A New Approach of Backbone Topology Design Used by Combination of GA and PSO Algorithms

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ABSTRACT

A number of algorithms based on the evolutionary processing have been proposed for communication networks backbone such as Genetic Algorithm (GA). However, there has been little work on the SWARM optimization algorithms such as Particle Swarm Optimization (PSO) for backbone topology design. In this paper, the performance of PSO on GA is discussed and a new algorithm as PSOGA is proposed for the network topology design. The simulations for specific examples show that the performance of the new algorithm is better than other common methods.

KEYWORDS: *Backbone, Cost, Genetic Algorithm, Network Topology design, PSO algorithm, SWARM intelligence.*

1. INTRODUCTION

The topological design of computer networks is a part of network planning which consists of finding a network topology configuration that minimizes the total communication cost, while considering some performance and reliability constraints [1] - [3]. Given the computational complexity of techniques that allow an optimal solution to this problem, heuristic methods are often proposed to reduce the search of candidate topologies and provide a suboptimal method. The Genetic Algorithm (GA) [10], [11], [13] and [14] and Particle Swarm Optimization (PSO) [15], [16] are such methods. Genetic Algorithms are part of evolutionary computing which is a rapidly growing area of artificial intelligence. And PSO is a part of SWARM intelligence [17] which has been built on collective treatments in uncentralized and self-organized terminals. These terminals usually have been comprised of a group of simple actors which are locally interacting with each other and their environment. The main purpose is to minimize the cost of topology by comparing it with Dijkstra's shortest path algorithms.

REVIEWING PREVIOUS LITERATURES

Different ways of solving a problem of topological design of network have been proposed: **R&CA** (Routing and Capacity Assignment): leads to solving a very complex writing problem [1]. **BXC** (Branch X-Change): there is possibility that deleting some of the old links decreases network efficiency and it has low speed when node numbers are more than 20 or 30 nodes [6]. **CBE** (Concave Branch Elimination): effectively deletes unnecessary nodes but does not permit new links to enter [7]. **CS** (cut Saturation): finding purred [4], [5]. **Mentor** (Mesh Network Topology Optimization and Routing): High cost is the problem of this approach [2]. **TS** (Tabue Search): In relation to other approximates approaches better efficiency and has low cost , but the only problem of this approach in defining movements (deleting, adding and replacing links with some conditionals) [7] - [9].

2. OVERVIEW OF NETWORK TOPOLOGY DESIGN

Network topology design is a part of network planning, and consists of finding a network topology configuration that minimizes the total communication cost, while considering some performance and reliability constraints. The literature was published by Cisco Systems, Inc., And other networking vendors talk about classic three-layer hierarchical model for network design topologies. The three-layer model permits traffic aggregation and filtering at three successive routing or switching levels. These three layers are as follows [12]:

1-The core layer (Backbone).

2- The distribution layer.

3-The access layer.

The core layer of a three-layer hierarchical topology is the high-speed backbone of the internet work. Since the core layer is critical for interconnectivity, you should design the core layer with redundant components. Fig.1 shows this segmentation.

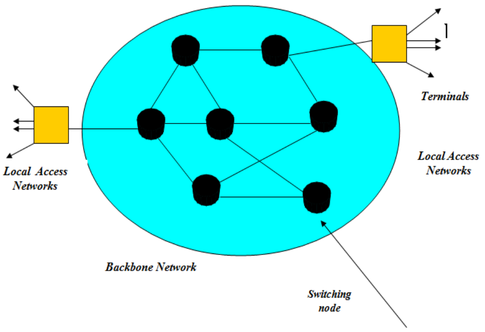


Fig.1. Segmentation of hieratical topology.

3. SCIENCE OF BIOLOGICAL PROCESS (BIONICS)

Strategies for solving old optimizing algorithm problems mostly depend on kind of aim, limit factors (linear, nonlinear), types of applied variation in sampling (true and natural). This is a fact that old optimizing approaches, causes limitations in solving mathematical programming and applied research approaches and this is mainly because of the intrinsic solving mechanism in those approaches. One of the main features of old optimizing algorithms is their inflexibility for the supposed problem and its adaptation to possible and dynamic changes. Among scientific and research society, there is a tendency to modeling and solving complex optimizing problem, using natural similarities. This is mainly because of the inefficiency of older optimizing algorithms for solving complex non-linear problems and bigger combined problems. The nature has been a source of inspiring and modeling for most of researches and scientific advances such as genetic algorithm, neural network, self-organizing systems and swarm intelligence.

