Genetic Algorithm Using Sub-path Codes for Mobile Robot Path Planning

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Abstract: In this paper, a new method for finding global optimal path planning is proposed using a Genetic Algorithm (GA). A map of known static environment as well as a start node and a target node connecting an optimal path which is required to be found are given beforehand. The chosen nodes in a known static environment are connected by sub-paths among each other. Each path is represented by a series of subpaths which connect the sequential nodes to form this path. Each sub-path radiating from each node is labeled by an integer. The chromosome code of a path is a string of series integers that represent the labels of sub-paths which are passed through traveling from start node to target node. Two factors are integrated into a fitness function of the proposed genetic algorithm: the feasibility of collision avoidance path and the shortest distance of path. Two examples of known static environment maps are taken in this study with different numbers of obstacles and nodes. Simulation results show the effectiveness and feasibility of the proposed GA using sub-path codes to find optimum path planning for mobile robot.

Keywords: Mobile Robot, Optimization, Genetic Algorithm, Fitness Function, Global Path Planning

الخوارزمية الوراثية التي تستعمل رموز الطرق الثانوية لتخطيط الطريق الالى النقال

الخلاصة:

في هذا البحث , تم اقتراح طريقة جديده لايجاد الطريق العام الامثل للربوت السيار باستخدام الخوارزمية الوراثية. ان خارطة البيئة المعروفة الثابتة كذلك عقدة البداية وعقدة النهاية اللتان تربطان الطريق المراد ايجاده تعطى مسبقاً. العقد المختارة في البيئة المعروفة الثابتة ترتبط فيما بينها بواسطة طرق فرعية .كل طريق عام يمثل بواسطة متوالية من الطرق الفرعية التي تربط العقد المتعاقبة لتكوين ذلك الطريق. اي طريق فرعي مشع من اي عقدة يرمز بعدد صحيح . ان رمز الكروموسوم الخاص بطريق عام هو سلسلة متوالية من الاعداد الصحيحة الخاصة برموز الطرق الفرعية التي يمر خلالها الربوت خلال رحلته من عقدة البداية الى عقدة الاعداد الصحيحة الخاصة برموز الطرق الفرعية التي يمر خلالها الربوت خلال رحلته من عقدة البداية الى عقدة النهاية. عاملان متكاملان اخذا في دالة الصلاحية للخوارزمية الوراثية المقترحة هما امكانية تنفيذ الطريق النهاية. معمرون الطرق مع المعالي من الطرق الفرعية التي يمر خلالها الربوت خلال رحلته من عقدة البداية الى عقدة النهاية. عاملان متكاملان اخذا في دالة الصلاحية للخوارزمية الوراثية المقترحة هما امكانية تنفيذ الطريق النهاية. المعروفة قد تم دراستهما مع اختلافهما في عدد العقد وعدد العوائق. النتائية البيئة الثابتة المعروفة قد تم دراستهما مع اختلافهما في عدد العقد وعدد العوائق. النتائج المحصلة من المحكاة تبين الفعالية والامكانية على التطبيق العملي للخورازمية الوراثية المقترحة الم المان من مجالات البيئة الفعالية والامكانية على التطبيق العملي للخورازمية الوراثية المقترحة التكوي المراق الفرعية لايجاد الفعالية والامكانية على التطبيق العملي للخورازمية الوراثية المقترحة التي المحصلة من المحكاة تبين

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1. Introduction

The mobile robot path planning is an important branch in mobile robot research field. Robot path planning refers to finding a best collision-free path among obstacles from the start place to the target place in a working environment while satisfying some optimization criteria [1].

In general, these methods mainly fall into two types in accordance with the properties of the environment. The first type is off-line global path planning depending on the model of known environments.

The second type is on-line local path planning depending on available sensors that detect the unknown environments [2].

The off-line global method in which the entire information concerning environment is obtained beforehand results in global optimal path with collision free obstacles.

