1}} = x_{r1,g} + F(x_{r2,g} - x_{r3,g})$$

In order to increase the diversity of the new parameter vectors, **crossover** is introduced. To this end, the vector:

$$U_{i,g+1} = (X_{0i,g+1}, X_{1i,g+1}, \dots \dots \dots)$$

With

$$\mathbf{U_{ji,g+1}} = \mathbf{V_{ji,g+1}}, \text{ for j} = <n>_{\mathrm{D}}, <n+1>_{D}, <n+2>_{\mathrm{D}}, \dots, <n+L-1>_{\mathrm{D}}$$
$$= \mathbf{X_{ji,g}}, \text{for all other j} \in [0, \mathrm{D} - 1]$$

is formed. The acute brackets < >, denote the modulo function with modulus D. The starting index, n is a randomly chosen integer from the interval [0,D-I]. The integer L, which denotes the number of parameters that are going to be exchanged, is drawn from the interval [1, D]. The algorithm which determines L works according to the following lines of pseudo code where rand() is supposed to generate a random number ϵ [0,1) :

```
L = 0;
do {
        L = L + l ;
    }while(rand()< CR) AND (L < D ) ) ;
```

Hence the probability Pr(L>=v) = $(CR)^{V-l}$, v > 0. CR ϵ [0,1] is the crossover probability and constitutes a control variable in the design process. The random decisions for both n and L are made anew for each newly generated vector$V_{i,g+1}$. The figure below provides a pictorial representation of DE'S crossover mechanism.

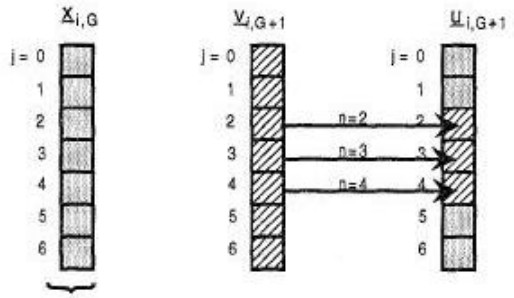


Fig. : Illustration of the crossover process for D=7, n=2 and L=3.

To decide whether or not it should become a member of generation G+1, the new vector $\mathbf{U_{i,g+1}}$ is compared to$\mathbf{X_{i,g}}$. If vector $U_{i,g+1}$ yields a smaller objective function value than $\mathbf{X_{i,g}}$, then $X_{i,g+1}$ is replaced by$U_{i,g+1}$; otherwise, the old value $X_{i,g}$ is retained for the next iteration.

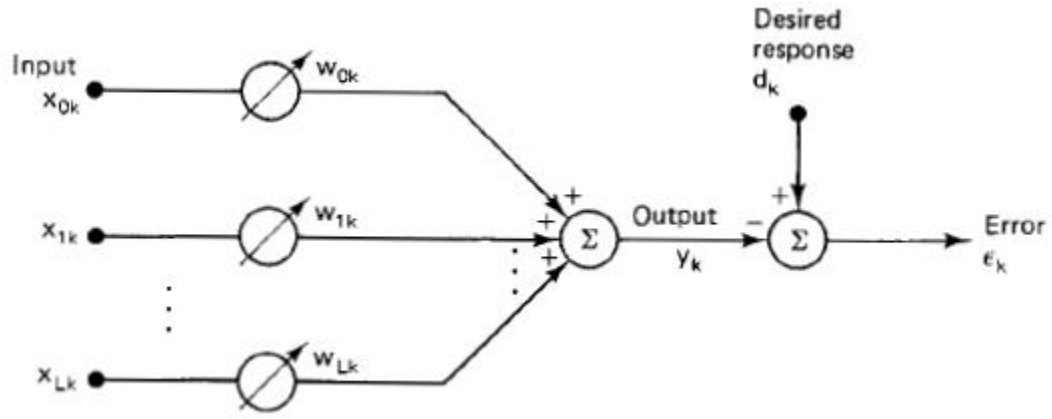
1.6) LEAST MEAN SQUARE ALGORITHM:

Least mean squares (LMS) algorithms are used in adaptive filters to find the filter coefficients that relate to producing the least mean squares of the error signal (difference between the desired and the actual signal). It is a stochastic gradient descent method in which the filter is adaptive based on the error at the current time. It was invented in 1960 by Stanford University professor Bernard Widrow and his first Ph.D. student, Ted Hoff.

The adaptive linear combiner output, y_k is a linear combination of the input samples. The error in measurement is given by

$$\boldsymbol{\varepsilon_k = d_k - X_K^T W_K}$$

where X_K^T is the transpose vector of input samples.



THE ADAPTIVE FILTER IN GENERAL FORM

To develop an adaptive algorithm ,it is required to estimate the gradient of ξ=E[ε_k^2] by taking differences between short term averages of ε_k^2 .Instead, to develop the LMS algorithm process, $\varepsilon_k^2$is taken as the estimate of ε_k Thus at each iteration in the adaptive process a gradient estimate form is as follows:

$$\hat{\nabla}_k = \begin{bmatrix} \frac{\partial \varepsilon_k^2}{\partial w_0} \\ \vdots \\ \frac{\partial \varepsilon_k^2}{\partial w_L} \end{bmatrix} = 2\varepsilon_k \begin{bmatrix} \frac{\partial \varepsilon_k}{\partial w_0} \\ \vdots \\ \frac{\partial \varepsilon_k}{\partial w_L} \end{bmatrix} = -2\varepsilon_k \mathbf{X}_k$$

With this simple estimate the steepest descent type of adaptive algorithm is specified as

$$\boldsymbol{W_{k+1} = W_k - \mu \nabla_k}$$
$$\boldsymbol{= W_k + 2\mu \varepsilon_k X_k}$$

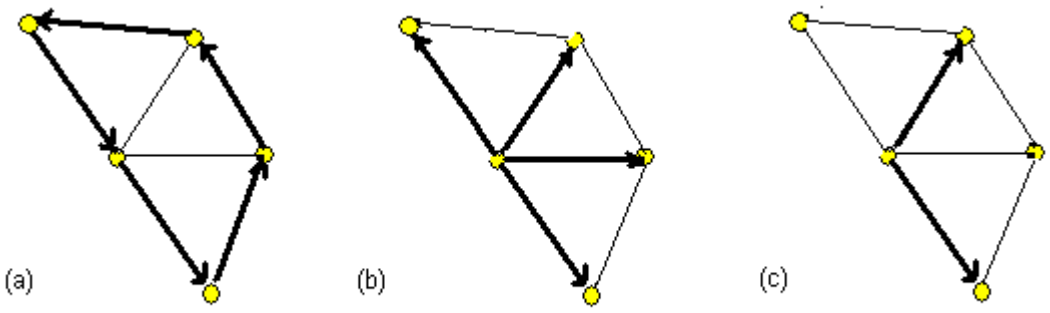
This is the LMS algorithm. Where "μ" is the **gain constant** that regulates the speed and stability of adaptation. Since the weight changes at each iteration are based on imperfect gradient estimates, the adaptive process is expected to be noisy. The LMS algorithm can be implemented without squaring, averaging or differentiation and is simple and efficient process.

CONVERGENCE OF WEIGHT VECTOR:

As with all adaptive Algorithms, the primary concern with the LMS Algorithm is its convergence to the weight vector solution, where error E [ε_k^2] is minimized.

1.7) INCREMENTAL ADAPTIVE STRATEGIES OVER DISTRIBUTED NETWORKS

Distributed processing deals with the extraction of information from data collected at nodes that are distributed over a geographic area. For example, each node in a network of nodes could collect noisy observations related to a certain parameter or phenomenon of interest. The nodes would then interact with their neighbours in a certain manner, as dictated by the network topology, in order to arrive at an estimate of the parameter or phenomenon of interest. The objective is to arrive at an estimate that is as accurate as the one that would be obtained if each node had access to the information across the entire network. In comparison, in a traditional centralized solution, the nodes in the network would collect observations and send them to a central location for processing. The central processor would then perform the required estimation tasks and broadcast the result back to the individual nodes. This mode of operation requires a powerful central processor, in addition to extensive amounts of communication between the nodes and the processor. In the distributed solution, the nodes rely solely on their local data and on interactions with their immediate neighbours. The amount of processing and communications is significantly reduced.



Three modes of co-operation (a) Incremental (b) Diffusion and (c) Probabilistic diffusion

The effectiveness of any distributed implementation will depend on the modes of cooperation that are allowed among the nodes. Three such modes of cooperation are as follows:

(a) Incremental

(b) Diffusion

(c) Probabilistic diffusion.

In an incremental mode of cooperation, information flows in a sequential manner from one node to the adjacent node. This mode of operation requires a cyclic pattern of collaboration among the nodes, and it tends to require the least amount of communications and power. In a diffusion implementation, on the other hand, each node communicates with all its neighbours as dictated by the network topology .The amount of communication in this case is higher than in an incremental solution. Nevertheless, the nodes have access to more data from their neighbours. The communications in the diffusion implementation can be reduced by allowing each node to communicate only with a subset of its neighbours. The choice of which subset of neighbours to communicate with can be randomized according to some performance criterion.

The need for adaptive implementations, real-time operation, and low computational and communications complexity, a distributed least-mean-squares (LMS)-like algorithm that requires less complexity for both communications and computations and inherits the robustness of LMS implementations. The proposed solution promptly responds to new data, as the information flows through the network. It does not require intermediate averaging as in consensus implementations; it neither requires two separate time scales.The distributed adaptive solution is an extension of adaptive filters and can be implemented without requiring any direct knowledge of data statistics; in other words, it is model independent.

1.8) SYSTEM IDENTIFICATION:

System identification is a general term to describe mathematical tools and algorithms that build dynamical models from measured data. A dynamical mathematical model in this context is a mathematical description of the dynamic behaviour of a system or process in either the time or frequency domain. Examples include:

- physical processes such as the movement of a falling body under the influence of gravity;
- economic processes such as stock markets that react to external influences.

One could build a so-called white-box model based on first principles, process but in many cases such models will be overly complex and possibly even impossible to obtain in reasonable time due to the complex nature of many systems and processes. A much more common approach is therefore to start from measurements of the behaviour of the system and the external influences (inputs to the system) and try to determine a mathematical relation between them without going into the details of what is actually happening inside the system. This approach is called System Identification. Two types of models are common in the field of system identification:

- **Grey box model:** Although the peculiarities of what is going on inside the system are not entirely known, a certain model based on both insight into the system and experimental data is constructed. This model does however still have a number of unknown free parameters which can be estimated using system identification. Grey box modeling is also known as semi-physical modeling.
- **Black box model:** No prior model is available. Most system identification algorithms are of this type.

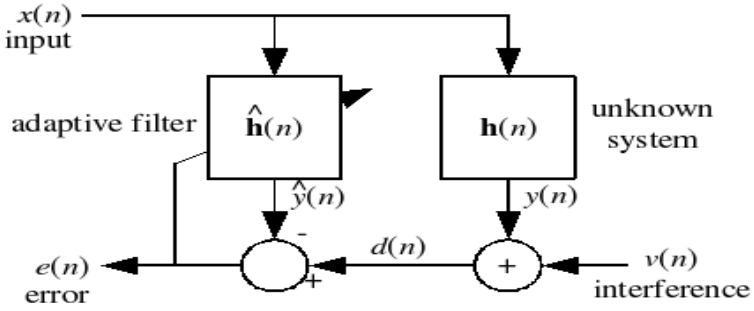


FIGURE: SYSTEM IDENTIFICATION USING ADAPTIVE FILTER

1.9) HAMMERSTEIN MODEL:

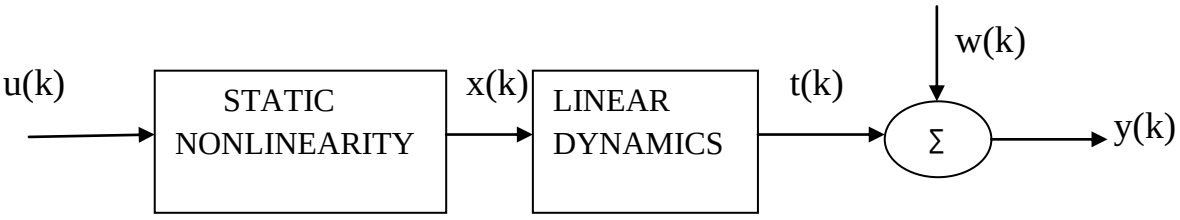
Hammerstein models are composed of a static nonlinear gain and a linear dynamics part. In some situations, they may be a good approximation for nonlinear plants. It has been approached following two major directions. The first one consists in supposing a polynomial (or polygonal) as the nonlinear element of the model. Then, the identification problem turns out to be a parametric one since it consists in estimating the parameters of the model linear and nonlinear parts. Parameter estimation is generally performed, based on adequate (known) structures of the model. The second direction, commonly referred-to nonparametric, considers that the nonlinear element of the model is not necessarily polynomial. It may be any continuous function. However, even in this case the identification process involves a truncated series approximation either of the nonlinear element or of related functions. Due to these finite series approximations, the identification problem amounts, just as in the parametric approaches, to estimating a finite number of parameters. The nonparametric methods usually involve probabilistic tools in the estimation process of the unknown parameters. The convergence of the parameter estimates has been analyzed, using stochastic tools, both for parametric and nonparametric methods. It is shown that consistency can be achieved, with a parametric instrumental variable method, using as input a strictly persistently exciting sequence or a white noise. Specific random inputs have been used in nonparametric methods to ensure consistency and other properties.

It appears that both parametric and nonparametric approaches involve, explicitly or implicitly, orthogonal function series approximations of the nonlinear element. This is a normal consequence of the fact that the plant nonlinear element is characterized by a continuous function F (v), defined on some real interval (say [vmin, vmax]), while the plant input sequence (say {v(t)}) is a discrete-time sequence (i.e. t=0, 1, 2, …). Actually, a continuous real function F(.), which is defined by an *uncountable* number of values F(v) (vmin≤v≤vmax), cannot be captured, except for particular cases, by a *countable* set of values, namely {v(t); t=0, 1, …}.

A parametric identification scheme is designed to deal with the case where the static gain is any (non-identically null) nonlinear function F.The proposed scheme identifies perfectly the model of the plant dynamics and a set of N points (v_i,F(v_i)) (i=1, …, N) of the static gain characteristic F,where N and the v_i's are chosen arbitrarily.

The points (v_i,F(v_i)) uniquely determine an Nth-degree polynomial P(v) that coincides with F(v) on the v_i's, then identifying the points (v_i, F(v_i)) amounts to identifying P(v). Furthermore, letting the plant input be chosen in the set {v_i, i=1… N}, allows substitution of P(v) to F(v) in the plant model; so doing, the initial identification problem is converted to one where the nonlinear element is polynomial. The mentioned substitution leads to a plant representation that is linear in the unknown parameters. It is worth noting, that the involved parameters are bilinear functions of the desired (unknown) parameters i.e. those of the plant dynamics, on one hand, and those of the static gain, on the other hand.

Finally, a persistently exciting input sequence is designed and shown to guarantee the convergence of the estimates to their true values. The proposed exciting input is an impulse type sequence.



The Hammerstein model structure

The Hammerstein systems are proved to be good descriptions of nonlinear dynamic systems in which the nonlinear static subsystems and linear dynamic subsystems are separated in different order. When the nonlinear element precedes the linear block, it is called the Hammerstein model as shown in figure above.

