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Research paper

Using Modified Genetic Algorithm for Enhancing Network Connections Distribution

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Abstract

In this paper, a developed Genetic Algorithm (dGA) has been proposed as an efficient method to find optimal distribution of network connections. There are many network devices can be used as a terminal station such as computers, hubs, routers or wireless networks. The proposed algorithm depends on the modifying of the traditional genetic algorithm (GA) parameters. The parameters of GA are initial population, encoding, evaluation, crossover, mutation, replacement and stopping criteria. The population consists of many chromosomes, each gene in a given chromosome represent a station of network. The chromosome has fixed length for all population. This paper aims to provide an efficient way to identify the population that gives the best paths for mesh topology network and detect optimal path, at the end the final population preserve only the shorter paths that gives best solution to reach goal.

Keywords: *Developed Genetic Algorithm (dGA), Mesh Topology, Optimal Path, eighth decimal encoding.*

1. Introduction

Genetic Algorithm (GA) is a numerical optimization techniques based upon the principle of natural selection [1]. It is one of the optimization algorithms used to find optimal solutions [2]. GA encodes a set of mathematical solutions i.e. chromosomes (CH). These construct population which contains set of individuals have fixed length. An important point of the GA is fitness function that represents the evaluations tool for each chromosome. It is considered as an essential to satisfy the Darwinian principle of the "survival of the fittest". It is a population-based search algorithm that replicates individual populations using many factors to obtain optimal solution [3]. The population is influenced by many major operations such as selection, crossover, mutation, replacement and stop criteria [4].GA has been applied in many applications such as design mesh networks [5], Implementation of shortest path in packet switching network [6], network security [7].

A simple definition of network is a set of nodes connected by lines called links. Whereas path is defined as going from one node to another in network [8]. Mesh topology unlike other types of topologies, allows multiple access links among network nodes. It provides reliability whenever one network element fails the network continues to work and do not make terminate data exchange operations by the bypass. Metropolitan area networks (MAN) often applied mesh topology network [9].

This paper is organized as follows.Section2 reviews the simple genetic algorithm. Section 3 shows the block diagram and the developed genetic algorithm . Experimental results of the proposed system and discussion in Section 4 . Section 5, draws the important conclusions.

2. Simple Genetic Algorithm

GA plays a significant role within artificial intelligence and robotics as an emerging paradigm. All genetic information of an individual string is stored in chromosome [10]. The main steps of GA are illustrated in the following algorithm [11]:

Step1: Initialize solution space. Here a random solution space is generated.
Step2: Encode the solution space .
Step3: Evaluate population using a fitness function.
Step4: While (best individual is not found).
Step5: Selection (for example, using the Roulette wheel Selection method).
Step6: Crossover (for example, using ordered crossover operator).
Step7: Mutation (for example ,Inversion).
Step9: Replacement of the old parent with new offspring (for example, using weak parent replacement).
Step10: Return the best solution found.

GA contains on certain number of individuals each one represents chromosome using encoding operation. The number of chromosomes in population depends on the problem. Each chromosome has a certain number of genes; each gene is represented in binary representation [12].

GA consist of many parameters, the parameters of GA are very important to determine the behavior and results of GA.

Population size is a first parameter of GA, the population consists of a number of chromosomes. The critical point of size population that large size of population makes the algorithm taking additional computation time and small gives poor solutions [13].
Encoding is a process of mapping object variables to a string. Which that all the genetic information of an individual have been stored in chromosome that represented in string of certain length. GA consists of many encoding schemes such as one dimension and two dimensional [10]. Evaluation, which is a mathematical function applied on chromosomes to calculate the fitness values[12].
Selection: a good string is selected to breed a new generation. The selection based on fitness can be minimized or maximized [14][15].
Crossover: represents mating pool of individuals to generate new children .Hoping that the mating pool will generate a better offspring. In GA crossover plays an important role. It is necessary to understand the role of a crossover to comprehend the GA as a whole [16][17][18].
Mutation plays important role to find unexplored genetic material into the population. Bit-flip mutation that probability of alleles flip is 1.0[19].
Replacement: a new offspring is created from old population members that locate these individuals in a new population. When the completely new population are created, old population, become new population [20].
Finally standard stopping criteria, there are many methods used for stopping in GA such as using: fixed number of generations, monitor the fitness and stop when it plateaus, monitor the genetic diversity and stop when it falls[21].