This method requires precise environment model. This means a prior knowledge of the environment must be obtained beforehand. The best path is realized by establishing proper model.

The on-line local method is used when the environment is partially or even completely unknown or when the environment changes with time for the mobile robot. In this case, usually a sensor is used to obtain environment information. Moreover it is required to replan the changed environment that makes the cost too high in order to adapt for the real-time requirement. The local method does not require precise environment model and can deal with uncertain situations in the environment. However, the local path planning methods may not get the global optimization effect due to the use of local information.

Many different methods, such as dijkstra's algorithm [3], potential field method [4], artificial neural networks approach [5,6] particle swarm [7,8]. optimization (PSO) simulated annealing [9], fuzzy expert systems [10], and genetic algorithms [11,12] have been developed to solve this problem. Most of these methods were based on the concept of space configuration. These techniques show a lack of adaptation and a non robust behavior. To overcome the weakness of these approaches researchers explored a variety of solutions [13].

There has been much attention to GAbased methods in recent years because of their success in solving many optimization problems and since we can view path planning as an optimization problem, we expect that GA can reasonably overcome it.

This paper focuses on the path planning method based on the global map. The process of global path planning includes two procedures: set up the environment model and search for the best path. The search criterion is to find out the shortest path when the model is established.

This paper presents a new algorithm, a combination of topological and grid map, to conduct environment modeling, then employs the proposed variable chromosome length GA with new encoding method of the branches radial from each node in the environment.

The remainder of this paper is arranged as follows: Section II describes the problem of the path planning; Section III introduces an overview on GA; Section IV proposes a method of path planning based on the proposed GA; Section V explains how the path planning problem is reformulated to be solved by the proposed GA; Section VI demonstrates simulation results of different environments with a different number of obstacles and nodes; and Section VII concludes this paper and presents some future works.

2. Problem Description

In this problem, we have a mobile robot moving in а known static environment. The environment space has obstacles located in specific manv positions. The mobile robot's mission is to search offline the shortest path to travel from a start node to a target node without colliding with the obstacles that appear on its way.

3. The Genetic Algorithm

The GA was invented by John Holland and developed by his students and colleagues in the 1970s. GAs are global, parallel, robust stochastic search algorithms, based on the principle of natural selection and natural genetic process that combines the notion of survival of the fittest, random search, and parallel evaluation of points in the search space [14].

GA manipulates a collection of potential solutions for a given problem. Each solution is represented as a genome (chromosome) which is basically a string of binary values, letters or numbers. Each chromosome is assigned a fitness value that indicates how successful this particular solution is compared to other chromosomes in the population.

GA starts by random creation of an initial population of chromosomes. It then applies genetic operators such as crossover and mutation, to create new chromosomes (offspring) from existing ones in the population, by either merging two or more parents chromosomes or by modifying an existing chromosome. The selection mechanism for parent chromosomes takes the fitness of the

parents into account, ensuring that the better solution has a higher chance to be selected.

At each generation, the newly generated individuals replace the existing ones. The population is evolved over generations to produce a better solution to the optimization problem [14,15].

4. Proposed Algorithm

A number of necessary preparation steps are needed in order to formulate the path planning problem to a form that GA can deal with, these steps are illustrated as follows;

- a) The known search environment is projected upon a gird map.
- b) The necessary and minimum nodes are chosen on the grid map in order to enable the mobile robot to reach each required place in the environment.
- c) Each node in the gird map of the environment is assigned by a symbol or name.
- d) The available subpaths between nodes are determined (i.e. the nodes linking between each other).
- e) Each radiated subpath (i.e branch) from any node is assigned by an integer.
- f) The coordinate values for each node in the grid map are calculated.
- g) The static obstacles present in the gird map of known search environment are counted.
- h) The starting node and target node are given beforehand in order to establish the required path.

5. Problem Formulation

a) Encoding of Chromosome.