4. GENETIC ALGORITHM

GA is a multi-purpose search and optimization algorithm that is inspired by the theory of genetics and natural selection [2]. The problem to be solved using GA is encoded as a chromosome that consists of several genes. A group of chromosomes referred to as a population represents the solution of the problem. In each iteration of the algorithm, the chromosomes in the population will undergo one or more genetic operations such as crossover and mutation. The result of the genetic operations will become the next generations of the solution. This process continues until either the solution is found or a certain termination condition is met. The idea behind GA is to have the chromosomes in the population to slowly converge to an optimal solution. At the same time, the algorithm is supposed to maintain enough diversity so that it can scan a large search space. It is the combination of these two characteristics that makes GA a good search and optimization algorithm.

4.1. Implementation of GA for proposed algorithm

Here it is assumed that different (or maybe the same) of backbone topology are initial populations with binary string representation and can be defined as follows:

Gen i in chromosome will be (one) 1 if link i in topology exists. Fig.2 is representation of the proposed algorithm.

Link 1 (0 or 1)	Link 2 (0 or 1)	Link i (0 or 1)	Link m (0 or 1)

Fig.2. Chromosome or representation of chromosomes in the proposed algorithm.

For example:

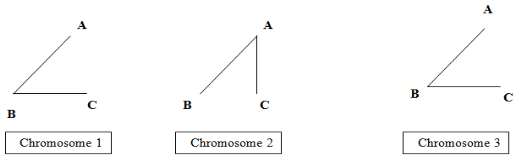


Fig.3. Three different of topologies

Table1. Initial chromosomes for Fig.3

Chromosome	Link AB	Link AC	Link BC
Chromosome	1	0	1
Chromosome	1	1	0
Chromosome	1	0	1

4.2. Reducing of chromosome length for big backbone

In our representation the number of links in topology is calculated by: $1/2(n)(n-1)$; thus the chromosome length will become so long. The most important reasons concerned with increasing length of chromosome leading to increasing problem complexity are: Population size; because problem's converges will be too slow, fitness function; because finding fitness function will be more complicated and time of generation production; because crossovering, replaces parents' chromosome genes in offspring and as a result mutation changes genes.

Our topology is broken down into 2 sub topologies thus the length of chromosome decreases to 1/4.

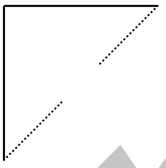
4.3. Fitness

Each possible solution by its value or qualification (fitness) can be marked for the problem. The fitness of each chromosome will be determined using a function called fitness function. Cost and connectivity are the variables used in producing the fitness function which are defined as:

$$\mathrm{Total\_cos\,t} = \sum_{i=1}^{m} d(C_i) + x_i \qquad (1)$$

$$\mathrm{Per\_connect} = \mathrm{Dis\_connec}/m \qquad (2)$$

Where $d(C_i)$ and x_i are the fixed cost and the variable cost of link i, respectively, dis_connec is the number of links that does not satisfy the node_connectivity (the minimum number of links that must be connected to any link) and m is the whole links in topology in full mesh state. For example in this topology



Per-connect = 2/3

We define the fitness function as below:

$$\mathrm{Fitness\_function} = 0.01 * \mathrm{link\_num} + (1.0/(\mathrm{diss\_connect} + 100 * \mathrm{link\_num} + 1.0) + 1.0/(\mathrm{cost} + 1.0)) \qquad (3)$$

And our mechanism for parent selection is truncation selection with this defined threshold in any generation.

T=average of Fitness_Function

Crossover operator is defined as one point crossover and point of crossover is selected randomly. Mutation operator changes a gene in the chromosome (adds or removes a link in the topology) randomly.

5. SWARM INTELLIGENCE

It's a kind of artificial intelligence which has been built on collective treatments in uncentralized and self-organized terminals. These terminals usually have been comprised of a group of simple actors locally interacting with each other and their environment. Although there is no centralized controlling imposed ways of their treatment, their local interaction is leading to general behaviors. Some examples of these systems can be observed in the nature. Ants groups, bird groups, animal bend, bacteria's colony, fish groups.

5.1. PSO Algorithm

PSO is initialized with a group of random particles (solutions) and then searches for optima by updating generations. In every iteration, each particle is updated by following two "best" values. The first one is the best solution (fitness) that has achieved so far. (The fitness value is also stored.) This value is called pbest. Another "best" value that is tracked by the particle swarm optimizer is the best value, obtained so far by any particle in the population. This best value is a global best and called gbest. When a particle takes part of the population as its topological neighbors, the best value is a local best and is called lbest. After finding the two best values, the particle updates its velocity and positions with following equation (a) and (b).