The Hammerstein model is represented by the following equations:

$$A(z^{-1})y(k) = B(z^{-1})x(k-1) + \left(1 \div C(z^{-1})\right)w(k)$$

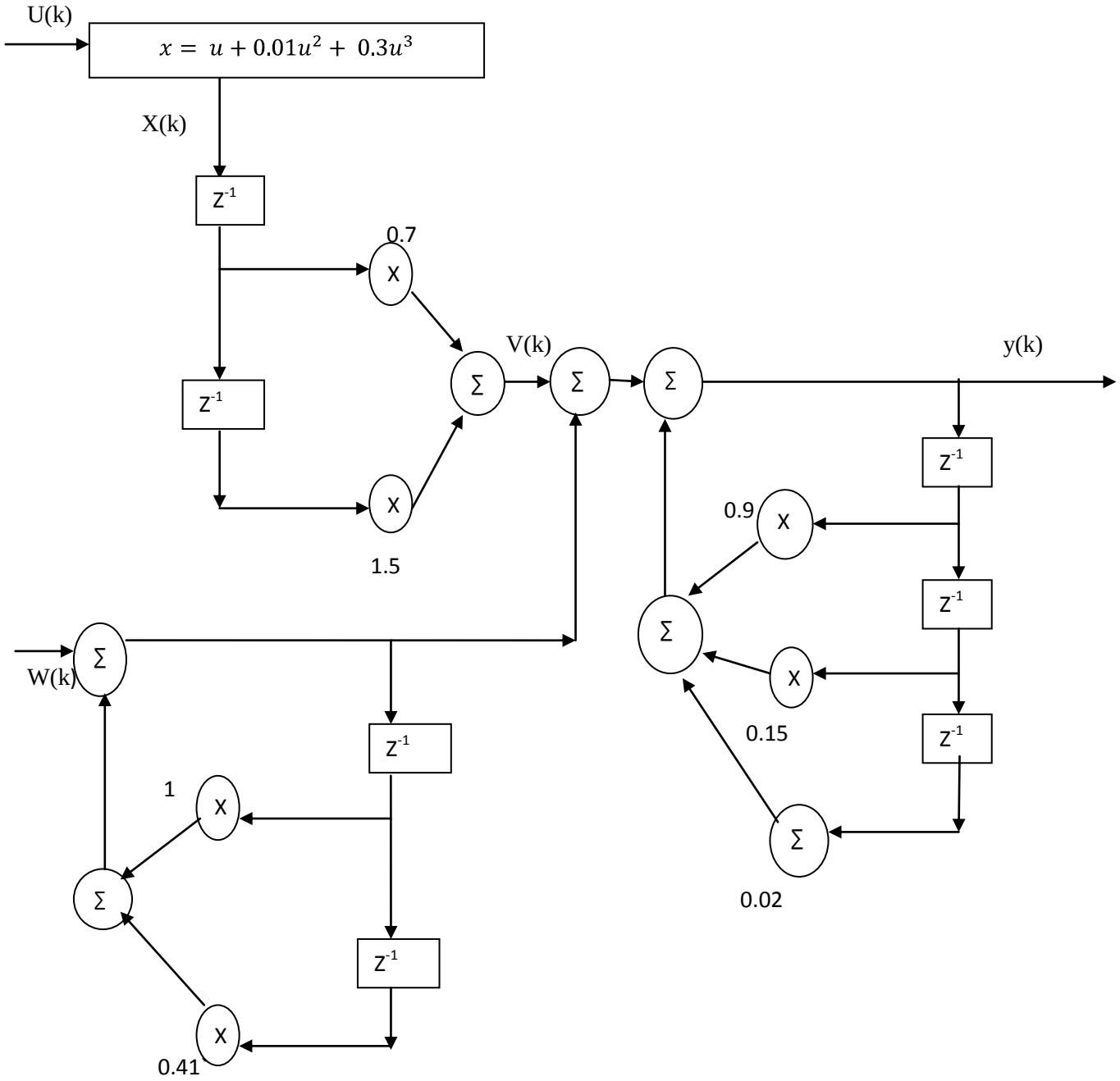
$$x(k) = f\left(u(k)\right)$$

$$A(z^{-1}) = 1 + a_1 z^{-1} + a_2 z^{-2} + \cdots + a_n z^{-n}$$

$$B(z^{-1}) = b_0 + b_1 z^{-1} + b_2 z^{-2} + \cdots + b_r z^{-r}$$

$$C(z^{-1}) = 1 + c_1 z^{-1} + c_2 z^{-2} + \cdots + c_m z^{-m}$$

HAMMERSTEIN MODEL



CHAPTER 2

AIM OF THE PROJECT

Our objective is therefore to study and analyse the various forms of Genetic algorithms and their application to the problems of Function Optimisation and System Identification. Since there are other methods traditionally adopted to obtain the optimum value of a function (which are usually derivative based), the project aims at establishing the superiority of Genetic Algorithms in optimizing complex, multivariable and multimodal functions.

1. The Genetic Algorithms need to be implemented to simple unimodal function optimization like sine x.

2. Then the process is to be extended to complex multimodal functions like schwefel's function.

3. The different forms of GA are to be comparatively studied analyzing their benefits in detail.

4. Then the Algorithm has to be extended to the System Identification problem and compared with the incremental LMS algorithm.

CHAPTER 3

IMPLEMENTATION AND SIMULATION:

3.1) FUNCTION OPTIMISATION USING REA L CODED GENETIC ALGORITHM:

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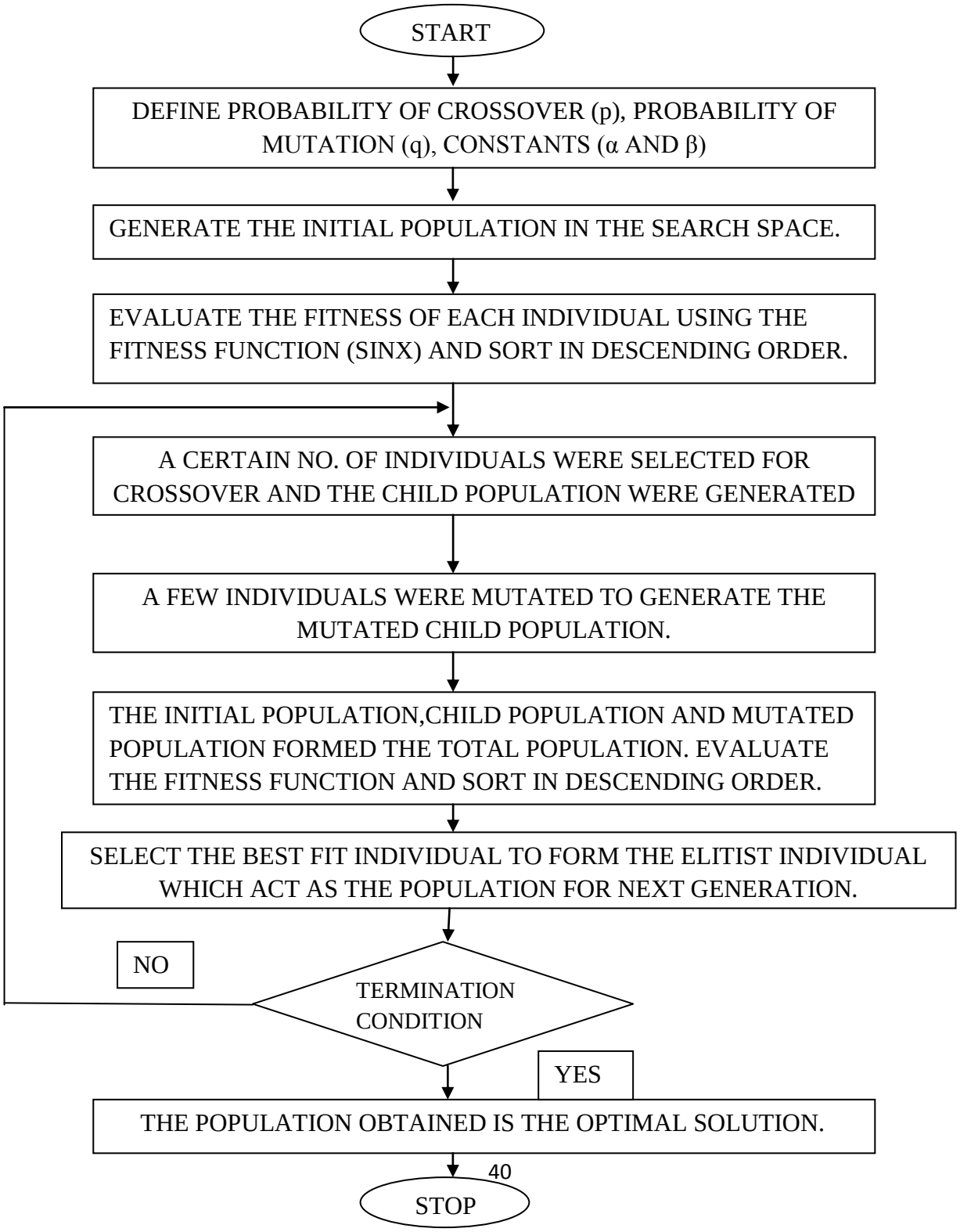


Algorithm for Function Optimisation using Real Coded GA:

STEP1: The parameters like Probability of Crossover (p), Probability of Mutation (q) are defined. The constants α AND β are also defined.

STEP 2: A set of possible solutions called the "initial Population" is initialized such that the values range uniformly throughout the search space. The size of the population is assumed to be "n"

STEP3: The Fitness Value was calculated for each of the individuals and the population is sorted in the decreasing order of the fitness. The fitness function used here is "sine" function.

STEP4: Using the "Roulette Wheel" method of selection, few individuals are selected to undergo crossover.

STEP5: The crossover between two individuals produced two child chromosomes. The child population is given by the formula

$$g_q^j(k+1) = g_q^j(k) + \alpha\, v_{qr}^j \omega_p \epsilon_q^j$$

$$g_r^j(k+1) = g_r^j(k) + \alpha\, v_{rq}^j \omega_p \epsilon_r^j$$

Where $g_q^j(k)$, $g_q^j(k)$ are the qth and rth individuals of the parent population set.

v_{qr}^j is the crossing vector. Given by the formula:

$$v_{rq} = g_r(k) - g_q(k)$$

ϵ is a normally distributed random number that determines the amount of gene crossing.

ω is the gene selection vector and the crossover takes place when the value is 1

α (0<α<=1) is the crossover range that defines the evolutionary step size and is equivalent to the step size in he LMS algorithm.

STEP6: Then using the probability of mutation a few individuals are mutated. The child produced by mutation is given by

$$g_q^j(k+1)' = g_q^j(k+1) + \beta\Phi$$

β is the mutation range or step size.

Φ is the random value which decides the amount of mutation in the individual.

STEP7: At the end of performing crossover and mutation we obtain the crossovered and the mutated child individuals. These along with the Parent population form super set for the next generation population.

STEP8: The fitness value evaluation and sorting of the individuals is followed by the selection of "n" best fit values as the next generation population.

STEP9: This process is repeated over and over again till the termination condition was reached. The termination condition applied here is the fixed number of iterations.

STEP10: The population obtained at the end of the specified number of iterations gives the optimal solution for the given problem.

SIMULATION:

Fitness function: sine x

Probability of crossover (p) =0.8

Probability of mutation (q) = 0.2

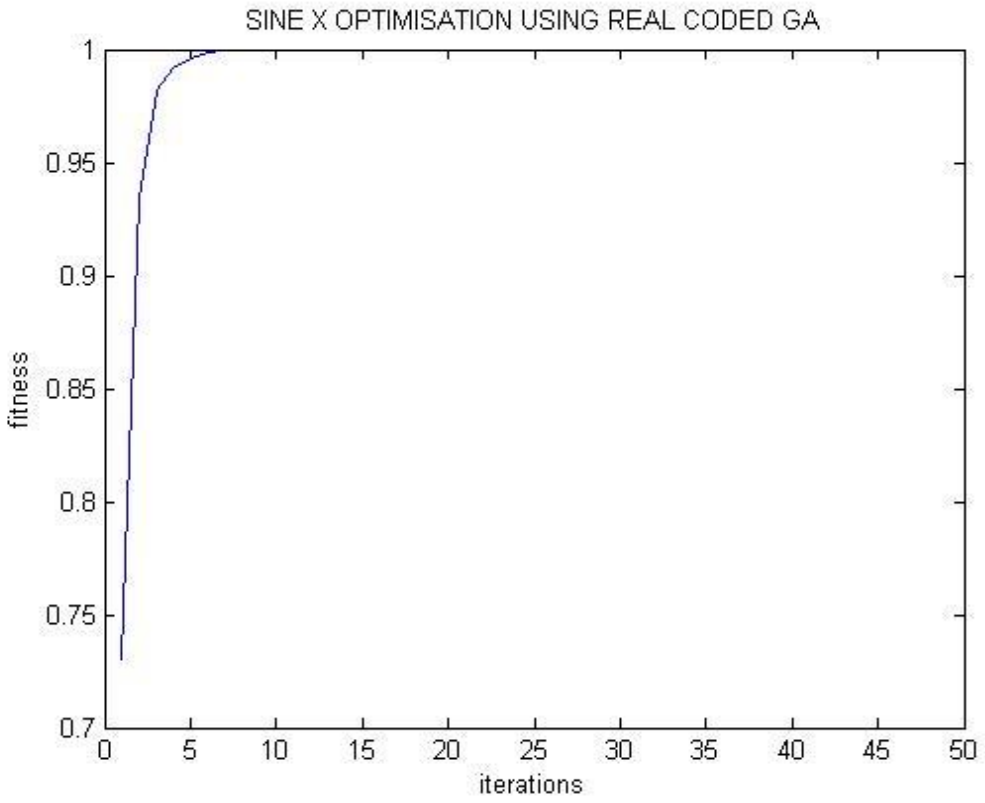
Alpha = 0.2

Beta = 0.2

Initial population size = 20

No of iterations = 50

SIMULATION RESULTS:



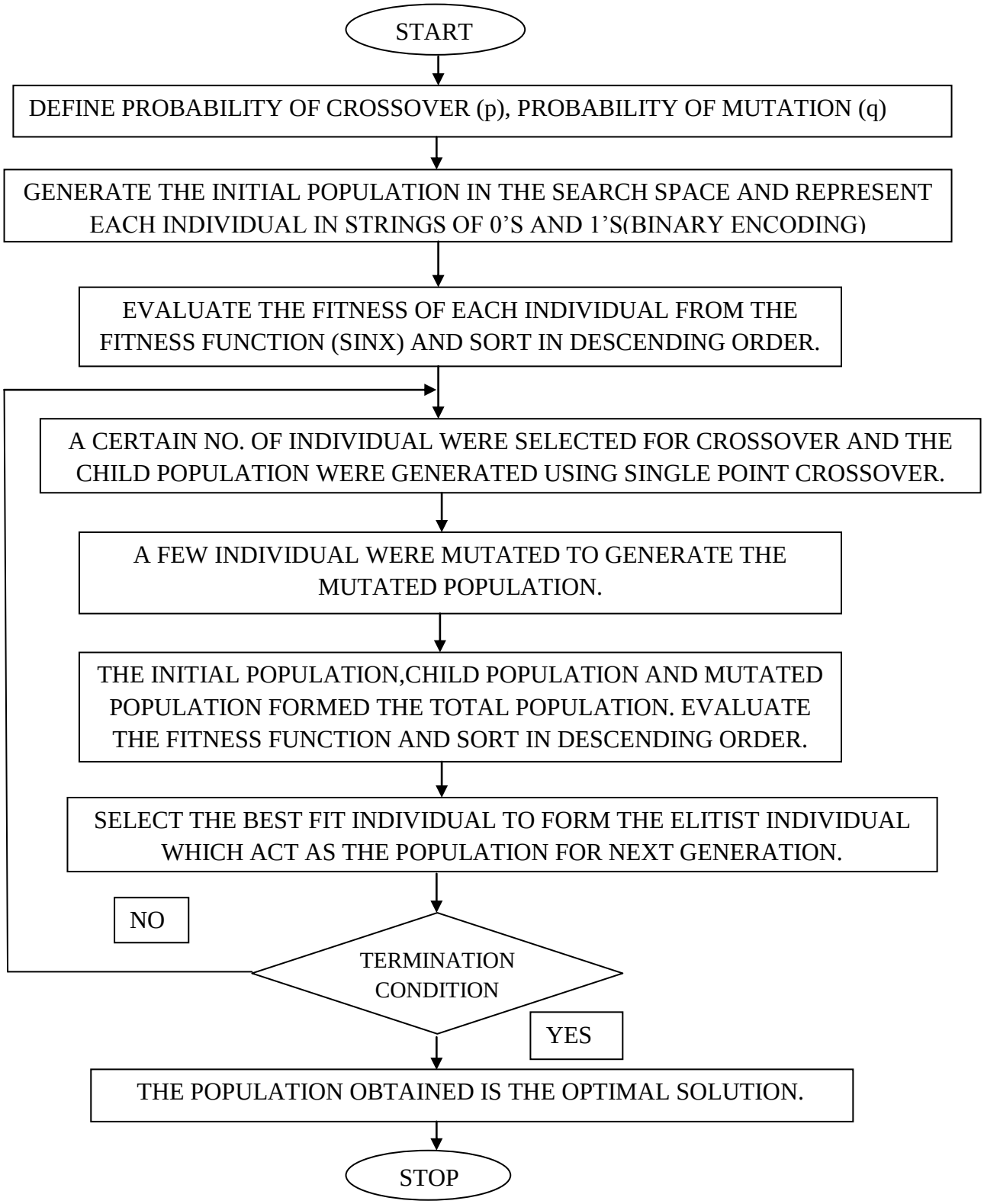
PLOT OF FITNESS VERSUS ITERATIONS IN SINE X OPTIMISATION USING REAL CODED GENETIC ALGORITHM

DISCUSSION:

The computation time for the above program was 0.06 seconds. It can be observed from the plot that the value of the fitness converges to he optimal value in about 8-10 iterations. This resembles a fairly good result in the optimization process.

3.2) FUNCTION OPTIMISATION USING SINGLE POINT CROSSOVER BINARY GENETIC ALGORITHM:

FLOWCHART



Algorithm for Function Optimization using Binary coded GA(Single Point Crossover Method):

STEP1: The parameters like Probability of Crossover(p), Probability of Mutation(q) are defined.

STEP 2: A set of possible solutions called the "initial Population" is initialized such that the values range uniformly throughout the search space. The size of the population was assumed to be "n". Each of the individual are called chromosomes and are in the form of string of 0's and 1's. Each bit in the chromosome is called a gene.

STEP3: The Fitness Value is calculated for each of the individuals and the population is sorted in the decreasing order of the fitness. The fitness function used here is the "sine" function.

STEP4: Using the "Roulette Wheel" method of selection, few individuals are selected to undergo crossover.

STEP5: The crossover between two individuals produced two child chromosomes. The point of crossover is generated randomly for each set of parents. And the genes after the crossover point are exchanged between the two parent chromosomes to give the child chromosomes which contain the attributes of both the parents.

STEP6: Then using the probability of mutation a few individuals are mutated. In the process of mutation a bit is randomly chosen from the parent and the bit value is reversed to obtain the mutated chromosome.

STEP7: At the end of performing crossover and mutation we obtain the crossovered and the mutated child individuals. These along with the Parent population forms the super set for the next generation population.

STEP8: The fitness value evaluation and sorting of the individuals is followed by the selection of "n" best fit values as the next generation population.