3. The Proposed System

The proposed system for solving the meth network topology, which relies on developing the optimization technique. Figure 1 shows the mechanism, which aims to enhance the search and distribution of the network. This satisfies at final generation.

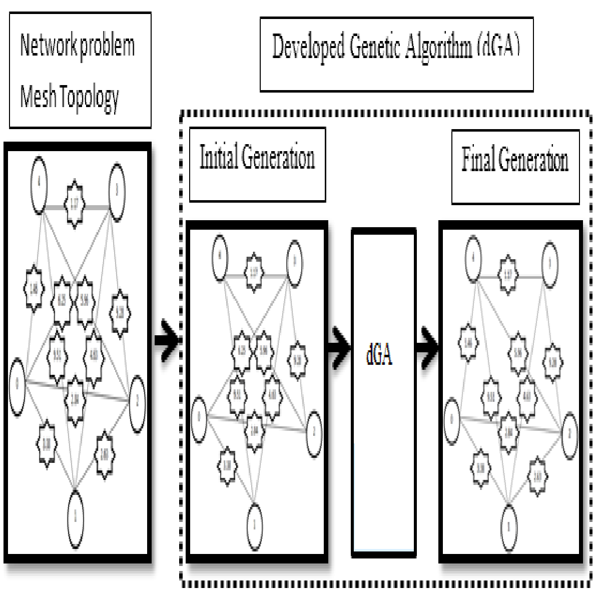


Fig. 1: The proposed mechanism of Network problem

3.1. The Proposed Developed Genetic Algorithm

Many operators are modified from the simple GA to get optimal solution with best fitness and time. Figure 2 states all stages which are updated.

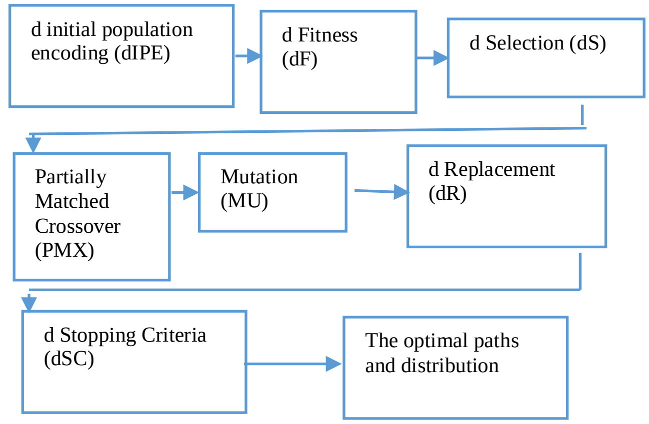


Fig. 2: Major operations of developed genetic algorithm

Where (d) refers to developing or modifying of original operation.

Name: dGA Algorithm
Input: m: size of population, n: length of chromosome
Output: optimal solution
Step1: dInitialPopulation_Encoding (dIPE)
m represents different feasible solutions randomly are generated, each solution has length n in array $p_{i,j}$ that encoding by **eighth decimal encoding** (0 to H).
Step 2: Random distance (RD)
Random symmetric distance is formed with size n*n in array $dis_{i,j}$
Step 3: dFitness (dF)
Each individual (i) in population has been evaluated using the flowing formula:
$x = \sum dis[p_{i,j-1}, p_{i,j}]$, where j from 1 to n-1.
$x = \sum dis[p_{i,n-1}, p_{i,0}]$.
Step 4: dSelection (dS)
Four different of individuals randomly are selected, best two individuals are assigned to parents (p1,p2) and the others have been used in replacement process (s1,s2).
Step 5: Partially Matched Crossover (PMX)
Input: Two parents
Output: Two children (Offspring)
5.1: Exchange two substrings between parents to produce children(c1,c2).
5.2: Determine mapping relations between two mapped sections.
5.3: Legalize offspring with mapping relationship.
PMX is used without using alleles values to produce (c1, c2).
Step6: Mutation (MU).
A random generation has been chosen and two children (c1or c2) are selected . Then swaping between genes are randomly selected, mutation may be occur once in every iteration.
Step 7: dReplacement (dR)
Return best two children from (c1, c2, s1, s2) to generate new population.
Step 8: dStopping criteria (dSC)
8.1 Maximum number of generations has reached.
8.2 (New population = old population) for n times.
8.3 The ratio of populations has reached to threshold.

New population /old population <= T threshold of fitness.
Step 9: If stop criteria not met go to step 3.