In this paper, the nodes of the map are not used to encode the path. The start node and target node are given beforehand. It is normal that each node in the gird map has one or many radiated sub-paths from it. These bidirectional subpaths connect each node with the other adjacent nodes. In order to illustrate the encoding of the chromosome in the path planning problem, consider an example of a simple map shown below in Figure (1).



Figure (1). Illustrative example for encoding the chromosome

Consider that node-a is the start node and node-g is the target node. As shown in the map, node-a has three radiated subpaths (1), (2) and (3). This means there are three choices to start the path from start node. If the mobile robot passes through subpath (1), the mobile robot reaches to node-b. When it is in node-b, there are also three radiated subpaths from this node. The mobile robot has also three choices and can pass through one of them. If the mobile robot passes through subpath (2), the mobile robot reaches to node-d. Again when it is in node-d, there are six radiated subpaths, if the mobile robot passes through subpath (2) which is radiated from node-d, the mobile robot reaches to node-g which is the target node. The path between start node and target node is a sum of a sequence of

subpaths, so the path illustrated above can be encoded by a string of integers. Each integer represents the label number of the radiated subpath of each node that the mobile robot passes through while traveling from start node to target node. Therefore, the code of the above path is 122. This means when the mobile robot is present in start node it passes through subpath(1) then when it is in second node it passes through subpath(2) and when it is in third node it passes through subpath(2). The first integer in the string represents which subpath outs from start node and the last integer in the string represent the subpath number of the node before the target node.

Since nodes do not have the same number of subpaths, we find the node which has the maximum subpaths in the environment. The number of maximum subpaths is taken as a reference in order to make each gene in the chromosome have equal alleles (instances).

So, for the nodes that have a number of subpaths less than the number of maximum subpaths, we assign some or all subpaths by one or more label integers to indicate to the same subpath as shown in Figure(2).



Figure(2). Illustrate the labeling method of subpaths

In this case two or more integers may be indicated to the same subpath of a certain node. We do this arrangement in order to make all genes in the chromosome have a fixed number of instances and genetic operations to be implemented easily.

The maximum chromosome length is equal to the number of map nodes. This result is straight forward but the chromosome length can be reduced to save the computation power. One can observe from the map topology that the optimal path to reach the target node is proportional to the number of obstacles. When the number of static obstacles is equal to *n*, the shortest path consists of at most (n+2) nodes or of (n+1) subpath or linear segment. This relation assumes that the obstacle shape is not complex and can be considered as mass point. When there are no obstacles in the environment n=0, the shortest path consists of a one subpath or liner segment from the start to target node. If there is one obstacle in the environment, the shortest path consists of two subpaths or linear segments. Thus, the number of chromosome length will be determined by the following equation (1).

L=n+1 (1) Where, L is the number of genes in the chromosome and n number of static obstacles. However, when the number of obstacles in the map is more than the number of nodes in the map, we consider the number of nodes in the map when we determine the maximum chromosome length.

b) Initial Population.

In the proposed GA the chromosome length is variable because the optimal path depends upon the given start node and target node.

The maximum chromosome length is determined from the number of obstacles and number of nodes in the map of the environment. Therefore, when we create a new chromosome, we choose a random length for it between 2 and L. So, each chromosome created in the initial population has its specific chromosome length. The value of chromosomes' length is stored in an additional location in the chromosome. Each gene in the chromosome is filled by a random integer between 1 and max subpath. Figure (3) details illustrates the of proposed chromosome.



Figure (3). The details of the chromosome

c) Creation Operation.

The creation operation is unique in that it does not require any existing chromosome.

It creates an entire new chromosome in the same way that a chromosome in the initial population is created. This operation is applied to create a predefined number of new chromosomes for new population in each generation.

d) Selection Operation.