STEP9: This process is repeated over and over again till the termination condition is reached. The termination condition applied here is the fixed number of iterations.

STEP10: The population obtained at the end of the specified number of iterations gives the optimal solution for the given problem.

SIMULATION:

Fitness function: sine x

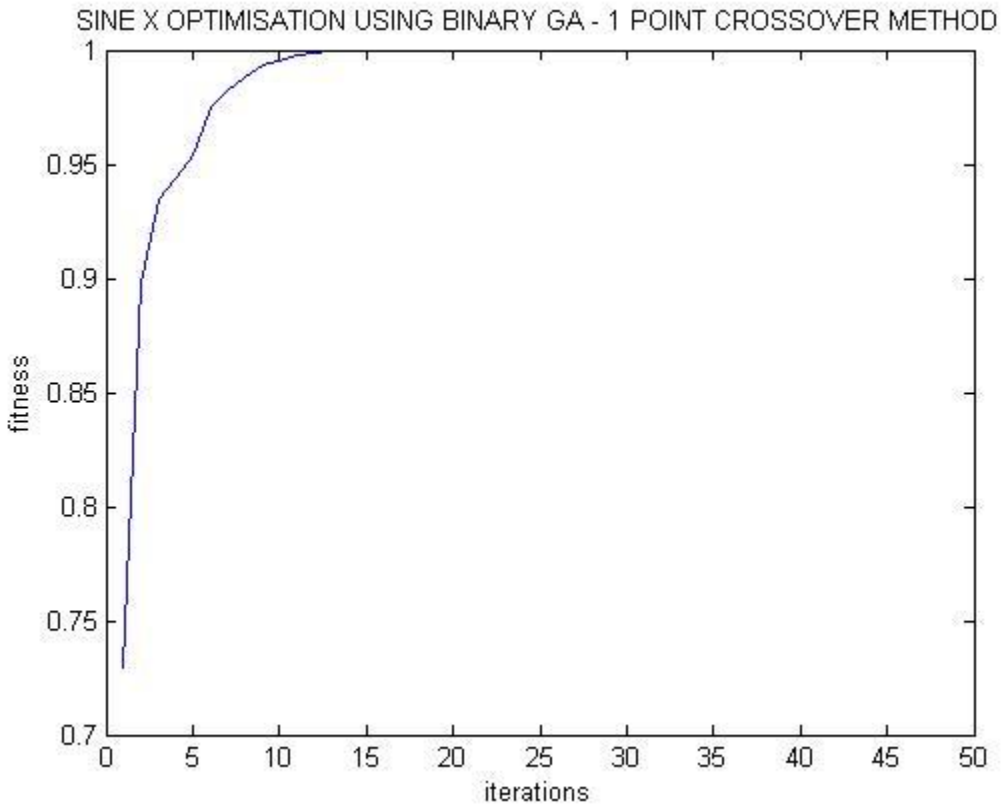
Probability of crossover(p)=0.8

Probability of mutation(q) = 0.2

Initial population size = 20

No of iterations = 50

SIMULATION RESULTS:



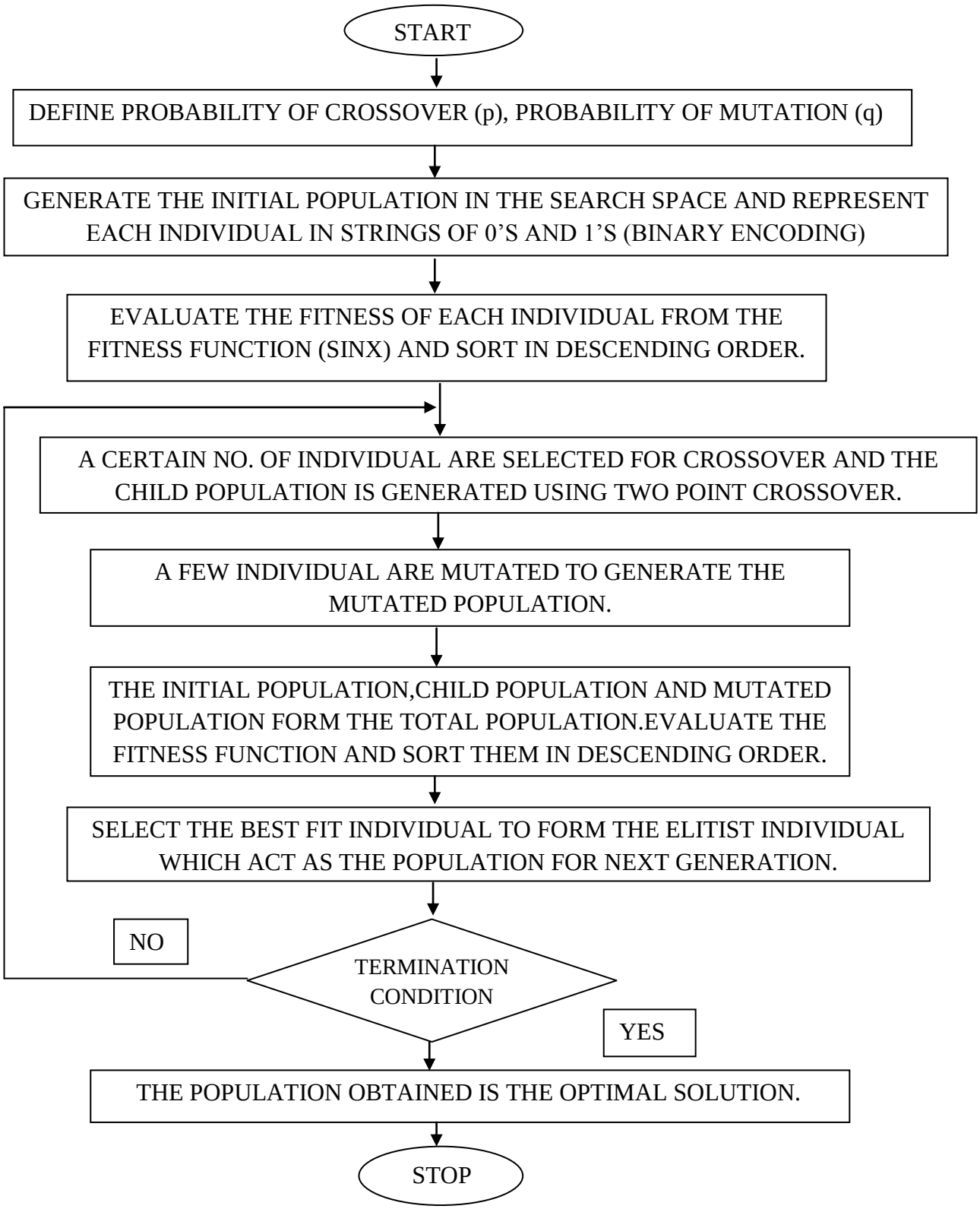
PLOT OF FITNESS VERSUS ITERATIONS IN SINE X OPTIMISATION USING BINARY CODED GENETIC ALGORITHM USING SINGLE POINT CROSSOVER TECHNIQUE

DISCUSSION:

The computation time for the above program was 0.26 seconds. The computation time is more from the real GA because of the need of converting data from real to binary form and vice versa. It can be observed from the plot that the value of the fitness converges to the optimal value in about 12-15 iterations. This resembles a fairly good result in the optimization process.

3.3) FUNCTION OPTIMISATION USING TWO POINT CROSSOVER BINARY GENETIC ALGORITHM:

FLOWCHART



Algorithm for Function Optimization using Binary coded GA (Two Point Crossover Method):

STEP1: The parameters like Probability of Crossover (p), Probability of Mutation(q) are defined.

STEP 2: A set of possible solutions called the "initial Population" is initialized such that the values range uniformly throughout the search space. The size of the population was assumed to be "n". Each of the individual are called chromosomes and are in the form of string of 0's and 1's. Each bit in the chromosome is called a gene.

STEP3: The Fitness Value is calculated for each of the individuals and the population is sorted in the decreasing order of the fitness. The fitness function used here is the "sine" function.

STEP4: Using the "Roulette Wheel" method of selection, few individuals are selected to undergo crossover.

STEP5: The crossover between two individuals produced two child chromosomes. The crossover is done by the exchange of genes between the two parents. The gene information to be exchanged is the bits in between the two crossover points. The points of crossover are generated randomly for each set of parents. And the genes between the crossover points are exchanged between the two parent chromosomes to give the child chromosomes which contain the attributes of both the parents.

STEP6: Then using the probability of mutation a few individuals are mutated. In the process of mutation a bit is randomly chosen from the parent and the bit value is reversed to obtain the mutated chromosome.

STEP7: At the end of performing crossover and mutation we obtain the crossovered and the mutated child individuals. These along with the Parent population forms the super set for the next generation population.

STEP8: The fitness value evaluation and sorting of the individuals is followed by the selection of "n" best fit values as the next generation population.

STEP9: This process is repeated over and over again till the termination condition is reached. The termination condition applied here is the fixed number of iterations.

STEP10: The population obtained at the end of the specified number of iterations gives the optimal solution for the given problem.

SIMULATION:

Fitness function: sine x

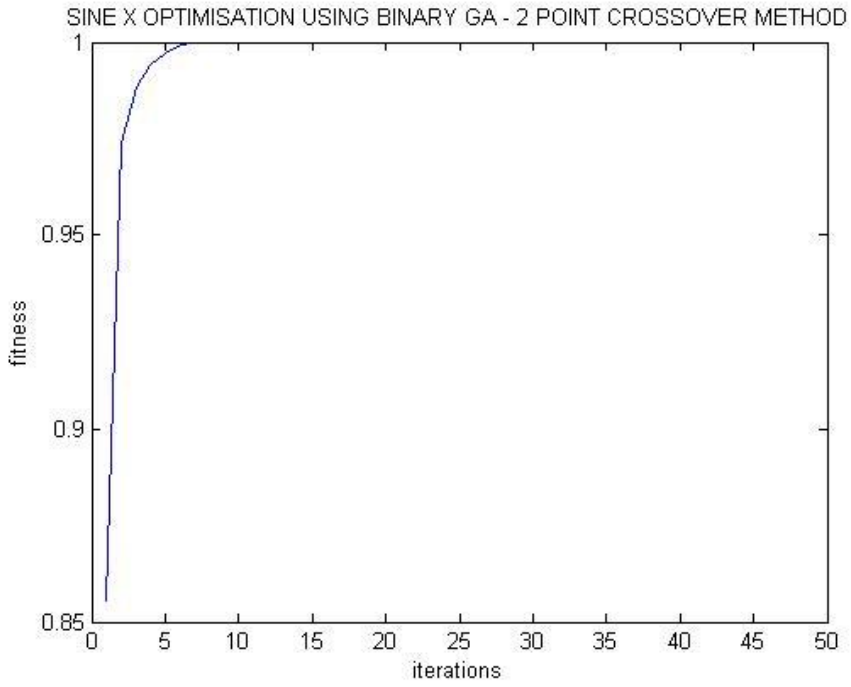
Probability of crossover(p)=0.8

Probability of mutation(q) = 0.2

Initial population size = 20

No of iterations = 50

SIMULATION RESULTS:



PLOT OF FITNESS VERSUS ITERATIONS IN SINE X OPTIMISATION USING BINARY CODED GENETIC ALGORITHM USING TWO POINT CROSSOVER TECHNIQUE

DISCUSSION:

The computation time for the above program was 0.28 seconds. The computation time is more from the real GA because of the need of converting data from real to binary form and vice versa. But is nearly same as that of the single point crossover binary GA because both involve equal number of computations.

It can be observed from the plot that the value of the fitness converges to the optimal value in about 8-10 iterations. This resembles a better result in the optimization process than the single point crossover technique where the convergence occurs after around 15 iterations.

3.4) FUNCTION OPTIMISATION USING SAWTOOTH GENETIC ALGORITHM:

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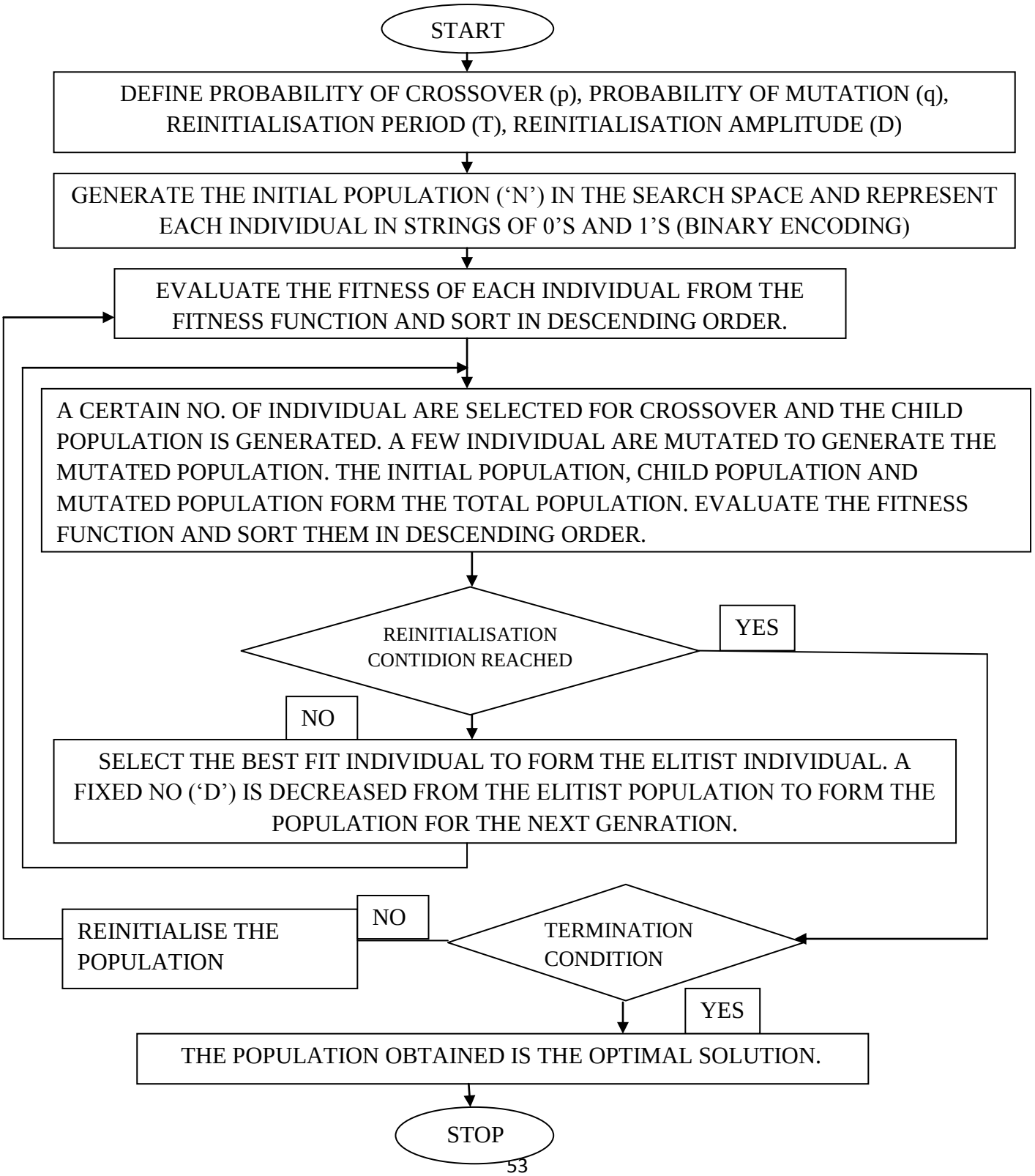


Algorithm for Function Optimisation using Sawtooth GA

STEP1: The parameters like Probability of Crossover(p), Probability of Mutation(q) are defined. The Period of Reinitialisation(T) and the Amplitude of Reinitialisation are defined.

STEP 2: A set of possible solutions called the "initial Population" is initialized such that the values range uniformly throughout the search space. The size of the population was assumed to be "n". Each of the individual are called chromosomes and are in the form of string of 0's and 1's. Each bit in the chromosome is called a gene.

STEP3: The Fitness Value is calculated for each of the individuals and the population is sorted in the decreasing order of the fitness.

STEP4: Using the "Roulette Wheel" method of selection, few individuals are selected to undergo crossover.

STEP5: The crossover between two individuals produced two child chromosomes. The point of crossover is generated randomly for each set of parents. And the genes after the crossover point are exchanged between the two parent chromosomes to give the child chromosomes which contain the attributes of both the parents.

STEP6: Then using the probability of mutation a few individuals are mutated. In the process of mutation a bit is randomly chosen from the parent and the bit value is reversed to obtain the mutated chromosome.

STEP7: At the end of performing crossover and mutation we obtain the crossovered and the mutated child individuals. These along with the Parent population forms the super set for the next generation population.

STEP8: The fitness value evaluation and sorting of the individuals is followed by the selection of "n-D" best fit values as the next generation population. So at each generation the population size is decreased by the amplitude.

STEP9: This process is repeated over and over again till the periodicity of reinitialisation is reached.

STEP10: A set of randomly generated individuals are reinitialized into the parent population set and the process is started all over again through selection, crossover and mutation.

STEP11: This stops when the termination condition is reached which here is the fixed number of iterations.

STEP12: The population obtained at the end of the specified number of iterations gives the optimal solution for the given problem.