DIPE is used to generate initial random population have different chromosomes. The size of the population is fixed, i.e. the number of individuals of the community is determined (from 0 to m), where m is a size of population. Each chromosome has a fixed length and maximum chromosome length is 18 .In population each individual should contain all genes i.e. chromosome consists of 0 to n-1, where n is length of chromosome. The proposed encoding is called eighth decimal encoding, this methods can be encoded genes of chromosome from 0 to H when n is set 18 where each chromosome is represented by the following genes according to the order of the Stations {0 ‹1 ‹2 ‹3 ‹4 ‹5 ‹6 ‹7 ‹8 ‹9 ‹A ‹B ‹C ‹D ‹E ‹F ,G ,H}. Next, the array of distance RD is defined, RD is symmetric that means the distance from node (1) to node (3) is the same distance from node (3) to node (1), the main diagonal values are set to zero because the distance from any node to itself is equal zero. Then, fF method is used to evaluate each individual in the population by the end fitness value is calculated by summation the distance values of string in sequence, As a result, minimum fitness value is better.
Furthermore, dS selection method is used to select four different individual randomly best two as parents (c1,c2) and the other two are used in replacement process (s1,s2). Next, PMX has been used for breeding and generation new children. It is used without assigning allele value. Then applying mutation, but MU is rare to occur. This step works on random generation, swap between genes of individuals random selected. Later, a steady state approach of replacement is applied, dR is used to replace week between two children (c1,c2) and two individuals selected in DS process (s1,s2), the best two between them are used to generate new population.
Finally dSC are used to terminate generation process ,in dGA stop when a) fixed number of generations reached, b) stop when ratio of population reach to threshold of fitness, c) when new population equal old population for several times.

4. Experimental Results and Discussion

The following results in the tables reflects sample of the network distribution.

- **Population**

N=1 n=5, m=5, where N is number of generation, m is the size of population, n is the length of chromosome.

Table 1: sample of population

No.	CH				
1	4	1	0	2	3
2	0	3	1	4	2
3	0	2	3	4	1
4	2	0	1	3	4
5	3	2	4	0	1

- **Distance**

Generate random symmetric distance matrix size n^2, where n length of chromosome.

Table 2: partial fitness

Nodes	0	1	2	3	4
0	0	3.38	2.84	6.25	1.46
1	3.38	0	2.63	4.63	9.51
2	2.84	2.63	0	9.28	5.96
3	6.25	4.63	9.28	0	1.17
4	1.46	9.51	5.96	1.17	0

- **Fitness**

Table 3: Total Fitness

No. of CH	CH	Summing Distances	Fitness
1	41023	**d[4][1]** 9.51 + **d[1][0]** 3.38 + **d[0][2]** 2.84 + **d[2][3]** 9.28 + **d[3][4]** 1.17	26.18
2	03142	**d[0][3]** 6.25 + **d[3][1]** 4.63 + **d[1][4]** 9.51 + **d[4][2]** 5.96 + **d[2][0]** 2.84	29.19
3	02341	**d[0][2]** 2.84 + **d[2][3]** 9.28 + **d[3][4]** 1.17 + **d[4][1]** 9.51 + **d[1][0]** 3.38	26.18
4	20134	**d[2][0]** 2.84 + **d[0][1]** 3.38 + **d[1][3]** 4.63 + **d[3][4]** 1.17 + **d[4][2]** 5.96	17.98
5	32401	**d[3][2]** 9.28 + **d[2][4]** 5.96 + **d[4][0]** 1.46 + **d[0][1]** 3.38 + **d[1][3]** 4.63	24.71

- **Selection**

Table 4: sample of selection

CH	Fitness	Action
(5) 32401	(5) 24.71	Smallest two fitness are parents and highest two fitness Candidates for replacement
(1) 41023	(1) 26.18	
(4) 20134	(4) 17.98	
(2) 03142	(2) 29.19	
Selected two parents (p1,p2) and two for replacement(s1,s2)		
(5) 32401	(5) 24.71	p1: parent one
(4) 20134	(4) 17.98	p2: parent two
(1) 41023	(1) 26.18	s1: Candidate for replacement
(2) 03142	(2) 29.19	s2: Candidate for replacement

- **PMX Crossover**

Apply the PMX for producing the offspring. let two parents (p1, p2). k1=2, k2=2 where k1and k2 is cut points cross over.