In the proposed GA, a tournament selection is used to create a new method. population. In this two chromosomes are chosen at random from the population. A random number r is then chosen between 0 and 1. If r < k(were k is a parameter, for example 0.75), the fitter of the two chromosomes is selected to be a parent chromosome, otherwise the less fit chromosome is selected. The two are then returned to the original population and can be selected again. Elitist mode is also used where a certain number of the best chromosomes of each generation are kept in the next generation, so as to improve the efficiency of the proposed GA.

e) Crossover Operation.

During the crossover operation, two chromosomes that have an efficient fitness value are randomly selected as parents based on the selected method. Each parent has its chromosome length. The crossover site in each parent is selected randomly between 1 and chromosomes length-1. The crossover operation can be implemented on the two parents, if the crossover operation does not result in any child of chromosome length more than the maximum length.

Otherwise mutation operation is made for these two parents. Figure (4) illustrates the crossover operation.



Figure (4). The crossover operation

f) Mutation Operation.

The parent chromosome is selected based on the fitness measure. Each gene in the chromosome may be mutated with a very small probability. When a gene is required to be mutated, another integer value between 1 and number of maximum subpaths is chosen randomly to replace the original gene. Figure (5) illustrates the mutation operation.



Figure (5) The mutation operation

h) Fitness and Evaluation.

The most difficult and important part in GA is the fitness measure. The success of GA to find the optimal or best solution depends totally on the fitness measure. Each chromosome in the population is assigned by a number representing the fitness value. The value of fitness is proportional to goodness degree of the chromosome to solve the underlying problem.

In our problem the shortest path between start node and target node is an optimal path. Thus, the fitness measure must be synthesized to guide the proposed GA to find this shortest path. Since each path consists of many segments of straight lines. The distance can be calculated by equation (2).

Distance =
$$\sum_{i=1}^{n+1} \sqrt{(x_{i+1} - x_i)^2 + (y_{i+1} - y_i)^2}$$

.... (2)

Since, each path begins from the start node, the first integer in the chromosome represents the first subpath which leads to the first intermediate node. The sequential integers of the chromosome also represent subpaths which lead to a sequence of intermediate nodes. Each path will be checked, if one intermediate node is the target node itself, the remaining of the chromosome will be neglected and the chromosome length will be also corrected. In this case the chromosome will not get punishment because the path is feasible.

If none of the intermediate nodes is a target node and the last subpath will not lead to the required target node, this chromosome will get a big punishment to decrease its fitness value because it is not feasible but it remains in the population.

If the last subpath leads to the target node, this chromosome will not get any punishment because it is feasible. The fitness function that would be minimized is illustrated as in equation (3).

 $Fitness = \frac{1}{Distance + Punishment}$ (3)

6. FINDING THE OPTIMAL PATH

In this paper, two examples of known static environments are suggested and expressed by two complex maps with relatively large number of obstacles and nodes. We suggest a specific number of nodes in each environment with the assumption that they are sufficient to reach any required place. Moreover, the mobile robot moves in these two environments without colliding with the existent obstacle.

Example-1: The environment map of this example is shown in Figure (6).



Figure(6). Environment map of example -1

When we apply the steps of the proposed algorithm on this map, we find the minimum number of required nodes is 35 and the number of obstacles in the environment is 30. The coordinates' values of any node and the nodes linking to it through the subpath are shown in Table (1).

Table (1). The coordinates values of each node and the terminal nodes of their subpaths for example-1.

