Path Planning of Mobile Robot Based on Genetic Algorithm and Gene Rearrangement

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***Abstract*—In this paper, a mobile robot path planning algorithm based on the rearrangement of gene is proposed for genetic algorithm and applied to solve the problem of mobile robot path planning. Firstly, it needs to build the robot path with the multi-plane model, and the genetic algorithm is used to search the optimal or sub optimal path. Then, with a new algorithm for the route of quadratic optimization, making the large rotation angle of optimization as a smooth path close to the flat angle under the premise of guarantee without intersecting any obstacles. The simulation results show that the algorithm combined with the classical genetic algorithm is better than the basic genetic algorithm, which can not only reduce the complexity of the genetic algorithm but also shorten the path length to obtain the relatively optimal path without collision.**

***Keywords*—Genetic algorithm, mobile robot, path planning, smoothing path**

I. Introduction

In recent years, with the development of the economy and technology, mobile robots have been widely used in the intelligent service, environment exploration, transportation and so on. To improve the work efficiency, it is an important study problem for researchers to find the optimal path when the robot moves from a starting point S to a destination point Q. For the continuous domain range, path planning is widely used in many fields of intelligent control, such as path planning of robot manipulator[1,2], trajectory planning of aircraft[3,4,5], cruise missile path planning[6] and so on. The optimal path is a collision free path with the shortest distance, the least energy consumption and the relative optimal path in a bounded range. However, the relatively optimal or sub-optimal path values are not identical due to the robot mechanical structure, different constraint conditions and application environment, so it's necessary to predict path planning environment and adapt to environmental changes. According to the different time, starting point and performance of the robot, if use the accurate algorithm to determine an optimal paths, it is necessary to solve the exponential growth of the path with the increase of the number of nodes, which is cumbersome, consuming a lot of running time and reducing the work efficiency. Therefore, genetic algorithm(GA), Ant colony algorithm, Annealing algorithm and other natural heuristic algorithms are used for path planning. Because the genetic algorithm has a good ability to optimize globally and to handle constraints, it solves the problem that of traditional optimization methods cannot solve such as the updating of network topology. Because of its implied parallelism, it has been widely applied in artificial neural network, fuzzy controller optimization and image processing etc.. Therefore, more and more scholars are engaged in the study of genetic algorithms. Jaesung Lee[7] set out the optimization of the initial population to improve the traditional genetic algorithm. As for genetic algorithm-based robot path planning, they proposed an effective initialization method. Based on the theories of the genetic algorithm (GA), the team of Adem Tuncer and Mehmet Yildirim[8] had proposed a new mutation operator and applied to the path planning problem of mobile robots in dynamic environments. The method have made some achievements compared with the previous ones. A GA with the new operator find converges more rapidly than the other methods do. The improved method could accomplish the task of path optimization in a shorter execution time. However, taking account of the safety and energy consumption of robot movement, this paper proposes a path optimization operator based on gene rearrangement for genetic algorithm, which can reduce the rotation angle of the robot, increase the smoothness of the path and reduce the energy consumption, at the same time, a shorter path than the relative optimal path was achieved. Finally, the simulation results proved the feasibility of the new operator in path planning.

The rest of the paper is organized as follows: Section 2 presents the path planning genetic algorithm; path optimization

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operator of the gene rearrangement is introduced in Section 3; simulation and comparison are presented in Section 4; finally, conclusions are sum-up in Section 5.

II. PATH PLANNING OF MOBILE ROBOT BASED ON GENETIC ALGORITHM

The following steps are used to solve the problem by applying genetic algorithm (GA): A chromosome coding method is designed; Population initialization; Evaluating fitness function for initial population fitness; The feasible solution is selected by selection, crossover and mutation operator. According to the principle of the fittest, the best value of the expectation is obtained through global search.

A. Environment modeling

The goal of path planning is to move the mobile robot from the starting point S to the destination point Q to find an optimal path. Using global path planning to get a collision-free path with constrained conditions. In this paper, the multi-faceted model representation is used to represent the environmental space. The motion space of the mobile robot is represented by two-dimensional planar graphics, and the vertices (x, y) of the obstacle are recorded with a circular list. The obstacle is set as static, random and known arbitrary irregular polygon. Compared with raster method, it is easy to solve the problem of complex environment information, and it takes fewer resources. In this paper, the environment model with different complexity and different rules is designed from simple to difficult. As shown in the following Fig. 1. It is assumed that the safe distance is D between the robot and the obstacle, and the process of the robot from the starting point to the destination point is treated as a particle.