Table 5: Pmx crossover (parents)

Name	CH	Fitness
Parent one P1:	3 2| 4 | 0 1	24.71
Parent two P2:	2 0| 1 | 3 4	17.98

Table 6: Pmx crossover (children)

Final offspring	CH	Fitness
Child one c1:	3 2|1| 0 4	17.92
Child two c2:	2 0|4| 3 1	12.73

- **Mutation**

Here, no mutation because it occurs in little probability.

- **Replacement**

Table 7: Replacement

Candidate for replacement	CH	Fitness	Put in new population
s1	41023	26.18	c1
c1	32104	17.92	
s2	03142	29.19	c2
c2	20431	12.73	

- **Results of Initial Generation**

Table 8: Results of Initial Generation

Initial Average Fitness	24.848

Initial Optimal fitness	17.98
Initial Optimal chromosome	20134

- **Results of Final Generation**

Table 9: Results of Final Generation

Final Average Fitness	19.904
Final Optimal fitness	12.73
Final Optimal chromosome	20431

- **Different Experiment of the Network Paths**

Many factors effect on the results of dGA such as number of generation (m), size of population (n), length of chromosome and cut points of crossover k1 and k2.
The output are average fitness for first generation (AVF), optimal fitness for first generation (OFF), average fitness for last generation (AVL), optimal fitness for last generation (OFL), average fitness for last generation of original genetic algorithm (AVLO), optimal fitness for last generation of original genetic algorithm (OFLO) and Fitness of mutation (FM).

- **Changing Number of Generations**

m=100, n=18, k1=8, k2=8 where m is size of population, k1 and k2 are cut points of crossover.
The result shows that Average Fitness and Optimal fitness for first generation is 87.4897 and 46.9 respectively. Changing number of generations is shown in table 10.

Table 10: Changing number of generation

m	AVL	OFL	FM
10	84.5349	46.9	76.8
100	64.9362	31.22	74.24
1000	41.9855	30.68	62.09
10000	39.3872	28.92	53.92
100000	39.2516	28.92	47.49
1000000	39.2516	28.92	49.75

The experiment (see figure3) shows that after optimal solution has reached, the increase in the number of generations does not affect the results because the individuals in population are better than children that generated from them.

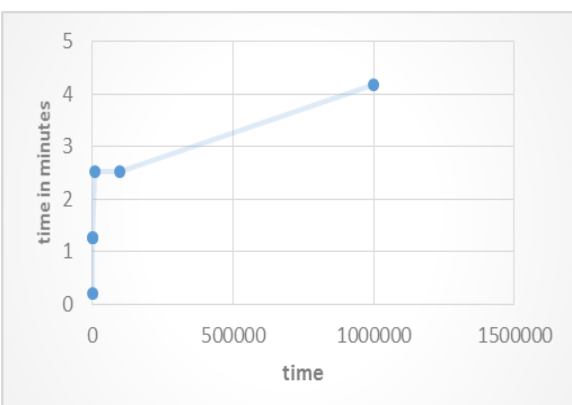


Fig. 3: Number of Generations and Time

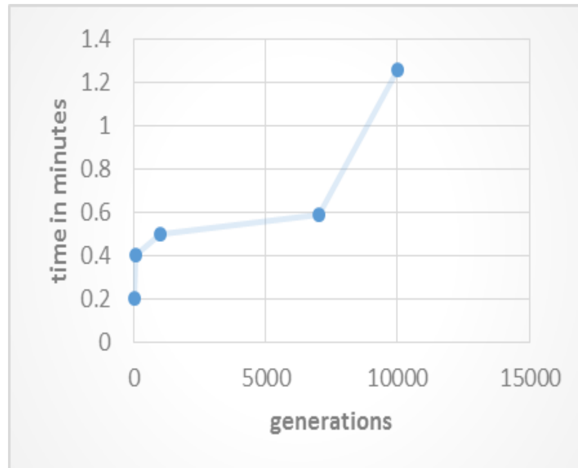
- **Changing Size of Population**

N=1000, n=18, k1=8, K2=8 where N is number of generation, n is length of chromosome, k1 and K2 are cut points of crossover. Changing size of population is shown in table 11

Table 11: Changing number of generation

m	AVF	OFF	AVL	OFL	FM
10	85.75	68.15	60.12	53.75	69.88
100	87.48	46.9	42.15	30.68	64.31
500	86.06	43.71	54.62	34.18	61.71
1000	85.60	43.71	64.97	35.11	102.17
2000	85.53	43.71	73.28	38.55	73.23
5000	85.57	40.13	80.12	40.13	117.1
10000	85.41	38.66	82.66	38.66	77.53

The experiment shows that the best size of population is one hundred and the worst size is ten thousand and increase in size of population lead to increase in time.