SIMULATION 1(Unimodal Function):

Fitness function: sine x

Probability of crossover (p)=0.8

Probability of mutation (q) = 0.2

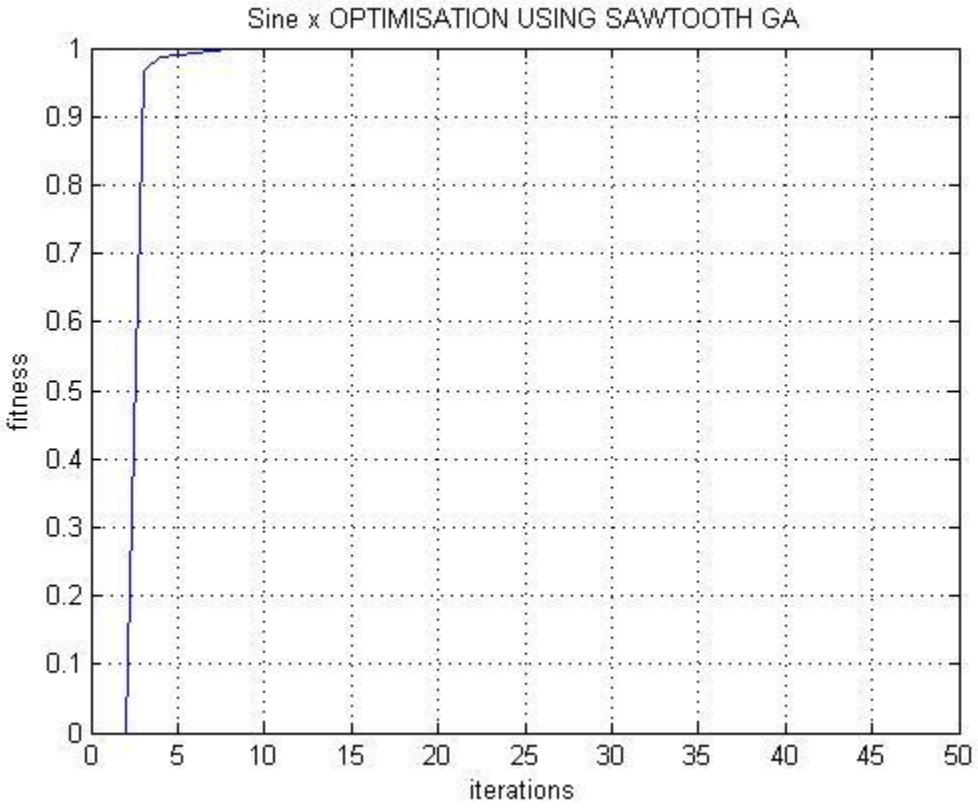
Initial population size = 25

No of iterations = 25

Period of Reinitialisation = 2

Amplitude of Reinitialisation = 10

SIMULATION RESULT:



PLOT OF FITNESS VERSUS ITERATIONS IN SINE X OPTIMISATION USING SAWTOOTH GENETIC ALGORITHM

SIMULATION 2(Multivariable Function)

Fitness function: Rosenbrock's Function

Probability of crossover(p)=0.8

Probability of mutation(q) = 0.2

Initial population size = 50

No of iterations = 75

Period of Reinitialisation =20

Amplitude of Reinitialisation = 40

ROSENBROCK FUNCTION:

In mathematical optimization, the **Rosenbrock function** is a non-convex function used as a test problem for optimization algorithms. It is also known as **Rosenbrock's valley** or **Rosenbrock's banana function**. This function is often used to test performance of optimization algorithms. The global minimum is inside a long, narrow, parabolic shaped flat valley. To find the valley is trivial, however to converge to the global minimum is difficult. It is defined by

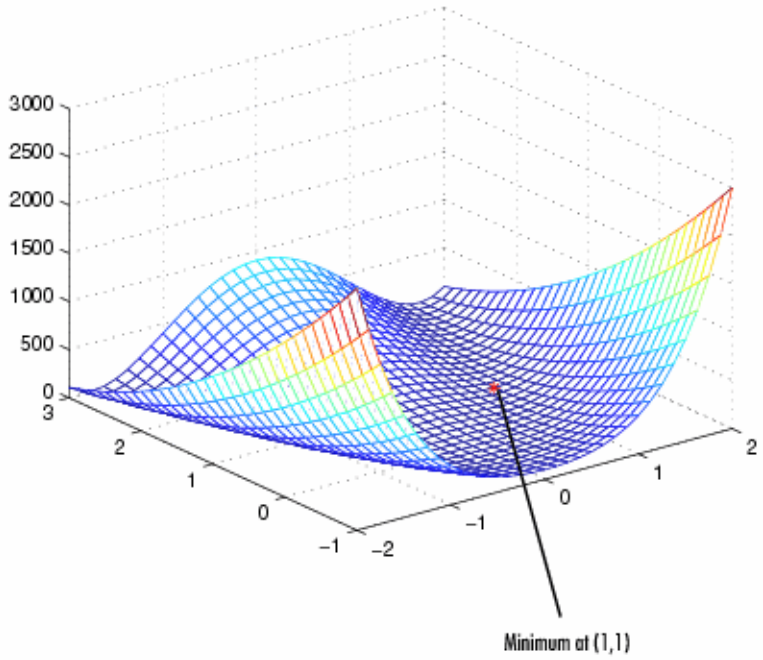
$$f(x,y) = (1-x)^2 + 100(y-x^2)^2.$$

It has a global minimum at (*x*,*y*) = (1,1) where f(x,y) = 0. A common multidimensional extension

$$f(x) = \sum_{i=1}^{N-1} \left[(1-x_i)^2 + 100(x_{i+1} - x_i^2)^2\right] \quad \forall x \in \mathbb{R}^N.$$

For $x_i \in [0,2]$ min f = 0 with x_i = 1, i=1,2,3…N

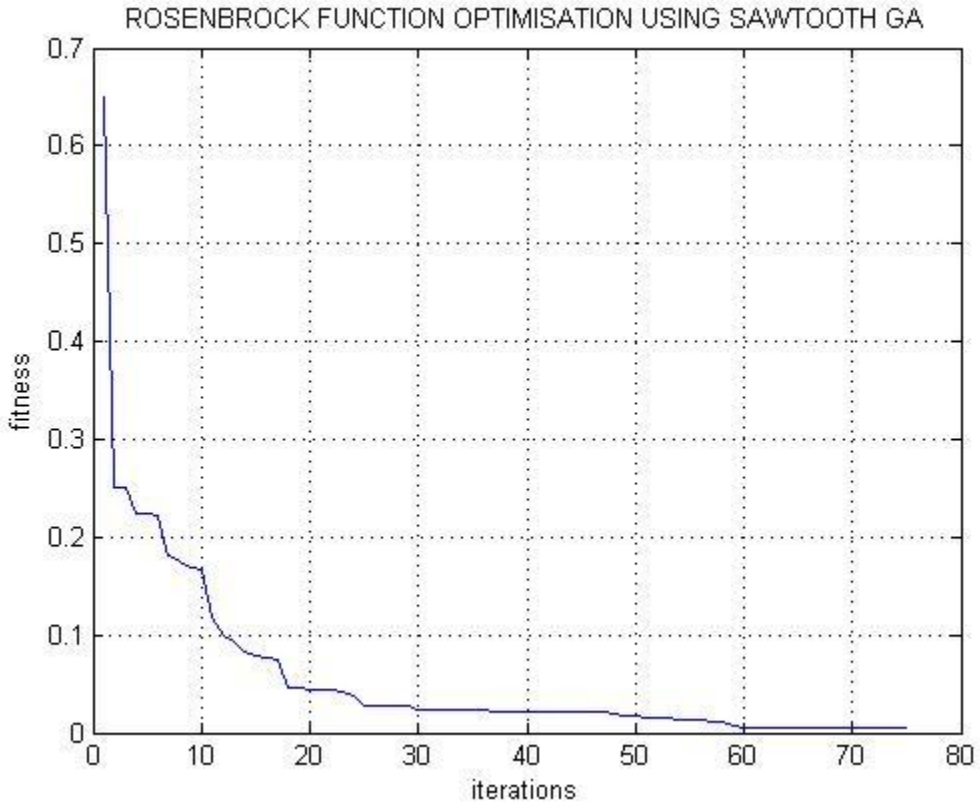
N = no of variables = 3



PLOT FOR ROSENBROCK FUNCTION

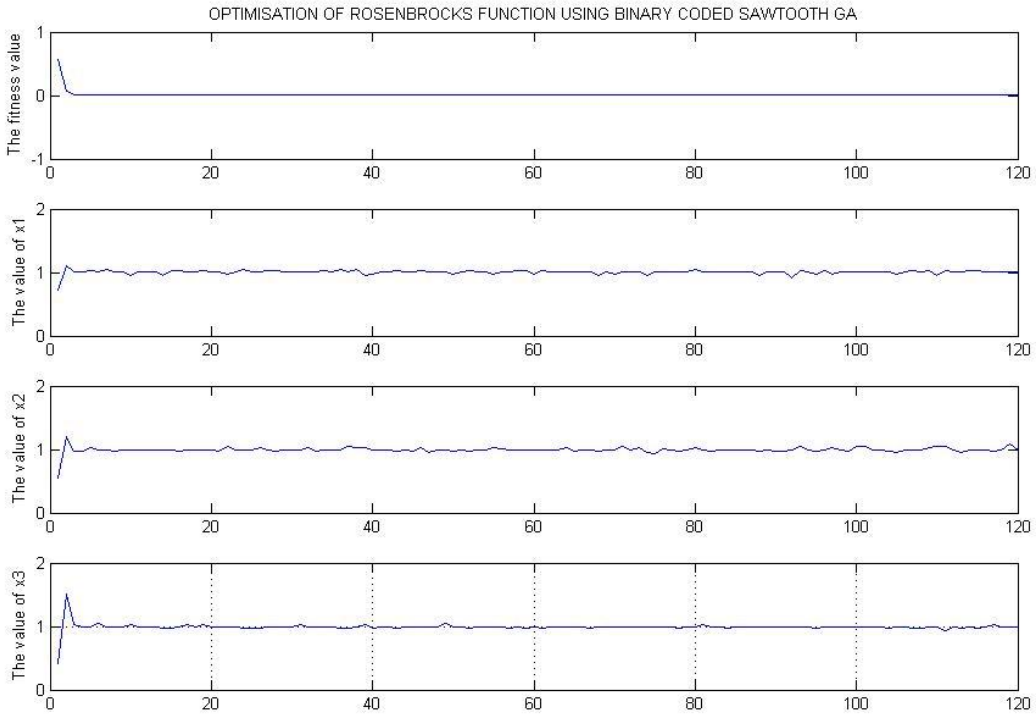
SIMULATION RESULT

i) USING REAL SAWTOOTH GA



PLOT OF FITNESS VERSUS ITERATIONS IN ROSENBROCK FUNCTION OPTIMISATION USING REAL SAWTOOTH GENETIC ALGORITHM

ii) USING BINARY SAWTOOTH GA



PLOT OF FITNESS VERSUS ITERATIONS IN ROSENBROCK FUNCTION OPTIMISATION USING BINARY SAWTOOTH GENETIC ALGORITHM

SIMULATION 3 (Multimodal Function)

Fitness function: Scwefel Function

Probability of crossover (p)=0.8

Probability of mutation (q) = 0.2

Initial population size = 100

No of iterations = 120

Period of Reinitialisation =16

Amplitude of Reinitialisation = 80

SCWEFEL FUNCTION:

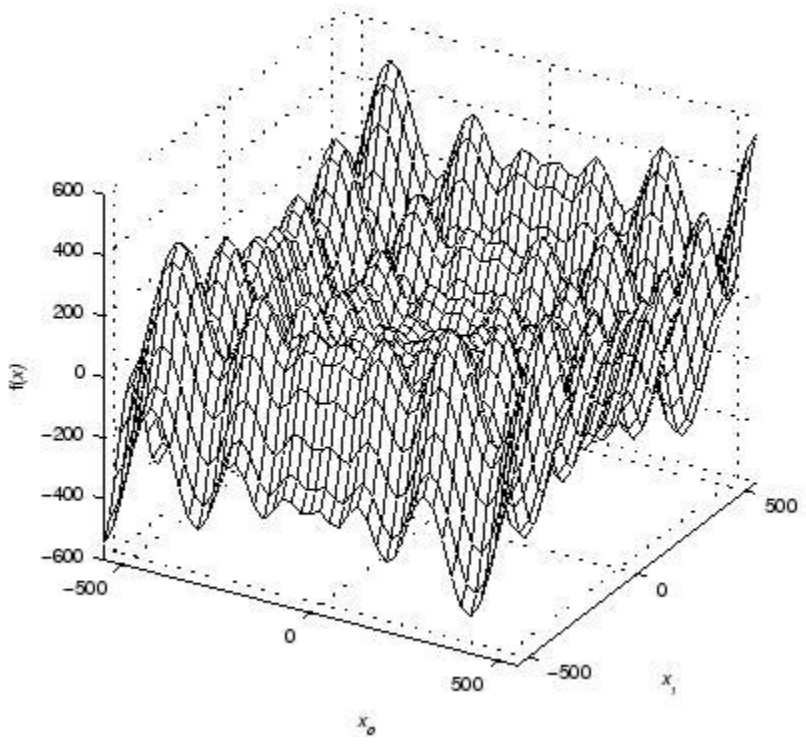
Schwefel's function is deceptive in that the global minimum is geometrically distant, over the parameter space, from the next best local minima. Therefore, the search algorithms are potentially prone to convergence in the wrong direction.

The function definition:

$$f_7(x) = \sum_{i=1}^{n} -x_i \cdot \sin\left(\sqrt{|x_i|}\right) \qquad -500 \le x_i \le 500$$

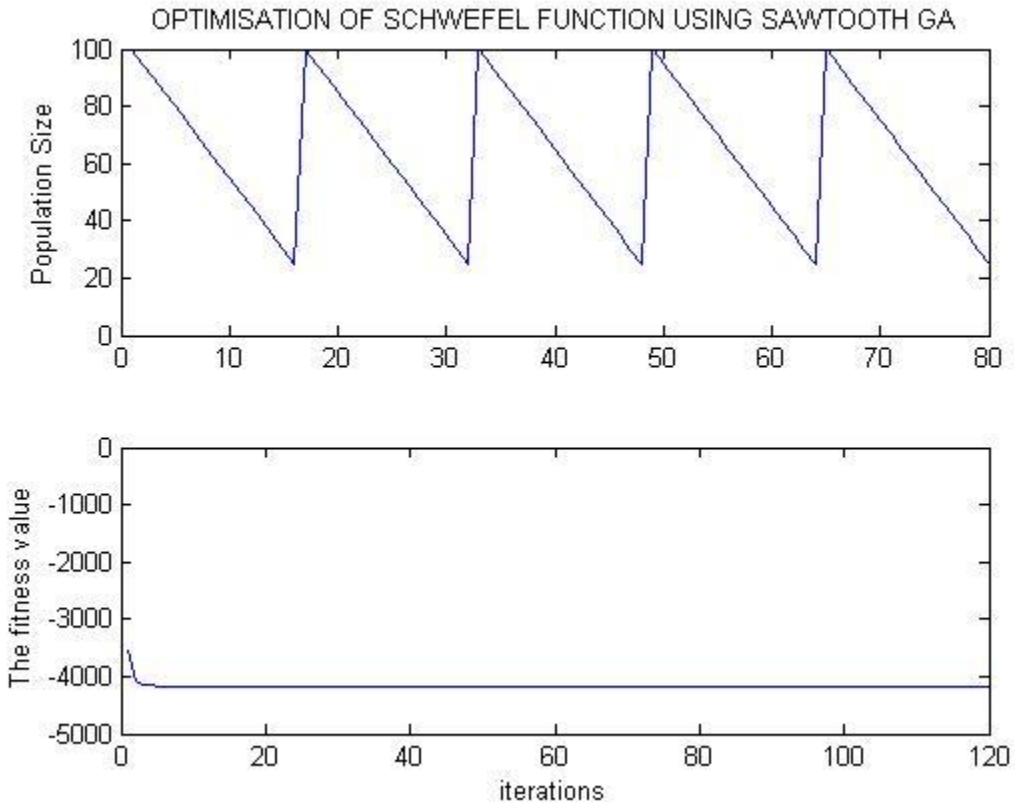
global minimum of f(x) is

f(x)= - 416.99N ; x_i=416.99 , i=1:N. Here N=10



PLOT FOR SCHWEFEL FUNCTION

SIMULATION RESULT:



PLOT OF FITNESS VERSUS ITERATIONS IN SCHWEFEL FUNCTION OPTIMISATION USING BINARY SAWTOOTH GENETIC ALGORITHM

DISCUSSION:

The computation times for the above programs are

Unimodal - 0.14 seconds.