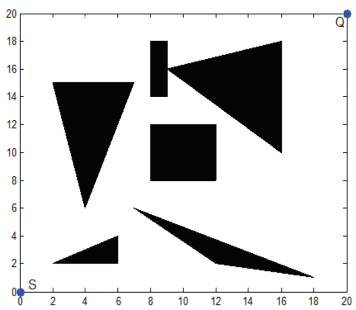

Fig. 1. Multi-plane model environment representation.

B. Chromosome coding

The encoding of chromosomes includes real coding, binary coding and tree coding, which influences the efficiency of path planning to some extent. In this paper, the real number encoding method is used to express the coordinates of the real points, and the path coordinates are encoded directly. The path of the robot is composed of several line segments, each of which is represented by a line of the indefinite starting point and end point connected to the node. The presented method is shown in Fig. 2. Symbol Ω represents a collection of a number of intermediate nodes. Suppose there are a total of n nodes, a point $p_i\,(i=1,2,3,\cdots,n)$ represents the i-th gene on the chromosome, that is $\Omega=\{p_1,p_2,\cdots,p_n\}$.

There are several advantages of real coding in relation to binary coding: (1) Using real numbers as chromosomes to participate in the genetic operation, eliminating time-consuming coding and decoding process; (2) Eliminate the "hamming cliff problem" in binary code; (3) Using real-coded chromosomes, there are many kinds of crossover mutation operators to breed new individuals, which improves the search efficiency of the algorithm. These points are processed in various ways in the next step to obtain the optimal path for robot motion.

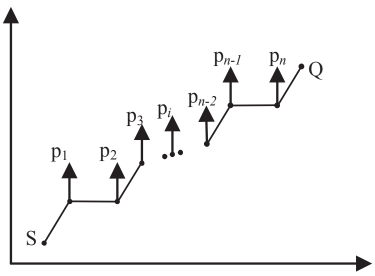

Fig. 2. Chromosome genes encoded by real numbers.

C. Population initialization

To design the optimal path for the mobile robot, the population must be initialized first. Because the initial path is randomly generated, so feasible path and unreachable path are included in the continuous domain, although the genetic operator can eventually find a relatively optimal path. But in the global search, the unreachable path would reduce the search efficiency, and the two unreachable paths are likely to produce unreachable paths when the chromosomes cross.

Therefore, this paper set an initial population in the generation of the path to retain the escape of obstacles and re-select the path encountered obstacles to speed up the convergence rate. The initialization method uses a single point of production, setting (x_0,y_0) as the starting point, (x_n,y_n) as the destination point, and meet $x_n \ge x_0, y_n \ge y_0$. The current point is i, while the $i+1$ point is produced. The following two conditions are available (equal to the probability of occurrence): (1) where $x_{i+1}\in[x_i,x_n]$, $y_{i+1}\in[y_0,y_n]$

$$\begin{cases} x_{i+1}=(x_n-x_i)*rand+x_i \\ y_{i+1}=(y_n-y_0)*rand \end{cases} \tag{1}$$

(2) where $x_{i+1}\in[x_0,x_n]$, $y_{i+1}\in[y_i,y_n]$

$$\begin{cases} x_{i+1}=(x_n-x_0)*rand \\ y_{i+1}=(y_n-y_i)*rand+y_i \end{cases} \tag{2}$$

Where $rand$ is a random function which can produce a random number of between 0 ~ 1 in MATLAB.

D. Fitness function

The fitness function is the evaluation of the adaptability of individual in the environment. However, after the mutation and crossover, there is a low fitness of individual who across the obstacle. So the fitness of the individual through the obstacle is set to 0, and the fitness of the other individual is expressed by (4). So the adaptive operator can be divided into two kinds of situations: If the individual passes through the obstacle, the fitness can be obtained by (3); if not through the obstacle, by (4).

$$F_j = 0 \tag{3}$$

$$F_j = \frac{C}{\sum_{i=1}^{n-1} \sqrt{(x_{i+1} - x_i)^2 + (y_{i+1} - y_i)^2}} \tag{4}$$

Where C is any constant, there is greater adaptability of the individual, there is higher fitness value. The fitness value is proportional to the probability that an individual is retained to the next generation.

