Route Planning Based on Gradient-Field Quantum Genetic Algorithm Model

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***Abstract*—A route planning method based on gradient-field quantum genetic algorithm model was presented in this paper. It introduces the gradient field of a grid map to quantum genetic algorithm model and uses quantum genetic algorithm (QGA) to optimize the cost function of route planning. By combining the quantum characteristics with the capabilities of the large diversity of the population, as well as fast convergence rate and high global searching, the optimization of route was guided and realized in our method by using the genetic operators with the essential characteristics of quantum and the gradient information of a grid map. Experimental results demonstrated that our method further effectively improves the quick convergence and capability of searching the optimal route.**

***Index Terms*—route planning, gradient field, QGA**

I. INTRODUCTION

Route planning has been extensively studied in detail within architectures, military and commercial use in the last decade. Route planning problem is essential to design a trajectory to optimize one route for avoiding the obstacles between a starting point and an ending point under several given constraint conditions. In the route planning, deterministic algorithm [1] and stochastic algorithm [2] are two chief kinds of route optimization algorithms. With the increase of computational complexity and controlled time-consuming requirements, several stochastic approaches, which have the capabilities of avoiding the uncertainty of computational time and giving a feasible route, for example genetic algorithm (GA) [3- 5], have been developed and widely used in the area of route planning.

Based on the particular physical characteristics of quantum such as quantum superposition and quantum entanglement, the quantum computing proposed, as a new computational model, is essentially different from traditional computational models. Moreover, it has altered our approach to further improve traditional signal and image processing techniques by introducing quantum computing to signal and image processing fields [6-8]. Narayanan [9] first proposed QGAby integrating traditional genetic algorithms based on quantum computational model. Han [10] further developedQGA by introducing quantum bit and quantum superposition in quantum characteristics.. Even if QGA has a similar process with traditional GA in implementing evolution, there are differences in the expressions in realizing chromosome coding using quantum bit and evolution mechanisms updating chromosome by the genetic operators with the essential characteristics of quantum. Therefore, compared with traditional GA, QGA has the strong capabilities of large diversity of population, quick convergence, and high global search. The artificial potential field method proposed by Khatib [11] to solve robot route planning problem has been extensively studied. However, there are some limitations, such as local minima and the difficulty of goal unreachable in route planning.

In this paper, we proposed a route planning method based on gradient-field quantum genetic algorithm model (GQGA). By introducing the gradient field of a grid map to QGA model and using quantum genetic algorithm to optimize the cost function of route planning, the proposed method guides the optimization of route by using the genetic operators with the essential characteristics of quantum and the gradient information of a grid map. By combining the quantum characteristics with the capabilities of the large diversity of the population, fast convergence rate and high global searching, our method further effectively improves quick convergence and the capability of searching the optimal route. Compared with traditional GA, experimental results demonstrated its potential and feasibility.

The remainder of this paper is organized as follows. Firstly, we introduce the fundamental concept of QGA in Section 2. Secondly, the proposed gradient-field quantum

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genetic algorithm model is described in Section 3. Then, Section 4 shows the experimental results with different parameters in our method and comparison with traditional QGA and GA. Finally, we give our conclusion in Section 5.

II. QGA

Based on the concepts of a quantum-bit and superposition of states of quantum mechanics, QGA encodes a chromosome using the quantum-bit with the superposition state, so that the chromosome can be expressed as the superposition of several states. Even if GQA is a probabilistic algorithm which is similar to a genetic algorithm, the potential of the large diversity of the population is gained using the novel quantum-bit representation.