Rosenbrock real coded- 1.36 seconds

Rosenbrock binary coded-19.7 seconds

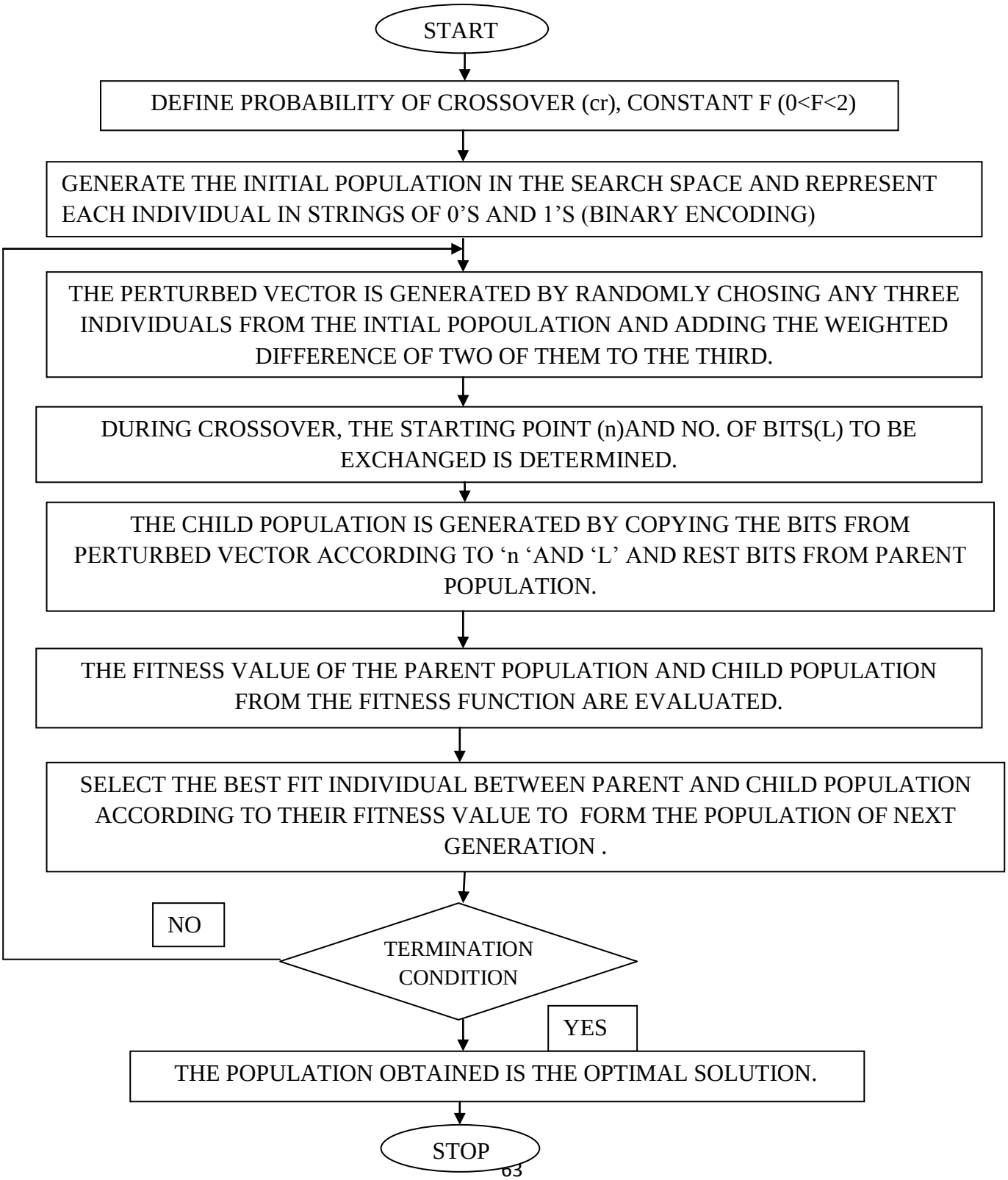
Schwefel - 55 seconds

The computation time is more from the real coded rosenbrock optimization than that of binary coded because of the need of converting data from real to binary form and vice versa.

It can be observed from the plot that the saw tooth GA gives a precise convergence of the function in both unimodal and multimodal functions.

3.5) FUNCTION OPTIMISATION USING DIFFERENTIAL EVOLUTION GENETIC ALGORITHM:

FLOWCHART



Algorithm for Function Optimization using Differential Evolution GA:

STEP1: The parameters like Probability of Crossover (Cr), weight of differential addition F are defined.

STEP 2: A set of possible solutions called the "initial Population" is initialized such that the values range uniformly throughout the search space. The size of the population was assumed to be "NP". Each of the individual are called chromosomes and are in the form of string of 0's and 1's. Each bit in the chromosome is called a gene.

STEP3: A perturbed vector is generated for each parent chromosome using the formula

$$v_i^{g+1} = x_{r1}^g + F * (x_{r2}^g - x_{r3}^g)$$

Where i, r1, r2, r3 are all integers ϵ [1, NP] and are mutually different from one another.

STEP4: Crossover operator is applied between the perturbed vector and its corresponding parent vector. The point of crossover is randomly selected between 0 – D-1, where D is the bit length of each chromosome. The number of bits to be exchanged is determined by the algorithm

```
L = 0;
do {
        L = L + l ;
    }while(rand()< CR) AND (L < D ) ) ;
```

STEP5: The crossover produces a child chromosome. Using the formula

$$\mathbf{U_{ji,g+1}} = \mathbf{V_{ji,g+1}}, \text{ for j} = <n>_D, <n+1>_D, <n+2>_D, \dots, <n+L-1>_D$$
$$= \mathbf{X_{ji,g}}, \text{for all other j} \epsilon [0, D-1]$$

Where v is the perturbed vector and u is the crossovered child.

< > implies the modulo function

STEP6: The fitness value of the Parent and the child is evaluated and the better fit of he two is selected as the next generation population.

STEP7: This process is repeated over and over again till the termination condition is reached. The termination condition applied here is the fixed number of iterations.

STEP8: The population obtained at the end of the specified number of iterations gives the optimal solution for the given problem.

SIMULATION:

Fitness function: sine x, x^2 and sphere function

Probability of crossover(Cr)=0.8

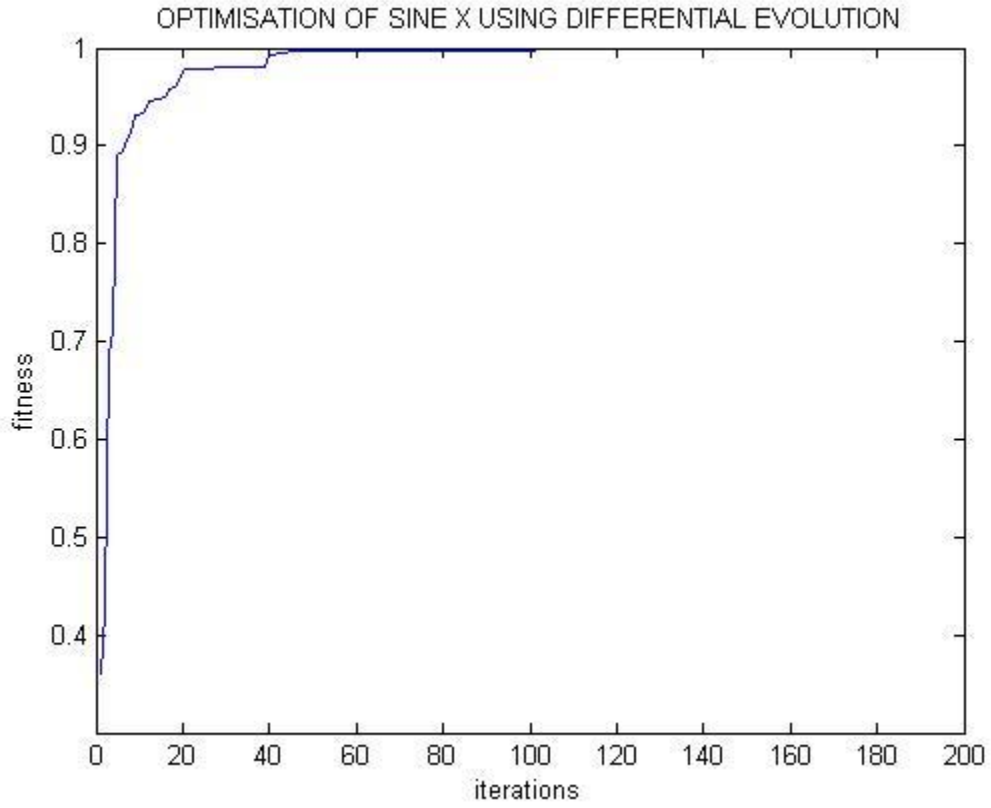
Initial population size = 20

SPHERE FUNCTION is given by

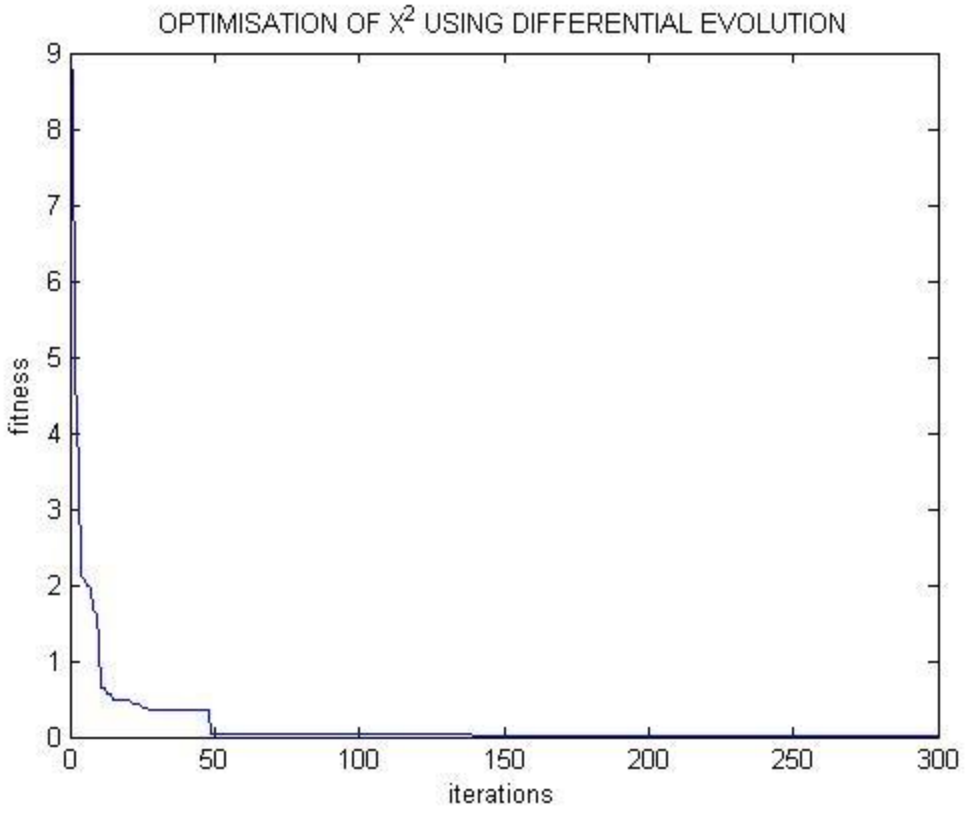
$$f(x) = \sum^{N} x_i \ for\ N = 1,2,3, \ldots..$$

For x(-200,200) the min value of the function is 0 at the points x_i = 0

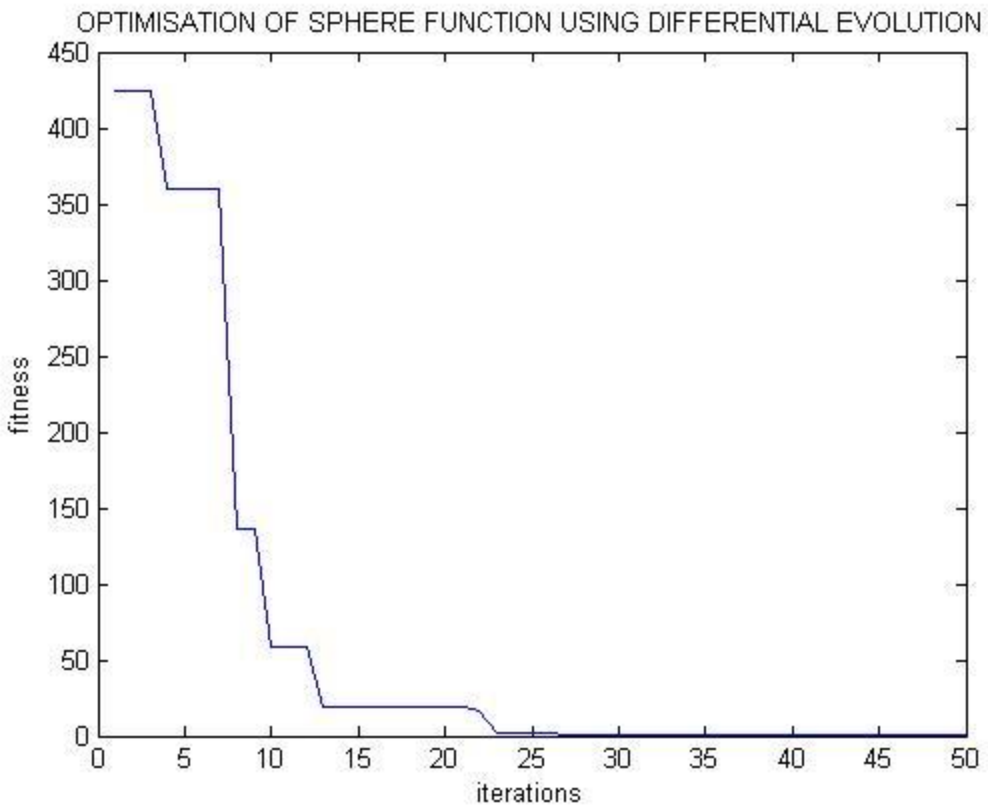
SIMULATION RESULTS:



PLOT OF FITNESS VERSUS ITERATIONS IN SINE X OPTIMISATION USING DIFFERENTIAL EVOLUTION GENETIC ALGORITHM



PLOT OF FITNESS VERSUS ITERATIONS IN X^2 OPTIMISATION USING DIFFERENTIAL EVOLUTION GENETIC ALGORITHM



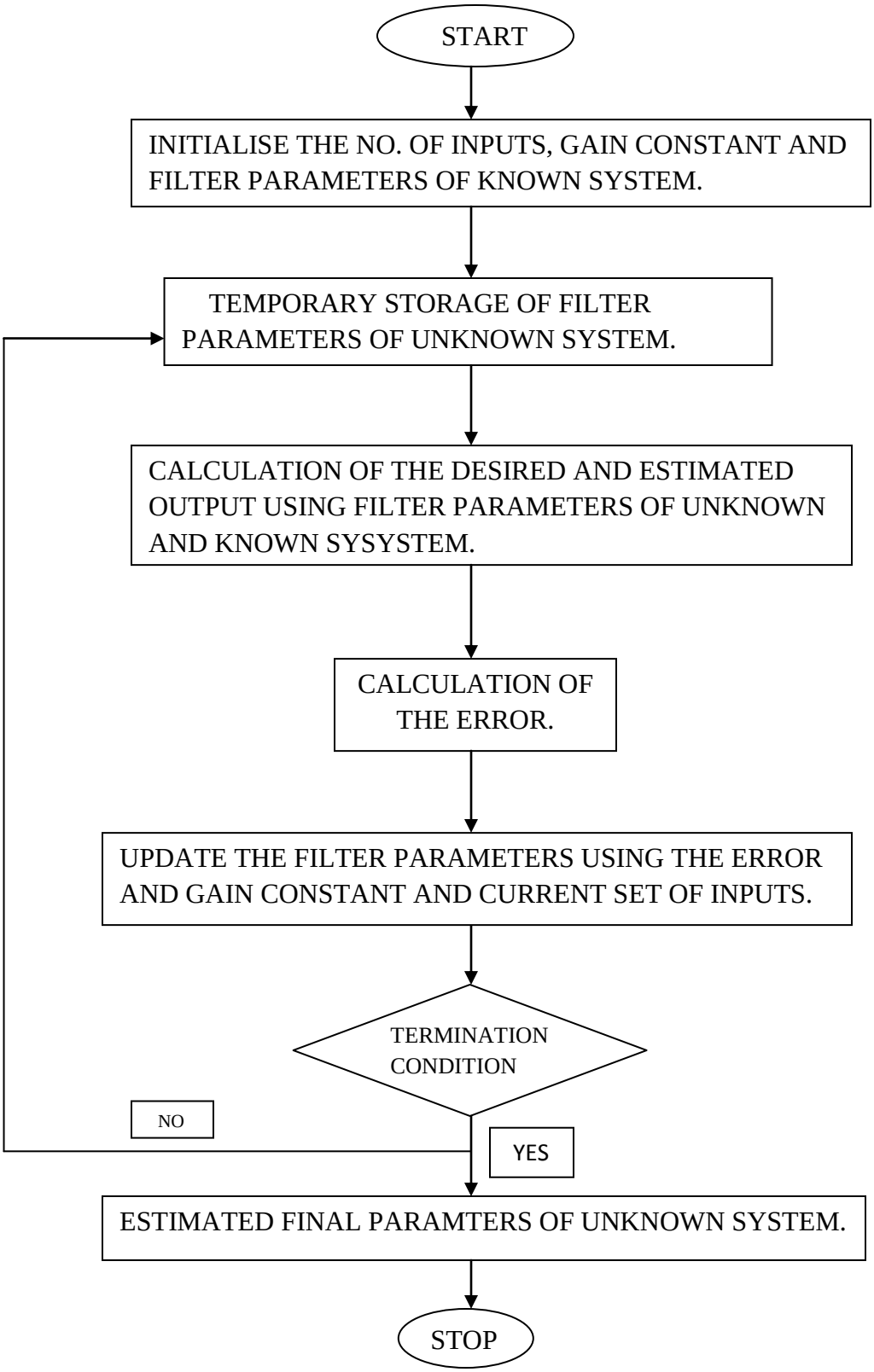
PLOT OF FITNESS VERSUS ITERATIONS IN SPHERE FUNCTION OPTIMISATION USING DIFFERENTIAL EVOLUTION GENETIC ALGORITHM

DISCUSSION:

The computation of the 1000 iterations in sin x optimization takes 7.29 seconds. It can be observed from the plots that the value of the fitness converges to the optimal value in both single variable and multi variable problems. But in case of a multi variable function the convergence takes a little longer which is due to the increase in the no of variables to be optimized.