E. Genetic operator

1) Select operator: By using the fitness function to choose the better gene reservation and inherit to the next generation. This paper adopts the way of roulette to ensure that the individual who passes the obstacle is not selected.

2) Crossover operator: A single point crossover method is used to ensure whether an individual crosses by means of generating random numbers. Randomly produces an integer within the range of genes as the starting point of the intersection, and randomly produces an integer in the range of populations as an object to be crossed. Assuming that the intersection of the *i*-th individual is *k* and the cross object is the *j*-th individual, then the new individual after the crossover of the *i*-th individual can be shown in Fig. 3:

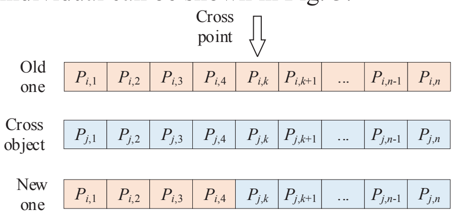

Fig. 3. Single point crossover method.

3) Mutation operator: Determine whether an individual is mutated by creating a random number. To ensure the diversity of the population, an integer that is within the range of the number of genes is randomly generated as a variation point so that a small change in the position on the chromosome results in a new gene fragment. The mutation probability is generally between 0.001 ~ 0.4, and the mutation probability is $P_m = 0.01$ obtained in this paper.

III. PATH OPTIMIZATION OPERATOR BASED ON GENE REARRANGEMENT

The optimization operator is based on individual gene characteristics and environmental characteristics of individual genes to determine, select, re-allocation and other optimization operations to achieve further enhance the individual fitness to improve the genetic algorithm convergence rate. The optimization operator mainly consists of three parts: primary optimization operator, immutable gene judgment operator and variable gene redistribution operator. Through the above three steps of the cycle operation, the path optimization task was realized finally. The operation process is shown in Fig. 4:

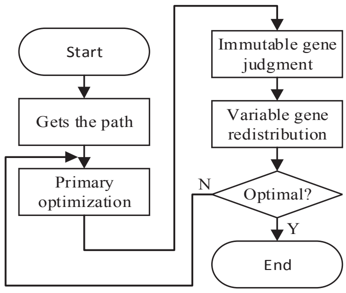

Fig. 4. Optimization flow chart.

A. Primary Optimization Operator

The primary optimization operator corrects the polyline in the path when the lines of the ends of the polyline are not obstructed to reduce the path length, the process is shown in Fig. 5. Assuming that the current path is a folded segment of S、$p1$、$p2$、Q, the segment SQ does not pass through obstacles, then the path is corrected to the segment SQ, $p1$、$p2$ two points evenly distributed between the segment SQ, two points are set to $p1', p2'$.

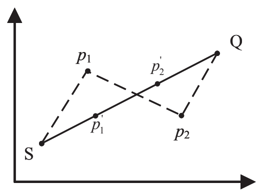

Fig. 5. Path correction diagram.

Set a path $P = \{p_1, p_2, p_3, \cdots, p_n\}$, where the coordinate point is $(x_i, y_i), i = 1, 2, 3, \cdots, n$, then the optimization of the path after the point i is completed in the following steps:

STEP1: Sequentially detects line segment between p_i and $p_n, p_{n-1}, p_{n-2}, \cdots, p_{i+2}$, if p_k $(k = i+2, i+3, \cdots, n)$ does not pass through any obstacles, then proceed to the next step;

STEP2: The Connecting line between p_i and p_k is considered as the new path of the individual, the other points between two points are evenly distributed on the line. Then the coordinates of the j point on the line can be expressed as:

$$\begin{cases} x_j = \dfrac{j*(x_k - x_i)}{k-i} + x_i \\ y_j = \dfrac{j*(y_k - y_i)}{k-i} + y_i \end{cases} \tag{5}$$

STEP3: After traversing all the points on the path in step 2, the path optimized by the primary optimization can be obtained. Where the vertex of the fold line in the path is an immutable gene, and the point on the line segment is variable genes.