*v[] = v[] + c1 * rand() * (pbest[] - present[]) + c2 * rand() * (gbest[] - present[])* *(a)*

present[] = present[] + v[] *(b)*

v[] is the particle velocity, present[] is the current particle (solution). pbest[] and gbest[] are defined as stated before. rand () is a random number between (0,1). c1, c2 are learning factors. usually c1 = c2 = 2.

There are two kinds of PSO: SPSO (Synchronous PSO) and APSO (Asynchronous PSO). In SPSO the processing is parallel processing and in APSO is serial processing. In our proposed algorithms, we use APSO and assume that V(velocity) will refer to the link which is added to the topology in each step and X(position) can be specified as the topology that will be gained by adding each link. And Initial topology (position) in PSO is the topology that has the best fitness after GA.

Finally, the suggested algorithm (PSOGA) can be written as:

1. Input the coordinates of backbone nodes.
2. Divide backbone nodes into two adjacent categories.
3. Align topology to each category, randomly.
4. Find the genotype of each topology according to the Fig. 2. (Align chromosome to each topology.)
5. Run GA on each chromosome found in step 2.
6. Run the PSO on the best chromosomes found from previous step.
7. Merge the best chromosomes found in step 4.
8. Finish.

6. IMPLEMENTATION OF PROPOSED ALGORITHM AND NUMERICAL RESULTS

The proposed algorithm is used in the design of network topologies which have 6,10,20 nodes and also **NSFNET** network that contains 14 nodes and their coordinates are in the appendix.

1. Topology design with 6 nodes:

In this case it is assumed that:

- Node_connectivity=3.
- Some of the parameters of the GA algorithm are shown in table 2.

Table 2. Some of the parameters of GA algorithm for topology design with 6 nodes.

Number of generations	Number of chromosomes in each generation	Crossover type	Crossover rate	Mutation rate
8	6	One point	50%	90%

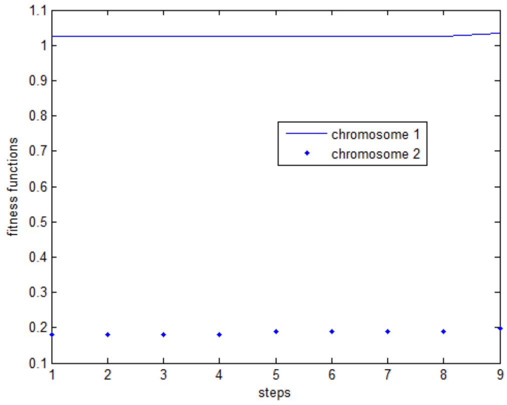


Fig.4. Fitness evolutionary of topology with 6 nodes.

Finally, these chromosomes are obtained:

0 0 0 0 0 1 0 1 0 0 0 0 0 0 0 0 1 0
0 0 1 0 0 0 0 1 0 0 0 0 0 0 0 1 0 0

2. Topology design with 10 nodes:

In this case it is assumed that:

- Node_connectivity=4.
- Some of the parameters of the GA algorithm are shown in table 3.

Table 3. Some of the parameters of GA algorithm for topology design with 10 nodes.

Number of generations	Number of chromosomes in each generation	Crossover type	Crossover rate	Mutation rate
12	10	One point	50%	90%

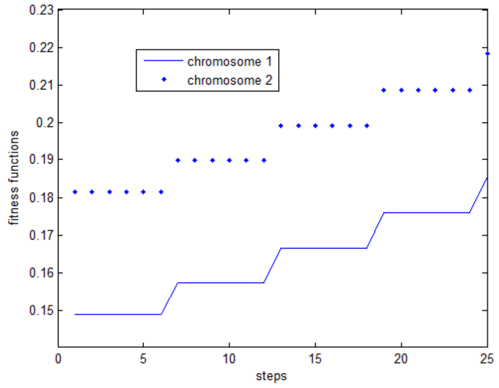


Fig.5. Fitness evolutionary of topology with 10 nodes.

Finally, these chromosomes are obtained:

0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 1 0 0 0 0
0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 1 0 0 0
0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 1 0 0 0 0
0 0 0 1 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 1

3. Topology design with 20 nodes:

In this case it is assumed that:

- Node_connectivity=5.
- Some of the parameters of the GA algorithm are shown in table 4.

Table 4. Some of the parameters of GA algorithm for topology design with 20 nodes.