3.6) SYSTEM IDENTIFICATION USING LMS:

FLOWCHART:



Algorithm for System Identification using LMS:

STEP 1: A known system was initialized with filter parameters

hknown =[0.26 0.93 0.26].

STEP2: The input signal set **X** was generated for a given signal power with zero mean.

STEP3: The unknown system was initially taken to be zero **hunknown** = [0 0 0].

STEP4: The input was convolved with both the known and the unknown system to obtain their corresponding outputs. A Gaussian distributed noise was added to the estimated output to account for the disturbance in the system.

$$desired\ output = hknown * X^T + \text{Noise}$$

$$estimated\ output = hunknown * X^T$$

STEP5: The difference between the outputs from the two filters gave the error in the system.

$$\text{Error} = \text{desired output} - \text{estimated output}$$

STEP6: From the error obtained in the above step the unknown filter's parameters were updated using the update equation

$$hunknown_{k+1} = hunknown_k + 2\mu * error_k * X_k$$

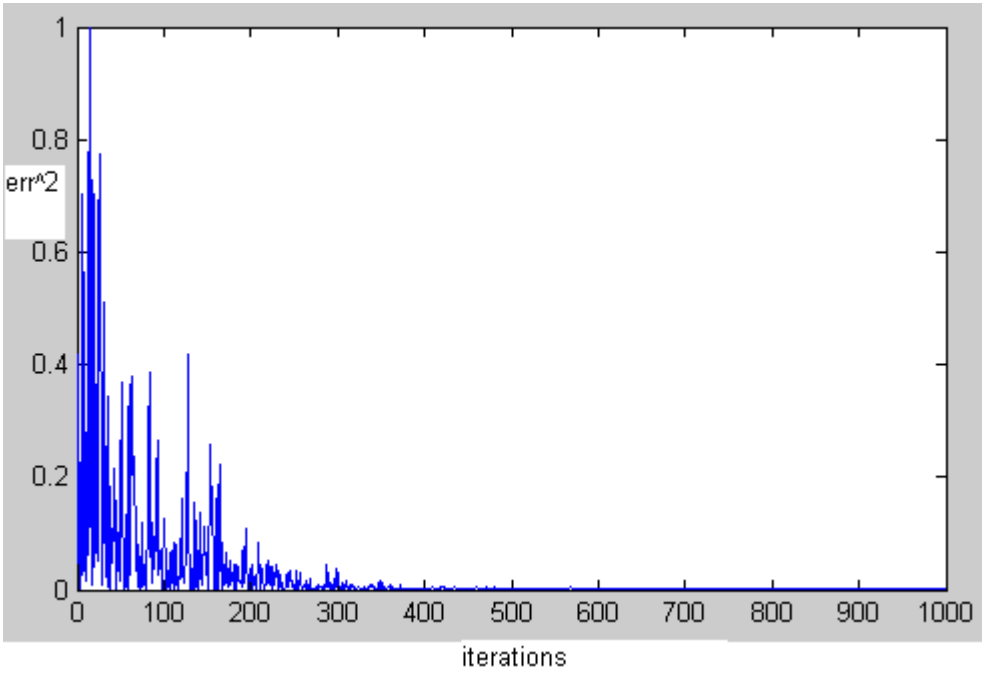
where μ is the gain constant.

STEP7: This procedure was repeated till the termination condition was reached. In the simulated programme the number of iterations served as the end condition.

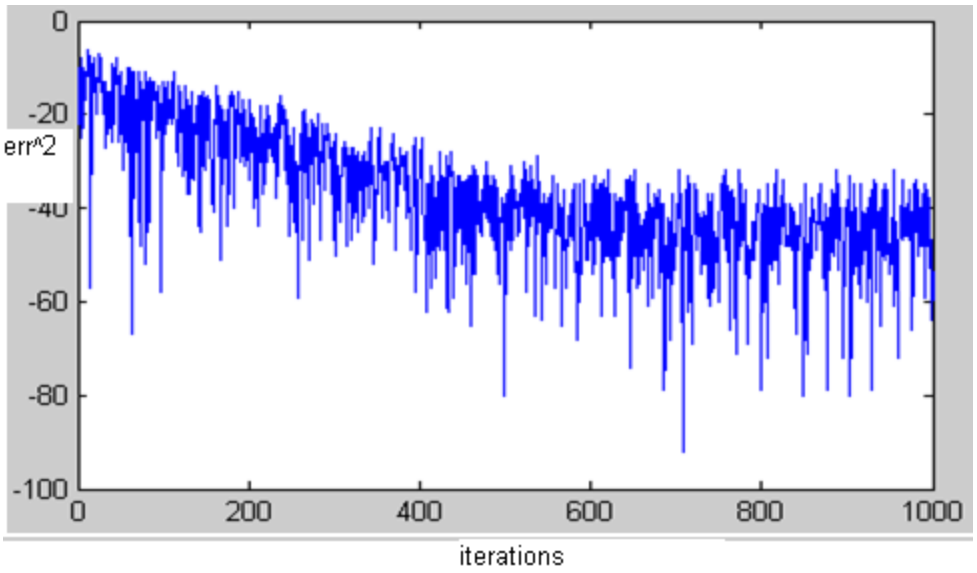
STEP8: The value of the filter obtained at the end of the specified iterations gives the final estimated system and has very close resemblance with the known system's characteristics.

STEP9: A graph was plotted between error square and the no of iterations to show the convergence. When error tends to zero the system is said to have converged with the known system. Hence the system is identified.

SIMULATION RESULTS:



PLOT OF ERROR SQUARE VERSUS NO OF ITERATIONS IN A SYSTEM IDENTIFICATION PROCESS IMPLEMENTING LMS ALGORITHM



SNR PLOT

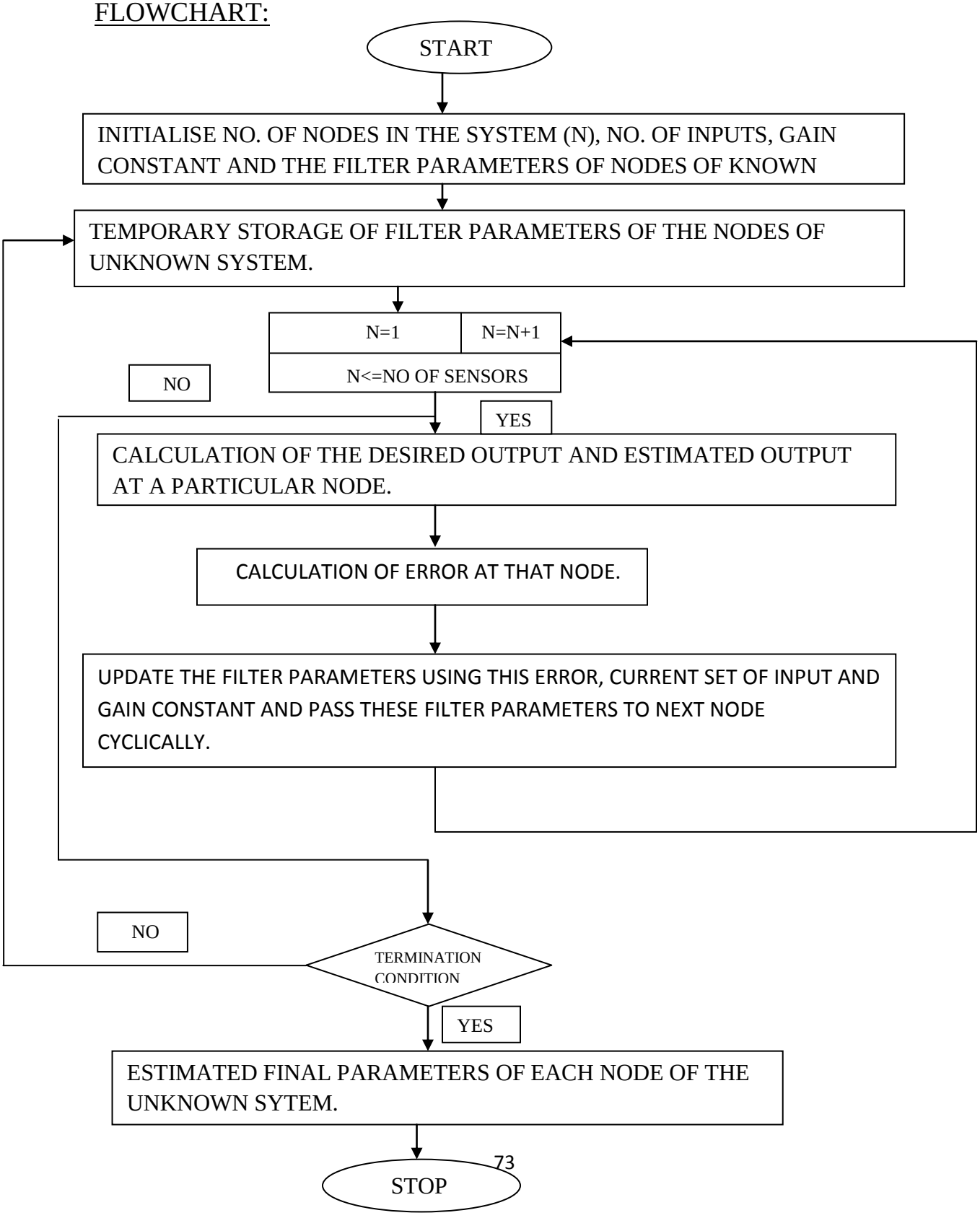
DISCUSSION:

The plot of error square shows the convergence of the filter parameters after 600 iterations as the error minimizes to zero.

The plot of error square in a logarithmic form roughly reflects the noise power which indicates the good performance of the Adaptive network in steady state. If the adaptive node is performing well then the estimated weights are a good estimate of the original weights, therefore the residual error should be close to the background noise.

3.7) SYSTEM IDENTIFICATION USING INCREMENTAL APPROACH (Random Input):

FLOWCHART:



COMPARATIVE ANALYSIS OF CENTRALISED AND INCREMENTAL APPROACH ALGORITHMS:

STEP 1: A known system of a few sensors was initialized with predefined filter parameters.

STEP 2: Input signal set **X** was generated for a given signal power with zero Mean.

STEP3: The parameters at the sensors were initially taken to be zero.
hunknown = [0 0 0] for each of the sensors.

STEP 4: The input was convolved with both the known and the unknown system at the first sensor to obtain their corresponding outputs. A Gaussian distributed noise was added to the estimated output to account for the disturbance in the system.

$$desired\ output = hknown * X^T + \text{Noise}$$

$$estimated\ output = hunknown * X^T$$

STEP 5: The difference between the outputs from the two filters gave the error in the system.

.

$$\text{Error} = \text{desired output} - \text{estimated output}$$

STEP 6: From the error obtained in the above step the unknown filter's parameters were updated using the update equation.

$$hunknown_{k+1} = hunknown_k + 2\mu * error_k * X_k$$

where **μ** is the gain constant.

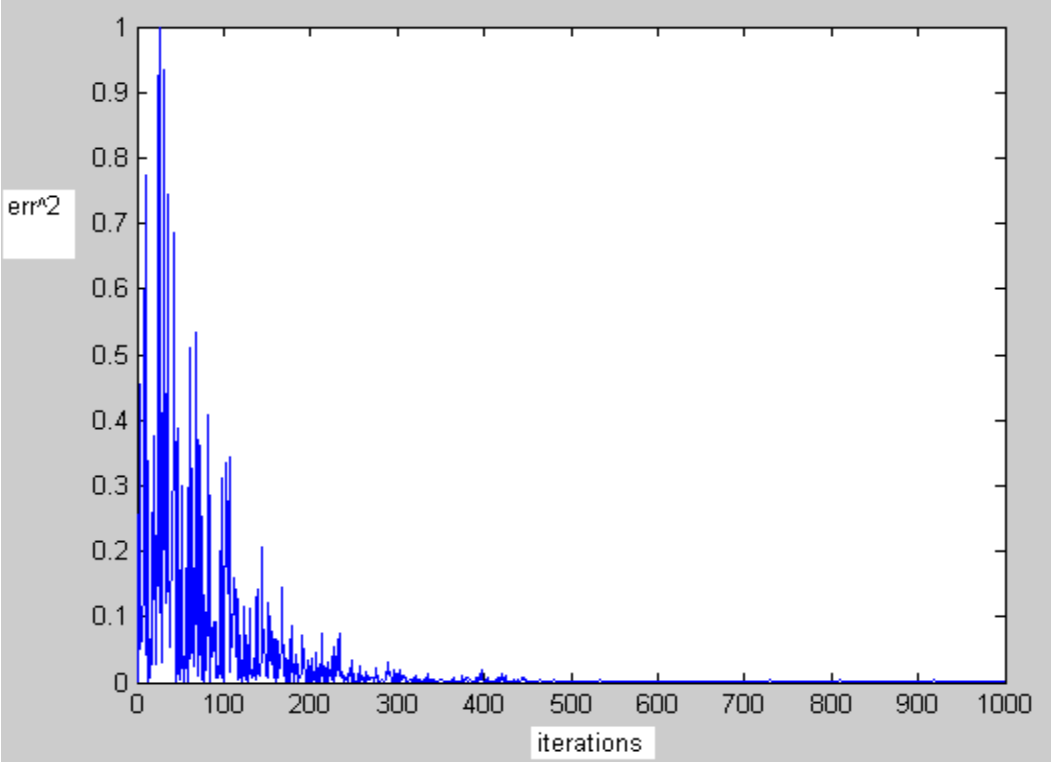
STEP 7: The updated parameters from the first sensor were passed as initial weights for the next sensor and the above processes were repeated.

STEP 8: Once we reached the last sensor the updated value of the filter parameter from the last sensor is passed onto the first sensor and the process was continued till we reached the termination condition.

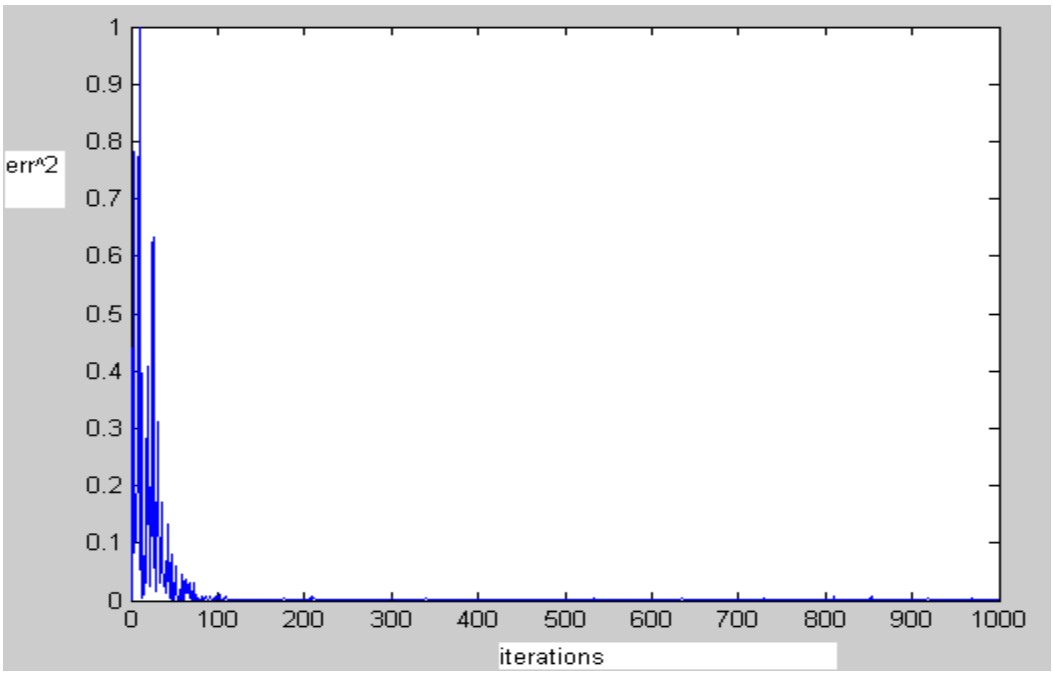
STEP 9: The convergence of the INCREMENTAL LMS technique was compared with that of a centralised LMS process where each sensor was treated as an independent system identification problem.

STEP 10: A graph of error square versus no of iterations was plotted for both the processes adopted and their convergence speed and efficiency were compared .

SIMULATION RESULTS:



PLOT OF ERROR SQUARE vs NO OF ITERATIONS IN A CENTRALIZED APPROACH



PLOT OF ERROR SQUARE vs NO OF ITERATIONS IN INCREMENTAL APPROACH

DISCUSSION:

A Relative study of the two graphs clearly enforces the better efficiency of the incremental LMS technique over the Centralized technique.

(a) In the plot for Centralized LMS the convergence occurs after over 600 iterations.

(b) In the plot for Incremental LMS the convergence is bit faster and is attained in about 200 iterations.

3.8) INCREMENTAL STRATEGIES OVER DISTRIBUTED SYSTEM:

INCREMENTAL ADAPTIVE STRATEGIES:

It is a reflection of a result in optimization theory that the incremental strategy can outperform the steepest-descent technique. Intuitively, this is because the incremental solution incorporates local information on-the-fly into the operation of the algorithm, i.e., it exploits the spatial diversity more fully. While the steepest-descent solution has fixed throughout all spatial updates, the incremental solution uses instead the successive updates.