After the primary optimization of the path distance is significantly shorter, smoothness has also been a certain increase. However, there is still a problem that the distribution of the variable gene points is not appropriate, resulting in a path with a large rotation angle, which not only consumes the kinematic energy of the robot but also increases the length of the path.

B. Immutable Gene Judgment Operator

After optimization of the path through the primary optimization operator, although the fitness of the individual has been improved obviously, the large rotation angle still exists, so further optimization of the path is needed. The analysis of the primary optimization operator shows that the reason that the path can not be further optimized is that the position distribution of the variable gene does not conform to the condition of further optimization, it is easy to find that only find a way to control the variable gene distribution can greatly enhance the probability that the variable gene is in the optimal position.

In this part, the work of determining the coordinate and quantity of the invariant gene in the path is completed. The vertex is judged by calculating the angle between the points in the path and the connection between the two adjacent points. If the angle is less than 180, it is considered that the point is the vertex, that is, the invariant gene, otherwise the variable gene. The angle between the two sides of the *i+1-th* point is calculated by (6):

$$\theta_{i+1} = arc\cos\left(\frac{(x_i - x_{i+1})(x_{i+2} - x_{i+1}) + (y_i - y_{i+1})(y_{i+2} - y_{i+1})}{\sqrt{((x_i - x_{i+1})^2 + (y_i - y_{i+1})^2)((x_{i+2} - x_{i+1})^2 + (y_{i+2} - y_{i+1})^2)}}\right) \tag{6}$$

C. Immutable Gene Judgment Operator

The control of variable gene distribution is the most critical step of the whole optimization operator, and the optimal distribution position of the variable gene can achieve the best results.

Assume that the path after the primary optimization operator is shown in Fig. 6 (a). Black squares are obstacles. It can be seen from the figure that the starting point of the path is S, the end point is Q, and the middle is composed of seven nodes, namely k_1、k_2、p_1、p_2、k_3、k_4、k_5, where p_1、p_2 are immutable genes, and k_1、k_2、k_3、k_4、k_5 are variable genes. It can be seen that the further optimization of the operation can not be achieved due to the unreasonable distribution of the variable gene position. So this part will achieve the re-allocation of variable genetic location, and control its distribution position. The path after redistribution is shown in Fig. 6 (b). The corner of the node p_1 is larger, so the number of the variable genes around it is significantly greater than p_2. The path which shown in Fig. 6 (c) can be obtained by further optimizing the path shown in Fig. 6 (b) using the primary optimization operator. It can be seen that after the redistribution of variable genes lead to a shorter path and a smaller corner by further optimization. According with the principle of shortest path distance and minimum energy consumption.

The relative optimal path is shown in Fig. 6 (d) after several optimization according to the above method. Compared with Fig. 6 (a) and (d), it can be seen that the optimized path is obviously better than the original path.

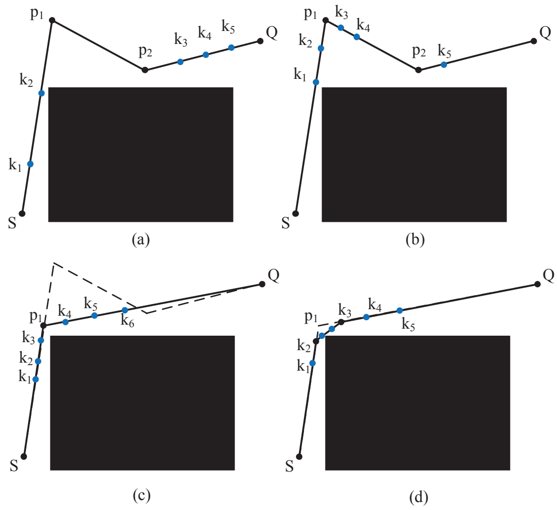

Fig. 6. Optimization process diagram.

According to the above, the realization of the operator consists of three parts: the distribution of the number of mutable genes around the immutable gene, the distribution of the number of mutable genes on both sides of the immutable gene, and the calculation of the variable genetic coordinates after redistribution.