Number of generations	Number of chromosomes in each generation	Crossover type	Crossover rate	Mutation rate
30	25	One point	50%	90%

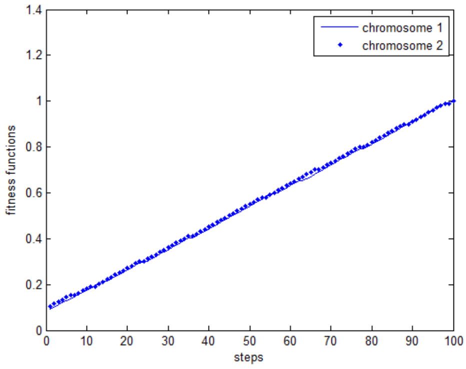


Fig.6. Fitness evolutionary of topology with 20 nodes

Finally, these chromosomes are obtained:

0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0
0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0
0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0
1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0
1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0
1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0
1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0
0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0

4. Topology design in NSFNET topology:

In this case it is assumed that:

- Node_connectivity=4.
- Some of the parameters of the GA algorithm are shown in table 5.

Table 5. Some of the parameters of GA algorithm for NSFNET topology

Number of generations	Number of chromosomes in each generation	Crossover type	Crossover rate	Mutation rate
25	18	One point	50%	90%

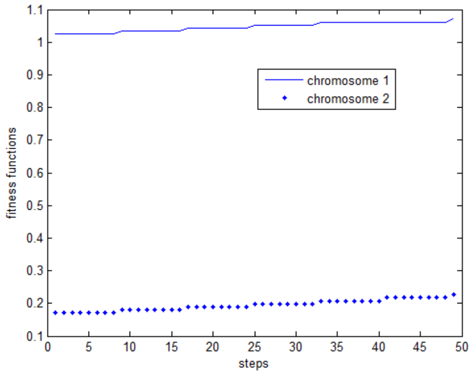


Fig.7. Fitness evolutionary of topology in NSFNET topology.

Finally, these chromosomes are obtained:

0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0
0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 1 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0
1 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0
0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 1 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0

7. CONCLUSION

Using Genetic Algorithm and PSO together in the backbone topology design in relation to the other mentioned algorithms leads to decreasing cost as well as decreasing its complexity. (In NSFNET design (in common method) the cost of topology (1-7 nodes) is: 0.29182058 and (7-14 nodes) is: 0.1890399) whereas in the proposed algorithm these values are: 0.254458 and 0.1492044 respectively.

Results of dividing the network to neighboring and dividing method for applying PSO Algorithm totally depend on needs characteristics and traffic between them and in every problem we can experiment the mentioned conditions about it and apply the best condition.

Because of variation in selection of fitness_function parameters, we can select other factors of topology for designing without need to make lots of changes in loading algorithms.

8. SUGGESTIONS

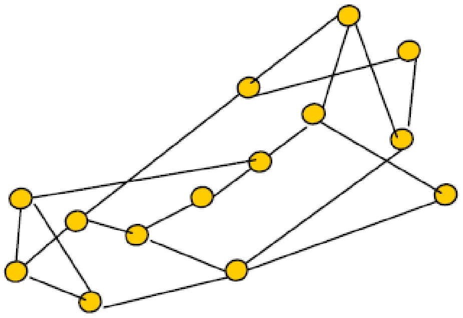
It's better to pay attention to these points when considering dividing nodes to neighbors. This action only applied to nodes with high amounts of backbone (ex: more than 10 nodes). Size of neighboring should be adjusted to the backbone's node numbers. Dividing nodes to the neighboring could be done according to the designers factors not only node numbers. Dividing nodes to the neighboring should be adjusted to the king of asking services from the network. For example in sensitive services to delay, could give weighting to the traffic among nodes.

APPENDIX

The node coordinates of backbone topologies:

x[1]=0; y[1]=0; x[2]=10;y[2]=-5;
x[3]=2;y[3]=10; x[4]=7;y[4]=5;
x[5]=12;y[5]=3; x[6]=20;y[6]=10;
x[7]=23;y[7]=0; x[8]=27;y[8]=10;
x[9]=32;y[9]=12; x[10]=25;y[10]=20;
x[11]=45;y[11]=10; x[12]=40;y[12]=12;
x[13]=40;y[13]=22; x[14]=35;y[14]=25;
x[15]=4;y[15]=73; x[16]=10;y[16]=71;

x[17]=56;y[17]=27; x[18]=82;y[18]=47;
x[19]=9;y[19]=54; x[20]=95;y[20]=61;
x[21]=63+10;y[21]=8+10;



NSFNET topology

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