A. Representation

Bit is a basic concept of classical information theory. In quantum system, the smallest unit of information stored in a two-state quantum computer is called a quantum-bit (qubit). Compared with the classical bit, a qubit may be in the '0' or '1' state, or in any superposition of the two. The state of a qubit $|\Psi\rangle$ can be represented as the following linear superposition between '0' and '1' state, namely:

$$|\Psi\rangle = \alpha|0\rangle + \beta|1\rangle \tag{1}$$

Where, $|0\rangle$ and $|1\rangle$ represent the classical '0' and '1' state respectively. α, β are two complex numbers that specify the probability amplitudes of the corresponding states. $|\alpha|^2$ and $|\beta|^2$ gives the probability that the qubit will be found in the '0' and '1' state respectively, and they satisfy $|\alpha|^2 + |\beta|^2 = 1$.

Based on quantum bit representation, a gene can be described by one or more quantum bits. Furthermore, a chromosome C consists of genes with quantum-bit encoding can be described as:

$$C = \begin{bmatrix} \alpha_1 & \alpha_2 & \cdots & \alpha_n \\ \beta_1 & \beta_2 & \cdots & \beta_n \end{bmatrix} \tag{2}$$

Where, n is the number of quantum bits, and $|\alpha_i|^2 + |\beta_i|^2 = 1$, $i = 1,2,\cdots,n$. If there is a system with n quantum-bits, the system can represent 2^n states at the same time. Therefore, because of the representation linear superposition of qubit states probabilistically, QGA has a better characteristic of diversity than classical approaches. As the qubit probability approaches to 1 or 0, the chromosome converges to a single state and the property of diversity disappears gradually, and then the convergence will be also obtained with the qubit representation.

B. Quantum Gates

As can be seen from the qubit state representation, a chromosome can be encoded as the superposition of several states. A quantum gate is defined as a variation operator, by which operation the qubit is updated to satisfy the normalization condition $|\alpha|^2 + |\beta|^2 = 1$. Therefore, with acting on quantum superposition states by a quantum gate, the probability amplitudes of all ground states can be changed, so that the corresponding chromosomes will be updated. In quantum genetic algorithms, quantum rotation gate will be often used to update the chromosome. The following quantum rotation gate $U(\theta)$ is used in this paper:

$$U(\theta) = \begin{bmatrix} \cos(\theta) & -\sin(\theta) \\ \sin(\theta) & \cos(\theta) \end{bmatrix} \tag{3}$$

Where, θ is the rotation angle. The corresponding update operation of qubit is described as:

$$\begin{bmatrix} \alpha_i' \\ \beta_i' \end{bmatrix} = \begin{bmatrix} \cos(\theta_i) & -\sin(\theta_i) \\ \sin(\theta_i) & \cos(\theta_i) \end{bmatrix} \begin{bmatrix} \alpha_i \\ \beta_i \end{bmatrix} \tag{4}$$

Where, $[\alpha_i, \beta_i]^T$ is i-th qubit in the chromosome. θ_i is a rotation angle of each qubit toward either 0 or 1 state depending on its sign. Its value is determined by the adjustment strategy. Its size determines the speed of convergence, and its sign determines the direction of convergence.

III. PROPOSED METHOD

A. Gradient-field of Grid Map

The edge map derived from an image has the property that it is larger near the image edges, so the gradient of the edge map has vectors pointing toward the edges, which are normal to the edges at the edges. And the edge map is nearly zero in homogeneous regions, where an image is nearly constant. Based on the general properties of edge maps, we can increase the cost value near the obstacle to obtain an optimal route. However, since these gradient vectors in the edge map generally have large magnitudes only in the immediate vicinity of the edges, the limitation of the influence range of the gradient vectors is leaded.

A gradient vector flow (GVF) method [12] proposed to enlarge the influence range was used in the paper, which will be helpful to obtain an optimal route. For a grid map $I(x, y)$, the gradient vectors field $V(x, y) = [u(x, y), v(x, y)]$ defined as any gray-level edge map can be obtained from its edge map $f(x, y)$ by minimizing the following energy equation:

$$\varepsilon = \iint \mu(u_x^2 + u_y^2 + v_x^2 + v_y^2) + |\nabla f|^2 |V - \nabla f|^2 \, dxdy \tag{5}$$