1) The distribution of the number of variable genes around the immutable gene: The distribution of this part mainly considers the influence of the path angle size on the variable gene quantity distribution. The larger the path angle, the greater the energy consumption of the robot moving. Therefore, the higher the probability of allocating the number of variable genes. So this section can be implemented in the following steps:

a) Step1: The number of variable genes was obtained from the previous step. It is assumed that the number of genes is *n* (including the starting point and the termination point) and the number of the invariant genes is *k*, and the number of variable genes is $m = n - k$.

b) Step2: The distribution of mutable genes is randomly assigned by roulette according to certain probabilities. If the rotation angle of the invariant gene is $\theta = [\theta_1, \theta_2, \theta_3, \cdots, \theta_k]$, then the probability of assigning the *i*-th immutable gene to a variable gene is as follows (7):

$$P_i = \frac{\theta_i}{\sum_{i=1}^{k}\theta_i} \tag{7}$$

c) Step3: The number of randomly assigned variable genes can be obtained by the roulette method. And the probability can be calculated by (7).

2) The distribution of the number of mutable genes on both sides of the immutable gene: In order to ensure that the variable genes are optimally distributed in the optimal location of the path optimization, the quantitative distribution of variable genes on both sides of the invariant gene is needed after the variable gene quantity is completed. Because the path segment length of the two sides of the invariant gene is not the same, and there may be a large gap in length. Therefore, the distribution of variable genes must take into account the influence of the length of the two sides of the invariant gene.

The section still allocates the number of variable genes by roulette. The probability of selecting the left side of the *i+1*-th immutable gene is P_l and the probability of the right side being selected is P_r. The probability that the variable gene is distributed on both sides of the invariant gene can be computed by (8).

$$\begin{cases} P_l = \dfrac{\sqrt{(x_{i+1}-x_i)^2+(y_{i+1}-y_i)^2}}{\sqrt{(x_{i+1}-x_i)^2+(y_{i+1}-y_i)^2}+\sqrt{(x_{i+2}-x_{i+1})^2+(y_{i+2}-y_{i+1})^2}} \\ P_r = \dfrac{\sqrt{(x_{i+2}-x_{i+1})^2+(y_{i+2}-y_{i+1})^2}}{\sqrt{(x_{i+1}-x_i)^2+(y_{i+1}-y_i)^2}+\sqrt{(x_{i+2}-x_{i+1})^2+(y_{i+2}-y_{i+1})^2}} \end{cases} \tag{8}$$

3) The calculation of the variable genetic coordinates after redistribution: The calculation of variable gene coordinates is divided into two parts: the left side and the right side of the immutable gene. Assuming that the left of the *i+1*-th immutable gene is p_i, the midpoint of the line between p_i and p_{i+1} is p_l, then the left variable gene position is distributed evenly between p_l and p_{i+1}. Similarly, assuming the right of the *i+1*-th immutable gene is p_{i+2}, the midpoint of the line between p_{i+1} and p_{i+2} is p_r. If the left variable gene number is n and the right variable gene number is m, then the coordinates of the *k*-th variable gene on the left or right can be computed by the formula (9).

$$\begin{array}{lll} left & \begin{aligned} x_k &= \frac{k*(x_{i+1}-x_i)}{2(n+1)} + \frac{x_{i+1}+x_i}{2} \\ y_k &= \frac{k*(y_{i+1}-y_i)}{2(n+1)} + \frac{y_{i+1}+y_i}{2} \end{aligned} & k=1,2,\cdots,n \\ right & \begin{aligned} x_k &= \frac{k*(x_{i+2}-x_{i+1})}{2(m+1)} + x_{i+1} \\ y_k &= \frac{k*(y_{i+2}-y_{i+1})}{2(m+1)} + y_{i+1} \end{aligned} & k=1,2,\cdots,m \end{array} \tag{9}$$

IV. SIMULATION EXPERIMENTS

In order to confirm the effectiveness of the above algorithms, the simulation experiments were carried out in three different environments: irregular environment (IE), narrow winding environment (NWE) and complex maze environment (CME). The initial environment consists of a coordinate system, and the shaded part is an obstacle area. GA parameters are set as follows: population size is 100; crossover probability is 0.8; mutation probability is 0.3; evolutionary algebra is 30 generation.