- **Changing Length of Chromosome**

N=100, m=100, k1=2, k2=2 where N is number of generation, m is size of population, k1 and k2 are cut points of crossover. Changing length of Chromosome is shown in table 12.

Table 12: Changing length of Chromosome

m	AVF	OFF	AVL	OFL	FM
5	23.435	12.16	22.665	12.73	20.93
7	31.380	12.73	23.855	12.16	30.64
10	49.065	34.09	39.225	25.49	45.56
15	71.309	39.51	54.432	33.21	58.95
18	87.489	46.9	66.224	46.9	83.35
5	23.435	12.16	22.665	12.73	20.93
7	31.380	12.73	23.855	12.16	30.64

The experiments show that the shorter length of the chromosomes gives better results than the longitudinal length of the chromosomes.

- **Changing Argument of Crossover**

- **Changing K1**

N=100, m=100, n=18, k2=2 where N is number of generation, m is size of population, n is length of chromosome, k2 is cut point of crossover from right. Changing k1 is shown in table_13.

Table 13: Changing k1

k1	AVF	OFF	AVL	OFL	FM
2	87.48	46.9	68.913	46.9	83.14
4	87.48	46.9	68.082	46.9	74.57
6	87.48	46.9	66.446	42.56	63.21
8	87.48	46.9	53.662	37.24	73.42
10	87.48	46.9	51.686	35.76	59.62

The experiment shows that a good results have obtained when the values of k1 are large.

- **Changing K2**

N=100, m=100, n=18, k1=2 where N is number of generation, m is size of population, n is length of chromosome; k1 is cut point of crossover from left. Changing k2 is shown in table_14.

Table 14: Changing k2

K2	AVF	OFF	AVL	OFL	FM
2	87.48	46.9	68.913	46.9	83.14
4	87.48	46.9	66.377	46.6	92.96
6	87.48	46.9	69.659	46.9	51.88
8	87.48	46.9	68.079	37.05	73.62
10	87.48	46.9	67.861	39.42	71.36

The experiment shows that a good results obtained when the value of k2 is large.

- **Changing K1 And K2**

N=1000, m=100, n=18 where N is number of generation, m is size of population, n is length of chromosome. Changing k1 and k2 are shown in table_15.

Table 15: Changing k1 and k2

K1	K2	AVF	OFF	AVL	OFL	FM
2	2	87.48	46.9	68.91	46.9	83.14
4	4	87.48	46.9	50.94	34.12	49.3
6	6	87.48	46.9	52.81	42.04	97.86
8	8	87.48	46.9	40.94	30.68	31.26
8	9	87.48	46.9	43.36	33.88	108.9
9	8	87.48	46.9	35.62	27.18	57.17

The experiment shows that when values of k1 and k2 larger, the results will be better.

- **Comparison of GA And Dga**

N=1000, m=100, n=18, where N is number of generations, m is size of population, n is length of chromosome. Comparison between original and developed algorithm for changing k1 and k2 are shown in table_16.

Table 16: Changing k1 and k2 for GA and dGA

K1	K2	AVLO	OFLO	AVL	OFL
2	2	121.05	61.16	68.91	46.9
4	4	125.29	79.73	50.94	34.12
6	6	121.67	102.09	52.81	42.04
8	8	121.3	105.51	40.94	30.68
8	9	120.63	112.9	43.36	33.88
9	8	121.08	112.07	35.62	27.18

The results show that the dGA is better than GA based on fitness function criteria.

5. Conclusion

The dGA can apply on different problems similar in general features. dGA system can apply to find optimal path of network , where the network can be computer , routers , hubs and/or wireless network. When reach to optimal generation, other iterations do not effect on results.

The experiments showed that the best size of population is one hundred and the worst size is ten thousand. Also, the system discussed the influence of the values of the cut points k1 and k2.Additionally, when repeat same experiment with the same arguments the results are vary slightly due to the effect of genetic mutation .

The dGA proved its efficiency for finding optimal generation and optimal path as well as satisfying best results in less time in a compared to simple GA. the different parameters of dGA have affected on the results such as number of generations, size of population, length of the chromosome , method of evaluation , selection, crossover ,mutation , replacement , and stopping criteria.

Finally, the proposed method is compared with the traditional GA. The results proved that the proposed method is better in terms of the fitness value, convergence, time and thus optimization in the distribution of network connections.

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