Using the calculus of variations, it can be shown that the GVF field can be found by solving the following Euler equations:

$$\begin{cases} \mu\nabla^2 u - (u - f_x)(f_x^2 + f_y^2) = 0 \\ \mu\nabla^2 v - (v - f_y)(f_x^2 + f_y^2) = 0 \end{cases} \tag{6}$$

Where, ∇^2 is the Laplacian operator. By solving the above (6) numerically, the improved gradient vectors field $V(x, y)$ will be obtained to enlarge the influence range of the gradient vectors. Based on the gradient vectors field of a grid map in the paper, an optimal route

can be evaluated to relative central positions among obstacles by increasing the cost value near the obstacle.

B. Route Encoding and Its Population Initialization

A route consists of several nodes including the corresponding location information in this paper, while a population is defined as a set composed of routes. We define an initial population set P as $\{p_1, p_2, \cdots, p_N\}$, where N is the number of routes p_k included in the population. A gene is considered as the location of each node in a route, while each route corresponds to a chromosome in a population. According to (2), we use qubit to encode the route p_k, namely

$$p_k = \begin{bmatrix} \alpha_{1,1} & \alpha_{1,2} & \cdots & \alpha_{1,n} & \alpha_{2,1} & \alpha_{2,2} & \cdots & \alpha_{2,n} & \cdots \\ \beta_{1,1} & \beta_{1,2} & \cdots & \beta_{1,n} & \beta_{2,1} & \beta_{2,2} & \cdots & \beta_{2,n} & \cdots \\ & & \cdots & \alpha_{m,1} & \alpha_{m,2} & \cdots & \alpha_{m,n} & & \\ & & \cdots & \beta_{m,1} & \beta_{m,2} & \cdots & \beta_{m,n} & & \end{bmatrix}, \quad (7)$$

Where, m and n correspond to the number of genes in a route and qubit in each gene respectively, and $|\alpha_{i,j}|^2 + |\beta_{i,j}|^2 = 1$ ($i = 1,2,\cdots,m$, $j = 1,2,\cdots,n$).

Based on the theory of quantum computing, qubit will only collapse to a single state when quantum state is observed and measured every time. Then the probability $|\alpha|^2$ or $|\beta|^2$ of the qubit will determine its observation value expressed by a single state. The measurement rule of observation value is defined as: for $[\alpha_{i,j}, \beta_{i,j}]^T$, if $|\alpha_{i,j}|^2 < |\beta_{i,j}|^2$, the observation value is 1; otherwise it is 0.

In this paper, a binary-encoded form was used to describe the location information of each node. Therefore, the correspondence between node locations and quantum bits can be built using above measurement rule. In addition, due to the gene described by qubit is multi-states, the state of each chromosome is the superposition of all possible states. Therefore, this will also ensure QGA to have population diversity.

C. Estimate of Cost Function

In genetic algorithm, the cost function is considered as an effective standard to measure an individual in a population. Usually, the smaller its cost value, the better an individual will be; otherwise, the individual is the worse. According to their cost value, the individuals are chosen to ensure that the better individuals can be selected in the next generation. Therefore, the cost function should correctly reflect the constraint conditions and requirements in route planning.

For the sake of simplicity, only obstacle constraint, distance constraint and gradient-field constraint of grid map are considered in this paper. The cost function J, consists in the obstacle cost f_{th}, the distance cost f_d and gradient-field cost f_g, is treated as the estimate index and described as:

$$J = \omega_1 f_{th} + \omega_2 f_d + \omega_3 f_g \quad (8)$$

Where, $\omega_i (i = 1,2,3)$ is the weight coefficient. f_g is defined as the sum of gradient-field magnitude on all node location in an route. Therefore, the smaller the value of a cost function J, the better the corresponding evolved route will be.