label	lue (m)	lue (m)	Rad nod	liated les ag	subp gainst no	aths f their des	rom e term	each inal			
lode	-Va	-Va		Su	ıbpatl	aths codes					
4	Х	Y	1	2	3	4	5	6			
0	0.3	7.3	1	2	3	1	2	3			
1	0.93	9.7	28	2	0	28	2	0			
2	1.75	7.75	0	1	29	4	0	1			
3	0.7	5.2	0	4	5	0	4	5			
4	2.3	5.87	8	27	2	3	5	8			
5	2.25	3.87	7	4	3	6	7	4			
6	2.3	2.2	11	10	5	11	10	5			
7	3.72	3.87	10	9	8	5	10	9			
8	3.72	5.75	23	25	27	4	7	23			
9	5.57	4.8	12	16	17	23	7	12			
10	4.37	2.3	11	13	12	7	6	11			
11	5.2	0.84	14	10	6	14	10	6			
12	6.25	3.5	13	16	9	10	13	16			
13	7.2	1.88	15	16	12	10	5	15			
14	6.63	0.7	13	11	13	11	13	11			
15	9	2	33	16	13	33	16	13			
16	8.22	3.87	34	18	9	12	13	15			
17	6.37	5.87	18	22	9	18	22	9			
18	7.7	5.87	20	19	17	16	20	19			
19	7.7	7.3	21	31	22	18	21	31			
20	9.15	6.25	34	21	18	34	21	18			
21	9.15	7.3	32	31	19	20	32	31			
22	6.37	8.13	19	24	25	23	19	24			
23	5.2	5.75	22	8	9	22	8	9			
24	6.25	9.57	31	26	22	31	26	22			
25	4.65	8.23	22	26	8	22	26	8			
26	4	9.7	24	30	28	27	24	30			
27	3.2	7.48	26	29	4	8	26	29			
28	2.4	9.7	26	30	1	29	26	30			
29	2.8	8.5	28	2	27	28	2	27			
30	3.2	10.7 5	26	28	26	28	26	28			
31	8.8	8.5	21	24	19	21	24	19			
32	10.3	7.07	21	34	21	34	21	34			
33	10.3	3.35	34	15	34	15	34	15			
34	9.4	5.06	32	20	16	33	32	20			

Start Node	Intermediate Sub paths and Intermediate nodes	Target node	The distance of path	Number of runs	Number of success Runs	Average of generation for success runs
1	$5, 4, 6, 6, 3, 2, 6$ $\rightarrow 2 \rightarrow 4 \rightarrow 8 \rightarrow 23 \rightarrow 9 \rightarrow$	15	12.8333	10	10	47
24	$4, 4, 3, 5, 4$ $26 \rightarrow 27 \rightarrow 4 \rightarrow 5$	9	10.1293	10	10	54
0	$2, 4, 6, 6, 3, 2, 1$ $\rightarrow 2 \rightarrow 4 \rightarrow 8 \rightarrow 23 \rightarrow 9 \rightarrow 16$	34	11.8859	10	10	190

are used (retain two best individuals), Table (2). Some optimal paths for example-1. Creation rate $P_r=0.2$, Crossover rate $P_c = 0.65$, Mutation rate $P_{m}=0.15$, Population size=100, Maximum Generation 1000 for each run. The results of some optimal paths between a certain start and target nodes are shown in Table (2).

> Figures (7, 8 and 9) show the optimal paths on the map environment.



Figure(7). The optimal path from node 1 to node 15 example-1



The chromosome of the proposed GA is represented by integer string, each subpath is represented by one integer, the maximum number of allele= 6, the chromosome length is variable with the maximum value 31 and minimum value 2. Tournament selection with elitism strategy In fact, the environment map of example-1 is relatively complex with large number of nodes and obstacles. However, the simulation results in Table (2) show that the proposed GA can find the optimal paths for different start nodes and target nodes. Moreover, the results show that the GA has succeeded to find the optimal paths with probability 100% because it did not fail in all runs. In addition, the results show that the proposed algorithm is able to find a path with little iterations (less than 10 generations) in the evolutionary stage of the GA.



Figure (9). The optimal path from node 0 to node 34 for example-1

Example-2: The environment map of this example is shown in Figure (10).



Figure(10). Environment map of example -2

When we apply the steps of the proposed algorithm on this map, we find the minimum number of required nodes is 49 and the number of obstacles in the environment is 74. The radiated subpaths from each node and the terminal node of each subpath are shown in Table (3). The coordinate's values of each node are shown in Table (4).