The network has N=20 nodes with unknown vector $w^0 = col\{1,1,\dots\dots,1\}/\sqrt{M}$, M=10, and relying on independent Gaussian regressors. The background noise is white and Gaussian. The output data are related via

$$d_k(i) = u_{k,i}w^0 + v_k(i)$$

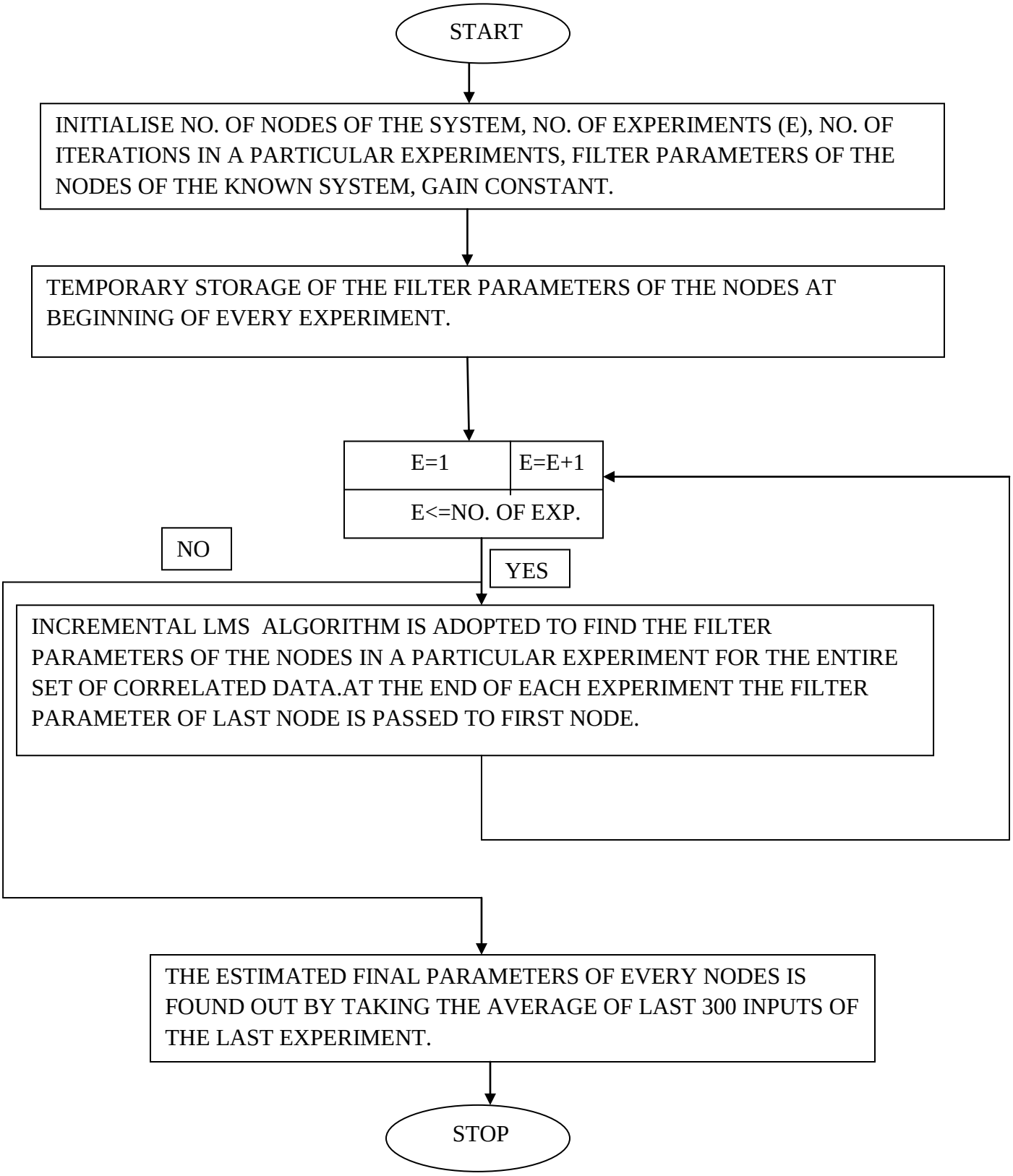
for each node. The curves are obtained by averaging over 300 iterations.

PERFORMANCE ANALYSIS:

Studying the performance of such an interconnected network of nodes is challenging (more so than studying the performance of a single LMS filter) for the following reasons:

1) Each node is influenced by local data with local statistics (spatial information);
2) Each node is influenced by its neighbours through the incremental mode of cooperation(Spatial interaction);
3) Each node is subject to local noise with variance (spatial noise profile).

FLOWCHART:


START
INITIALISE NO. OF NODES OF THE SYSTEM, NO. OF EXPERIMENTS (E), NO. OF ITERATIONS IN A PARTICULAR EXPERIMENTS, FILTER PARAMETERS OF THE NODES OF THE KNOWN SYSTEM, GAIN CONSTANT.
TEMPORARY STORAGE OF THE FILTER PARAMETERS OF THE NODES AT BEGINNING OF EVERY EXPERIMENT.
E=1
E=E+1
E<=NO. OF EXP.
NO
YES
INCREMENTAL LMS ALGORITHM IS ADOPTED TO FIND THE FILTER PARAMETERS OF THE NODES IN A PARTICULAR EXPERIMENT FOR THE ENTIRE SET OF CORRELATED DATA.AT THE END OF EACH EXPERIMENT THE FILTER PARAMETER OF LAST NODE IS PASSED TO FIRST NODE.
THE ESTIMATED FINAL PARAMETERS OF EVERY NODES IS FOUND OUT BY TAKING THE AVERAGE OF LAST 300 INPUTS OF THE LAST EXPERIMENT.
STOP

Algorithm:

STEP 1: The Network has 20 sensors pursuing the same unknown vector w^0

$$w^0 = col\{1,1,1 \ldots .,1\}/\sqrt{M}$$

With M = 10 that specifies the filter length.

STEP 2: Input signal set **X** was generated for each of the nodes from the given signal power profile. The signal generated is a set of **"Correlated Data".**

STEP3: The parameters at the sensors were initially taken to be zero. **hunknown** = [0 0 0] for each of the sensors.

STEP 4: The input was convolved with both the known and the unknown system at the first sensor to obtain their corresponding outputs.

A Gaussian distributed noise was added to the estimated output to account for the disturbance in the system. The noise was obtained from the given signal to noise ratio for each node.

$$\boldsymbol{desired\ output = hknown * X^T + Noise}$$

$$\boldsymbol{estimated\ output = hunknown * X^T}$$

STEP 5: The difference between the outputs from the two filters gave the error in the node.

.

$$\textbf{Error = desired output – estimated output}$$

STEP 6: From the error obtained in the above step the unknown filter's parameters were updated using the update equation

$$\boldsymbol{hunknown_{k+1} = hunknown_k + 2\mu * error_k * X_k}$$

where $\boldsymbol{\mu = 0.03}$ is the gain constant.

STEP 7: The updated parameters from the first sensor were passed as initial weights for the next sensor and the same above processes were repeated.

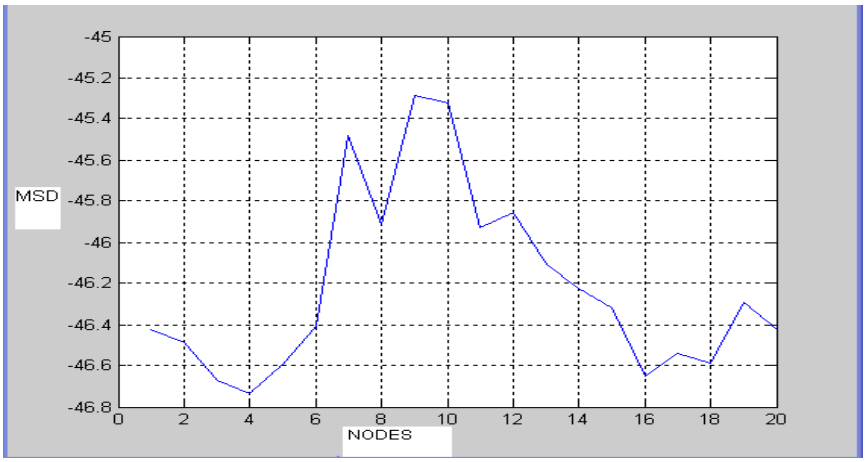
STEP 8: Once we reached the last sensor the updated value of the filter parameter from the last sensor was passed onto the first sensor. This completed one **iteration** of our operation.

STEP 9: At the end of the required no of iterations all the inputs have been evaluated once at their respective sensors. This completes one **Experiment**.

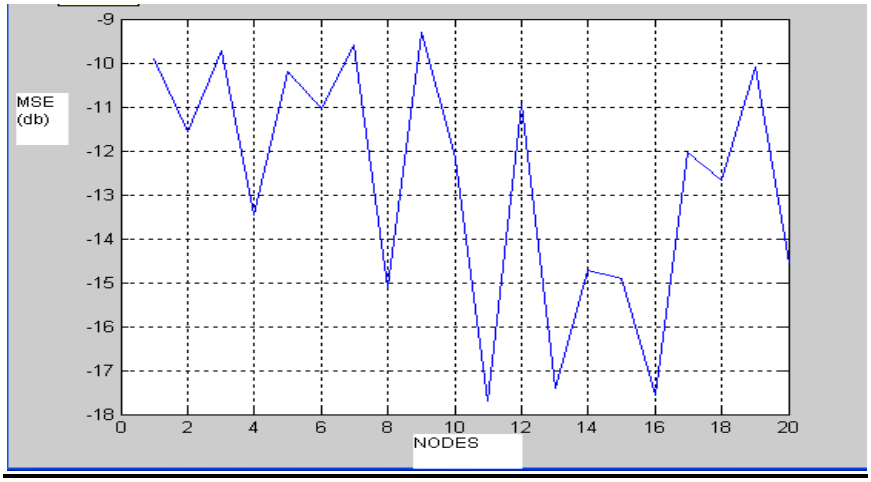
STEP10: At the end of all the experiments the average weights of the last 300 iterations was obtained.

STEP 11: A graph of MSE(Mean Square Error), EMSE(Excess Mean Square Error) and MSD(Mean Square Deviation) was plotted against each node.

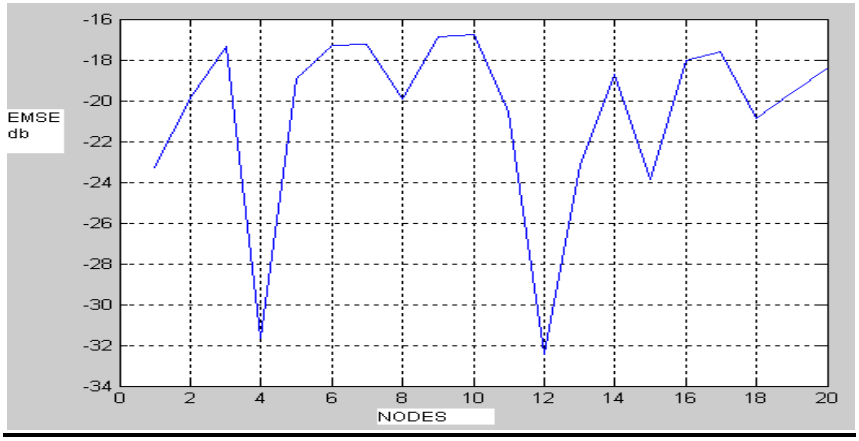
SIMULATION RESULTS:



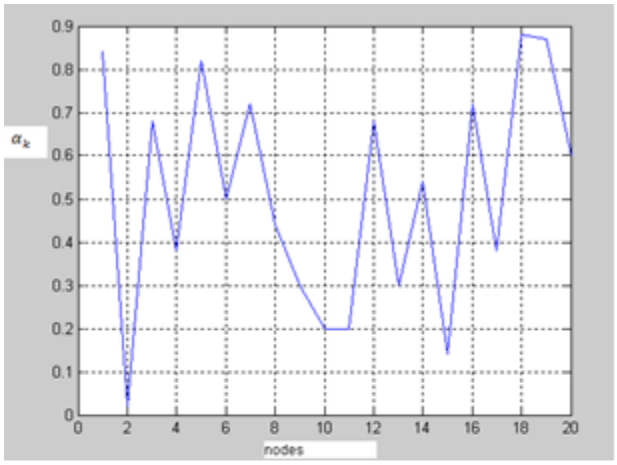
MEAN SQUARE DEVIATION ACROSS NODES



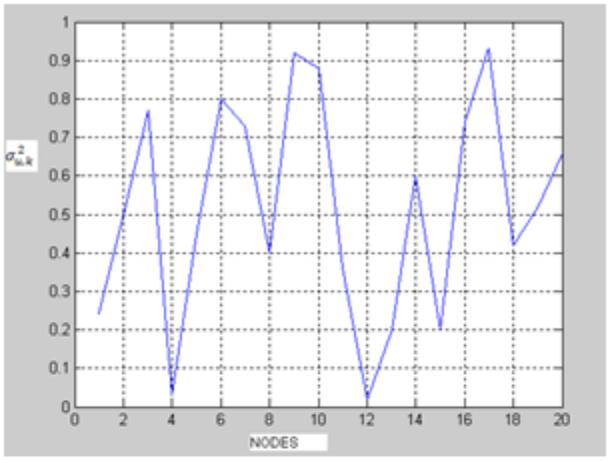
MEAN SQUARE ERROR ACROSS NODES



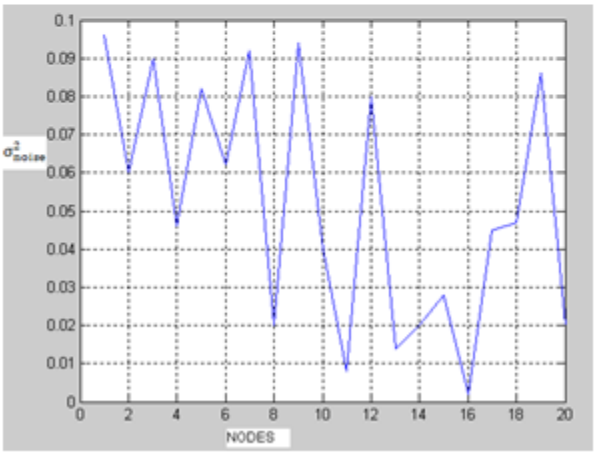
EXCESS MEAN SQUARE ERROR ACROSS NODE



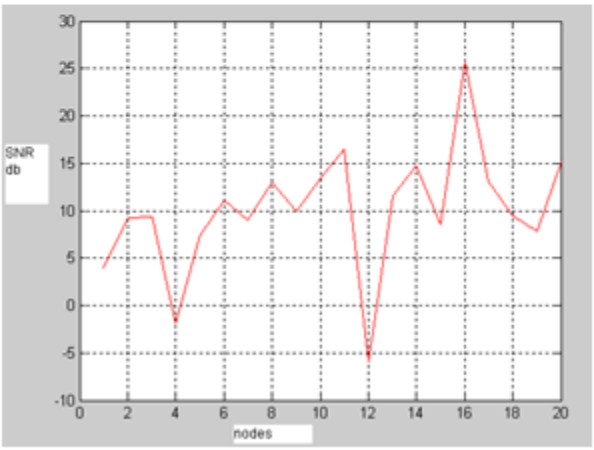
CORRELATION INDEX ACROSS NODES



NODE POWER PROFILE



NODE NOISE POWER PROFILE



SIGNAL TO NOISE RATIO ACROSS NODES

Computer simulations were done in MATLAB environment to make a thorough study of the performance of the Incremental type LMS Algorithm. In order to plot performance curves 100 different experiments were performed and the values of the last 300 iterations after the convergence were averaged. The quantities of interest:

MSD(Mean Square Deviation)

MSE(Mean Square Error)

EMSE(Excess Mean Square Error) were obtained.

In the Simulation N=20 nodes were taken with each regressor size of (1X10) collecting data from time correlated sequence $\{u_k(i)\}$, generated as

$$u_k(i) = \alpha_k . u_k(i-1) + \beta_k z_k(i) \qquad i > -\infty$$

$$\alpha_k \in [0,1)$$

$z_k(i)$ is a spatially independent white Gaussian process with unit variance

$$\beta_k = \sqrt{\sigma_{u,k}^2 . (1 - \alpha_k^2)}$$

The correlation indices and the Gaussian noise variances were chosen a random. The corresponding Signal to Noise Ratio obtained at each node.