A. Irregular environment

Fig. 7 is the path planning for an irregular environment, where path 1 is the path after a primary optimization, and path 2 is the two optimized path after the gene rearrangement. (0, 0) point as the starting point, (20, 20) point as the destination point. It can be seen from the graph that after two times optimization, the path is significantly shorter than the previous path, the smoothness is higher, and the point of the variable gene is distributed around the invariant gene point.

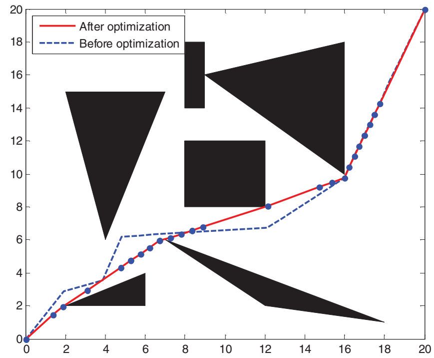

Fig. 7. Smooth path in irregular obstacle environment.

B. Narrow winding environment

Fig. 8 is the path planning under the narrow winding environment, it can be seen that using the algorithm mentioned above to minimize the large rotation angle. Not only increases the security of the robot, but also reduces the energy consumption. And can be seen from the figure, the larger the corner where the more concentrated distribution of gene points.

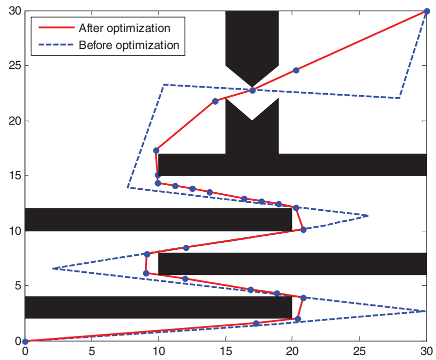

Fig. 8. Smooth path in narrow winding environment.

C. Complex maze environment

Fig. 9 is the path planning in complex maze environment. Firstly, a better path is found by genetic algorithm, and then the path optimization operator of gene rearrangement can be optimized to approximate the angle of the larger path. As shown in Figure 9, from the starting point (0, 0) to the end point (45, 45), the larger the corner, the more densely the gene points. A path with a sharp corner (Before optimization) is optimized to a smoother path (After optimization) through the redeployment of the gene point.

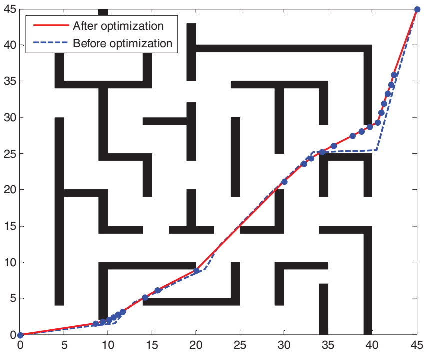

Fig. 9. .Smooth path in complex maze environment.

According to the above simulation diagram to draw TABLE I.

TABLE I. DATA COMPARISON TABLE

#	Path length		Angle sum（degree）	
	Before optimization	***After optimization***	***Before optimization***	***After optimization***
IE	31.5238	29.9951	216.0551	72.0687
NWE	135.9031	87.6393	744.6351	634.4359
CME	71.4325	67.9287	236.6041	108.4325

From the date of table can be seen, no matter how complex the environment is, our path optimization operator not only to short the path again, but also to greatly reduce the rotation angle to increase the security of the robot. From the tabular data, we can see that the algorithm is superior to the standard genetic algorithm in both path length and turning angle. The main reason is that this paper is primarily aimed at the path optimization operator, thus speeding up the speed of evolution, and reducing the path length in various environments based on genetic algorithm.

V. CONCLUSION

In this paper, a genetic algorithm based gene rearrangement optimization operator is proposed to optimize the path of the mobile robot. According to the size of the rotation angle of the path, the gene points are redistributed on the chromosome, and the large corner path is optimized as a smooth path near the straight angle under the conditions without encountering obstacles. This operator compared with the improved genetic algorithm in the previous literature posses the obvious advantage, this method not only can greatly reduce the path length, but also can smooth the big rotation angle to make the robot turn more nimble, also reduced the energy consumption. The experimental results show that this method does some further optimization on the optimal path to some extent. Finally, the path optimization operator of gene rearrangement achieves two times optimization and path smoothing in the safe distance, which is not only easy to realize but also converges faster.

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