Table(3) The radiated subpath from each node and the terminal nodes of subpaths for example-

label	Radiated subpaths from each nodes against their terminal nodes											
Vode				Sub	paths	s code	es					
~	1	2	3	4	5	6	7	8	9			
41	40	42	31	40	42	31	40	42	31			
42	43	40	41	43	40	41	43	40	41			
43	45	44	42	40	45	44	42	40	45			
44	45	46	43	45	46	43	45	46	43			
45	38	39	47	46	44	43	40	32	33			
46	47	44	45	47	44	45	47	44	45			
47	46	45	39	46	45	39	46	45	39			
48	47	39	36	37	47	39	36	37	47			

label	Radiated subpaths from each nodes against their terminal nodes										
lode				Sub	paths	s code	S				
2	1	2	3	4	5	6	7	8	9		
0	5	4	2	1	5	4	2	1	5		
1	0	2	8	15	0	2	8	15	0		
2	0	7	8	1	0	7	8	1	0		
3	12	6	5	12	6	5	12	6	5		
4	5	6	9	7	0	5	6	9	7		
5	3	6	4	0	3	6	4	0	3		
6	3	12	21	20	11	9	7	5	3		
7	4	9	10	13	8	2	4	9	10		
8	2	7	13	14	15	1	2	7	13		
9	6	11	10	7	4	6	11	10	7		
10	9	18	17	13	7	9	18	17	13		
11	6	20	19	18	9	6	20	19	18		
12	21	6	3	21	6	3	21	6	3		
13	7	10	17	14	8	7	10	17	14		
14	8	13	17	16	29	15	8	13	17		
15	1	8	14	29	1	8	14	29	1		
16	14	17	28	29	14	17	28	29	14		
17	10	18	25	26	27	28	16	14	13		
18	11	19	25	17	10	11	19	25	17		
19	20	24	18	11	20	24	18	11	20		
20	21	23	19	11	21	23	19	11	21		
21	22	23	20	6	12	22	23	20	6		
22	37	23	21	37	23	21	37	23	21		
23	22	37	36	35	24	20	21	22	37		
24	23	35	25	19	23	35	25	19	23		
25	24	35	34	26	17	18	24	35	34		
26	25	34	27	17	25	34	27	17	25		
27	26	34	33	28	17	26	34	33	28		
28	17	27	33	30	29	16	17	27	33		
29	15	14	16	28	30	31	15	14	16		
30	28	33	32	40	31	29	28	33	32		
31	29	30	40	41	29	30	40	41	29		
32	33	45	40	30	33	45	40	30	33		
33	34	38	45	32	30	28	27	34	38		
34	35	38	33	27	26	25	35	38	33		
35	23	36	39	38	34	25	24	23	36		
36	37	48	39	35	23	37	48	39	35		
37	48	36	23	22	48	36	23	22	48		
38	32	45	43	42	41	31	30	32	45		
39	40	42	31	40	42	31	40	42	31		
40	42	31	40	42	31	40	42	31	40		

Y Axis	9.81	9.44	9.7	10.31	10.57	11	9.81	10.69	10.66	10.05			
X Axis	8.32	2.2	0.58	1.44	2.39	4.07	5.07	5.7	72.9	10.05			
Node label	39	40	41	42	43	44	45	46	47	48			
Y Axis	4.57	5.07	5.07	4.7	7.11	8.33	8.44	7.83	7.44	7.57	8.44	8	8.83
X Axis	5.58	4.56	3.32	0.85	1.82	0.46	3.19	4.69	6.82	8.45	9,57	11.07	6.57
Node label	26	27	28	29	30	31	32	33	34	35	36	37	38
Y Axis	2.85	3.31	2.56	3.95	3.7	3.31	3.31	3.07	3.92	4.94	5.07	4.46	4.32
X Axis	4.55	2.69	1.07	2.44	4.58	6.82	7.94	9.06	10.07	11.07	10.07	8.57	6.95
Node label	13	14	15	16	17	18	19	20	21	22	23	24	25
Y Axis	0.31	1	1.07	1.07	1.07	0.73	2.08	1.57	1.82	2.33	3.07	2.81	2.57
X Axis	4.82	2	4.07	10.07	5.94	8.3	9.06	5.45	3.32	7.2	6.32	7.81	10.57
Node				~	4	2	6	7	8	6	10	11	12