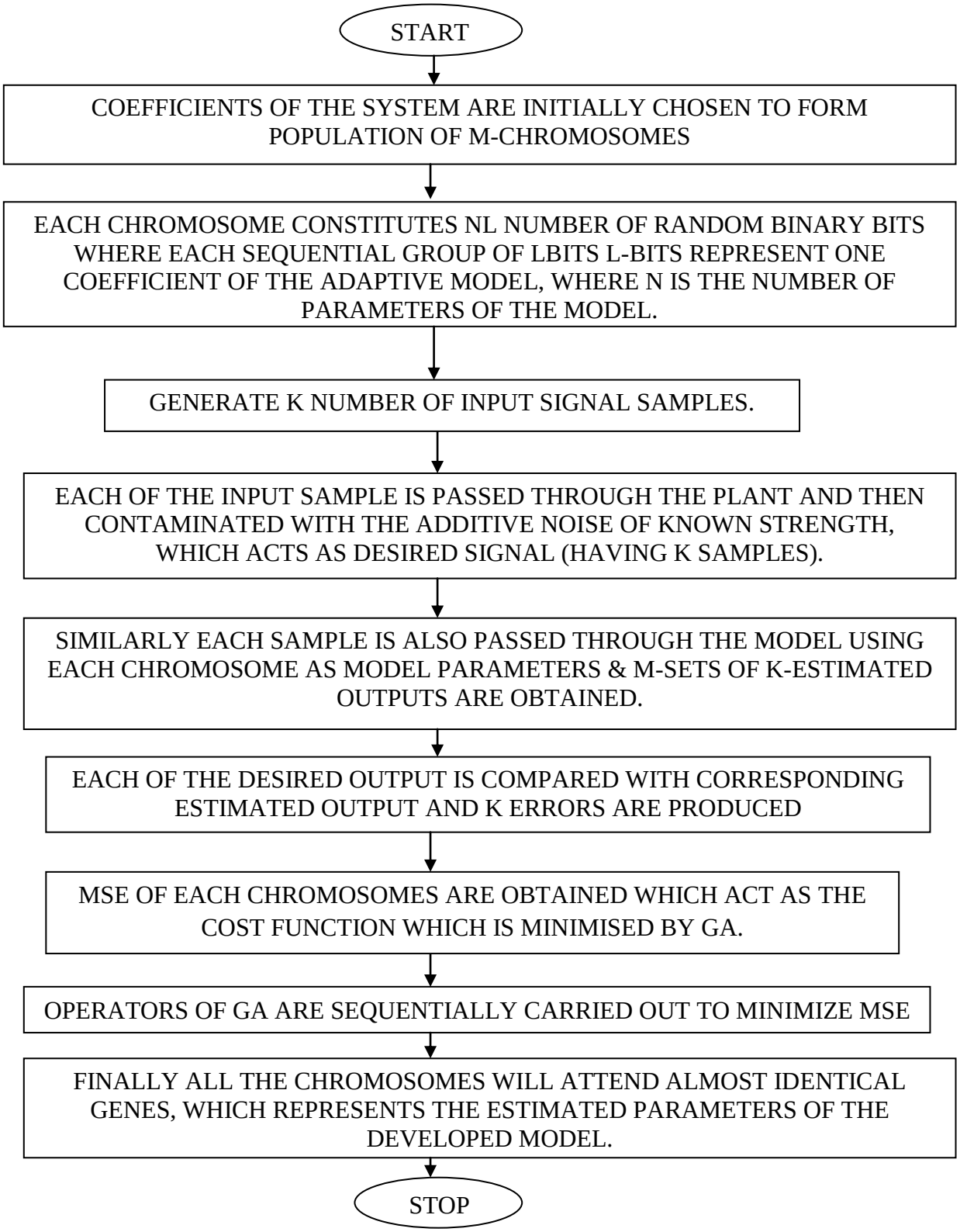
DISCUSSION:

The MSE roughly reflects the noise power which indicates the good performance of the Adaptive distributed network in steady state. If the adaptive node is performing well then the estimated weights are a good estimate of w^0 therefore the residual error should be close to the background noise.

The graphs obtained for the MSE and EMSE were in close resemblance with the graphs obtained in the IEEE paper "Incremental Adaptive Strategies over Distributed Networks" implemented by Lopes and Sayed. There was some difference observed in the plot of MSD.

3.9) SYSTEM IDENTIFICATION USING GENETIC ALGORITHM:

FLOWCHART



Algorithm for System Identification using Genetic Algorithm:

STEP 1: A known plant was initialized with filter parameters

hknown =[0.26 0.93 0.26].

STEP2: The input signal set **X** was generated for a given signal power with unit amplitude.

STEP3: The unknown system was initially taken to be zero **hunknown** = [0 0 0].

STEP4: The input was convolved with both the known and the unknown system to obtain their corresponding outputs. A Gaussian distributed noise was added to the estimated output to account for the disturbance in the system.

$$desired\ output = hknown * X^T + \text{Noise}$$

$$estimated\ output = hunknown * X^T$$

STEP5: The difference between the outputs from the two filters gave the error in the system.

$$\text{Error} = \text{desired output} - \text{estimated output}$$

STEP6: The population is sorted on the basis of the mean square error associated with it.

STEP7: The selected individuals undergo crossover and mutation to produce the net generation population.

STEP8: This procedure is repeated till the termination condition is reached. In the simulated programme the number of iterations served as the end condition.

STEP9: The value of the filter obtained at the end of the specified iterations gives the final estimated system and has very close resemblance with the known system's characteristics.

STEP10: Different graphs are plotted to show the outputs of the known and the unknown plant for a given set of inputs.

SIMULATION:

Probability of crossover(p)=0.8

Probability of mutation(q) = 0.2

Alpha = 0.2

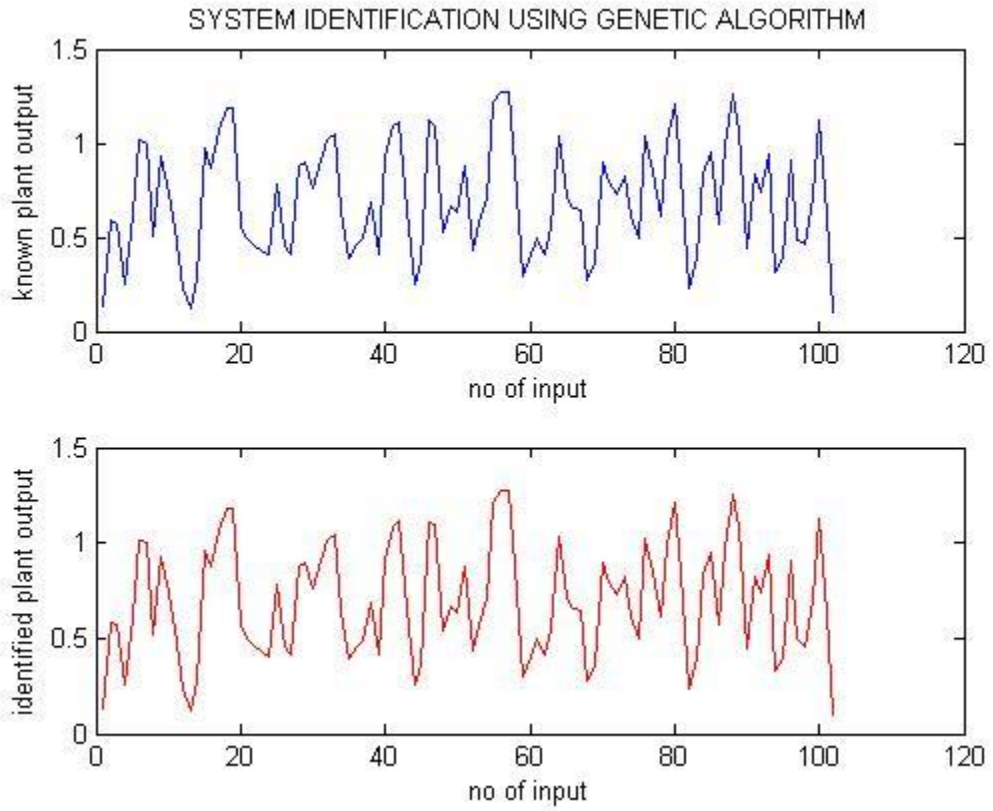
Beta = 0.2

Initial population size = 50

No of iterations = 500

No of inputs = 100

SIMULATION RESULT:



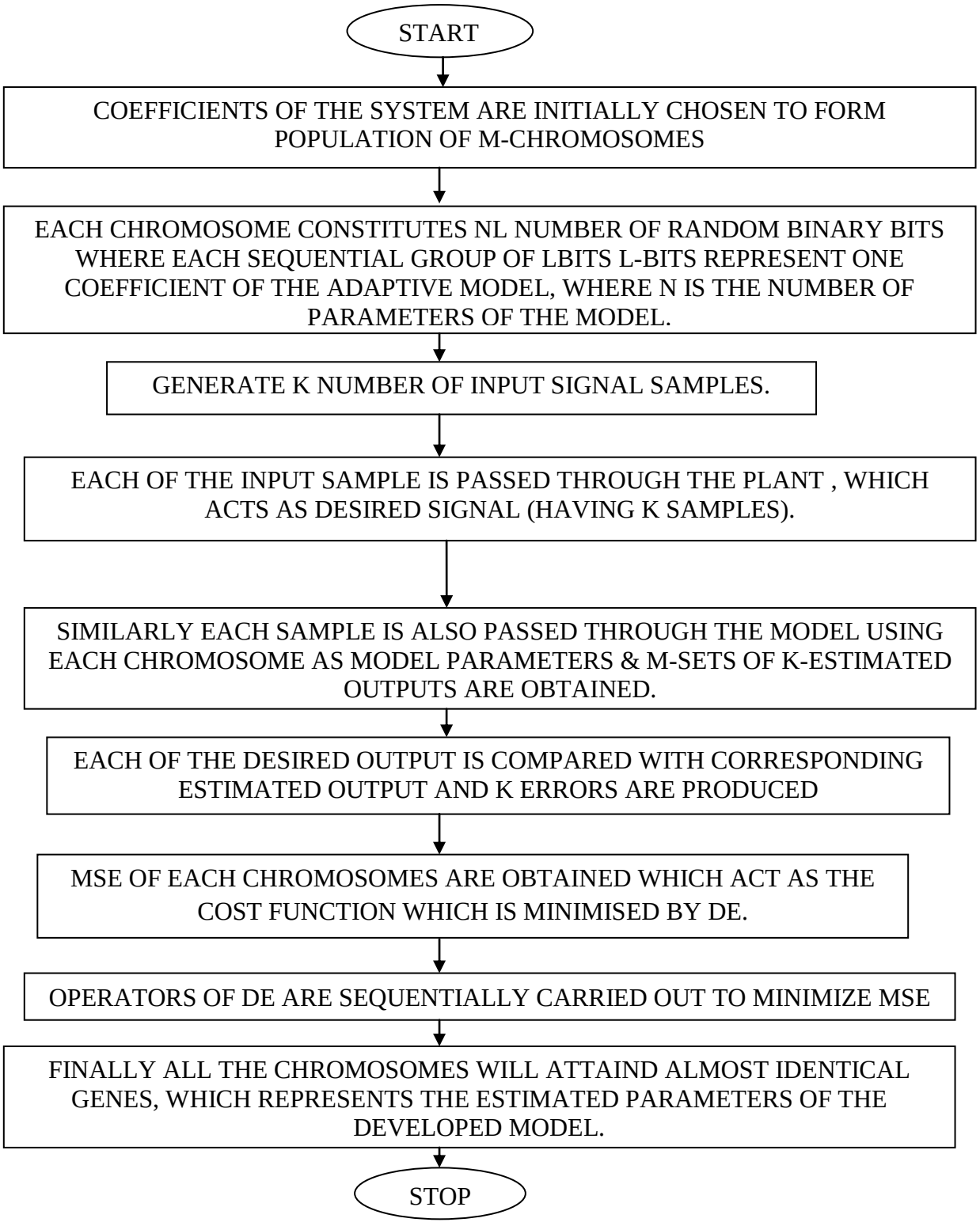
PLOT SHOWING THE OUTPUT OF THE KNOWN AND THE IDENTIFIED PLANT FOR THE GIVEN SET OF INPUTS

DISCUSSION:

The system in the problem was perfectly identified with the mean square error tending towards zero. This proves the efficiency of the GA in system identification problem.

3.10) SYSTEM IDENTIFICATION USING DIFFERENTIAL EVOLUTION GENETIC ALGORITHM:

FLOWCHART



Algorithm for System Identification using LMS:

STEP 1: A known plant was initialized with filter parameters

hknown =[0.26 0.93 0.26].

STEP2: The input signal set **X** was generated for a given signal power with unit amplitude.

STEP3: The unknown system was initially taken to be zero **hunknown** = [0 0 0].

STEP4: The input was convolved with both the known and the unknown system to obtain their corresponding outputs.

$$desired\ output = hknown * X^T$$

$$estimated\ output = hunknown * X^T$$

STEP5: The difference between the outputs from the two filters gave the error in the system.

Error = desired output – estimated output

STEP6: The population is sorted on the basis of the mean square error associated with it.

STEP7: The selected individuals generate their respective perturbed vectors. The parent chromosome is crossovered with the perturbed vector to form the child. The child if fitter replaces the parent individual else the parent chromosome is retained in the next generation.

STEP8: This procedure is repeated till the termination condition is reached. In the simulated programme the number of iterations served as the end condition.

STEP9: The value of the filter obtained at the end of the specified iterations gives the final estimated system and has very close resemblance with the known system's characteristics.

STEP10: Different graphs are plotted to show the outputs of the known and the unknown plant for a given set of inputs.

SIMULATION:

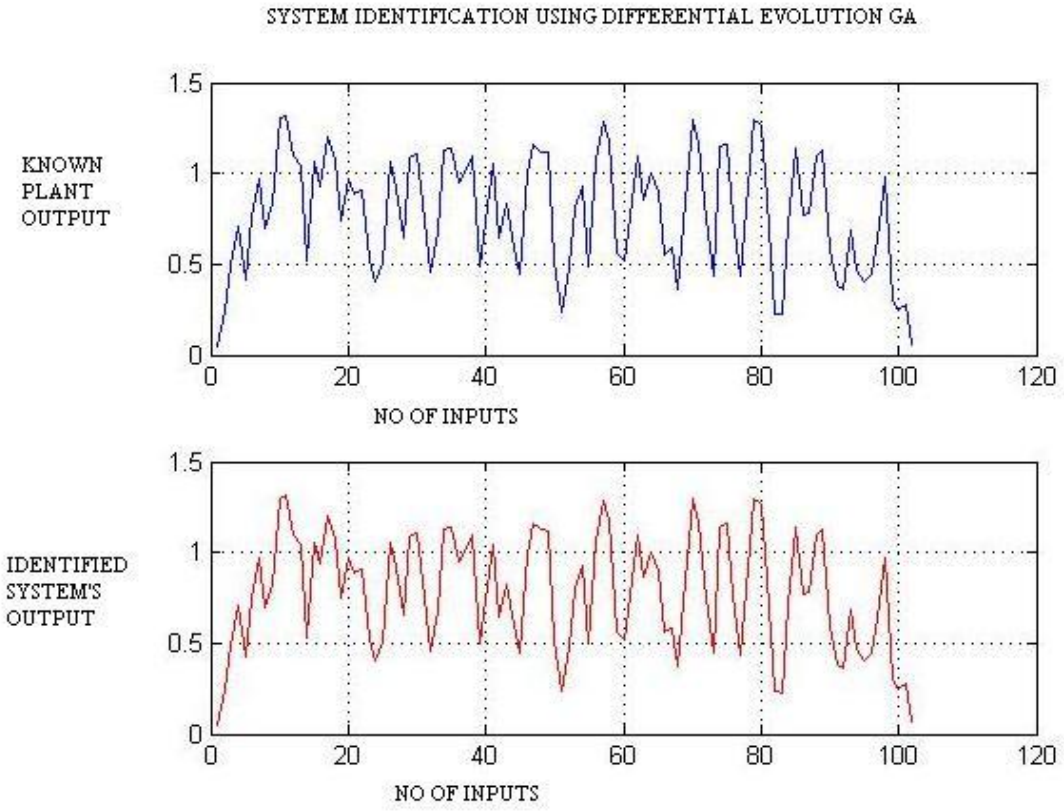
Probability of crossover(Cr)=0.8

Initial population size = 50

No of iterations = 1500

No of inputs = 100

SIMULATION RESULT:



PLOT SHOWING THE OUTPUT OF THE KNOWN AND THE IDENTIFIED PLANT FOR THE GIVEN SET OF INPUTS

DISCUSSION:

The system in the problem was perfectly identified with the mean square error tending towards zero. The application of Differential evolution algorithm to the system identification problem shows closer approximation of the filter parameters.

The graph shows that the output of the estimated plant closely follows the output of the known plant for the given set of inputs.

CHAPTER 4

4. CONCLUSION

The results obtained by simulation of the Function Approximation problem reveals the superiority of the Genetic Algorithm over the other methods of optimization in both unimodal and multimodal functions. The different algorithms of the real coded GA, binary coded GA, Sawtooth GA and Differential Evolution GA have their own advantages and disadvantages in the different optimization problems. Real coded GA has faster convergence than Binary GA. Further Twp point crossover Binary GA is better than Single point crossover Binary GA because it brings better randomness in the search space. Sawtooth GA worked efficiently for both unimodal and multimodal function because of the variabile population factor. Differential Evolution (DE) proves to be a promising candidate for optimizing real valued multi-modal objective functions.
The results obtained by simulation of the System Identification problem shows both Real coded GA and Differential Evolution GA are effective tool to design the model which is the replica of the system. The output produced by the known plant and the system model by Real Coded GA and Differential Evolution GA perfectly matched.

System identification using LMS algorithm gives lesser error than in GA technique. But the efficiency of LMS algorithm is restricted to linear systems and becomes unstable as the number of parameter increases. The increase in he number of parameters also increases the computational complexity in LMS but in GA there is very little increase in the computation.

Thus, this paper summarizes a number of current developments in genetic algorithms. It includes both theoretical aspects of genetic algorithms and its variants and some potential applications which incorporate the use of genetic algorithms.

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