Table(4). The coordinates values of each node for Example-2

The chromosome of the proposed GA is represented by an integer string, each subpath is represented by one integer, the maximum number of allele= 9, the chromosome length is variable with maximum value 49 and minimum value 2. Tournament selection with elitism strategy is used (retain two best individuals), Creation rate $P_r=0.2$, Crossover rate, $P_c=0.65$, Mutation rate, $P_m=0.15$, Population size=100, Maximum generation is 3000 for each run.

The results of some optimal paths between certain start nodes and certain target nodes are shown in Table (5). Figures (11,12,13) show the optimal paths on the map of environment.

Really, the environment map of this example is a complex map with 49 nodes and 74 obstacles. This means there are many available paths between any start node and target node. These paths are competing between each other through the adaptation process of GA according to fitness measure. In addition, these paths have approximated distances which make the competing not easy and need relatively large generations.

So, we employ it to test the ability and the efficiency of the proposed algorithm to solve complex path planning problems.

The results of this test are shown in Table (5). Again the proposed GA succeeds to find different optimal paths for different start nodes and target nodes. Moreover, all 10 runs result in the global optimal path for each required path.

The average of generations for succeeded runs is more than that in example-1 because the map is more complex as well as that the available paths are longer and the number of segments of the paths is larger too. So, more time is needed for searching about global optimal path because there is at least one path, connecting the starting node to target node since all nodes are connected together.

However, the potentials of the proposed GA and the high speed of the new computer processors are sufficient to find the global optimal paths in reasonable generations and time. Therefore, the proposed GA can successfully be implemented online to find the global

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optimal path for the mobile robot in complex environments.

Average of generation for succeeded runs	UUC	0.67	163	661	180		
Numberof succeeded runs	U1	10	U1	10	10		
Number of runs	10	10	10	10	10		
The distance of path	13.851139		13.14582		12.035		
Target node	Ţ	41	97	48	47		
Intermediate Sub paths and Intermediate nodes	8, 5, 9, 4, 6, 4, 5	$6 \rightarrow 11 \rightarrow 18 \rightarrow 17 \rightarrow 28 \rightarrow 30 \rightarrow 31$	7,3,3,3,2,2,2	$1 \rightarrow 8 \rightarrow 13 \rightarrow 17 \rightarrow 25 \rightarrow 35 \rightarrow 36$	6, 3, 2, 3, 2, 2, 3, 2	$0 \longrightarrow 4 \longrightarrow 9 \longrightarrow 11 \longrightarrow 19 \longrightarrow 24 \longrightarrow 35$	
Start node	,	r		1	0		





Figure (11). The optimal path from node 3 to node 41 for example-2



Figure (12). The optimal path from node 1 to node 48 for example-2



Figure (13). The optimal path from node 0 to node 47 for example-2

7. CONCLUSIONS & DISCUSSION

In this paper, a new path planning method based on variable chromosome length GA is proposed to find off line the optimal path in two-dimension known static environments. The grid is used to establish the work environment of mobile robot. The sequence integers of subpaths labels are used to encode the chromosome of the proposed GA. The proposed fitness function and punishment rules are sufficient to lead the process of adaptation of GA to the global optimal path. The simulation results show the high efficiency of the algorithm for path planning of mobile robots in known static environment map.

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