D. Quantum crossover

In traditional GA, the crossover operator is generally invalid when a crossover operator is generally implemented between two chosen individuals which are same in a population. Based on quantum coherence property, quantum interference crossover [9] is treated as quantum crossover operator in this paper. Therefore, all chromosomes in the population will be involved in quantum crossover operation, and new chromosomes are created by rearranging chromosomes along the diagonal in the procedure. For example, when the size of population and chromosome are chosen as 4 and 5 respectively (see Table I), A1-B2-C3-D4-A5 is a new chromosome after quantum crossover operation.

As can be seen, quantum crossover operator can avoid the problems that traditional crossover operators are invalid in the evolution when two routes are same. Furthermore, route information in the population is made full use as much as possible. Therefore, premature convergence is overcome. This also improves the efficiency of crossover operators the searching speed of the algorithm.

TABLE I.
QUANTUM INTERFERENCE CROSSOVER

No.	Chromosome				
1	A1	A2	A3	A4	A5
2	B1	B2	B3	B4	B5
3	C1	C2	C3	C4	C5
4	D1	D2	D3	D4	D5

E. Quantum gates strategy

Quantum gate mutation operator described by quantum gates strategy in Eq.(3) is used as the mutation operator in this paper. According to the task of route planning, we use the rotation-angle adjust strategy shown in Table II, in which a gene is randomly selected in the current route and its observation value from its qubit $[\alpha_{i,j}, \beta_{i,j}]^T$ is obtained. Then compared the cost values of the current route p with its current optimal route b, the angle and direction of rotation are determined further and the current route is finally updated.

In Table II, $b_{i,j}$ and $g_{i,j}$ represent observation values of the j-th qubit at the i-th gene in the current optimal route b and current route p respectively. The rotation angle is $\theta_{i,j} = sign(\alpha_{i,j}, \beta_{i,j}) \cdot \|\theta_{i,j}\|$ where $sign(\alpha_{i,j}, \beta_{i,j})$ and $\|\theta_{i,j}\|$ represent the direction and the angle of rotation respectively.

There is a direct connection between the size of rotation angle and the algorithm convergence. If the angle is too large, premature convergence can easily take place and affects accuracy of convergence. Otherwise, if the angle is too small, the speed of convergence will be significantly influenced. The dynamic adjustment strategy about rotation angle has many advantages over the stationary one. Therefore, the size of rotation angle is randomly selected in the range of $(0.005\pi,0.1\pi)$ in this paper.

TABLE II
ADJUSTING STRATEGY ABOUT A ROTATION ANGLE

$g_{i,j}$	$b_{i,j}$	J(p)>J(b)	$\|\theta_{i,j}\|$	sign($\alpha_{i,j}$,$\beta_{i,j}$)			
				$\alpha_{i,j}\beta_{i,j}>0$	$\alpha_{i,j}\beta_{i,j}<0$	$\alpha_{i,j}=0$	$\beta_{i,j}=0$
0	0	True/False	0	0	0	0	0
1	0	True	$\|\theta_{i,j}\|$	-1	+1	± 1	0
1	0	False	0	0	0	0	0
0	1	True	$\|\theta_{i,j}\|$	+1	-1	0	± 1
0	1	False	0	0	0	0	0
1	1	True/False	0	0	0	0	0

IV. EXPERIMENTS AND ANALYSIS

All simulation experiments in this paper were completed in PC platform running Windows XP with Inter Core2 Duo E5300 2.60GHz CPU and 1G memory. A 512×512 digital grid map shown in Fig. 1 was used in our experiments, in which the dark areas are defined as the simulated obstacles. The value of obstacle cost f_{th} is chosen as 5000, and the weight coefficient ω_1 , ω_2 and ω_3 are chosen as 0.3,0.4and 0.3 respectively. We define the reciprocal of a cost function J as the fitness function F , namely $F=1/J$. In addition, 'F_Route' and 'A_J' represent the average number of iterations and the average optimal cost value respectively, when the first feasible route is found in each evolution.

A. Chosen different parameters in GQGA

The method by choosing different numbers of gene and chromosome in a population is firstly implemented in our experiments. The two points chosen as the start-point and end-point of each route correspond to the point S and point T in Fig. 3. According to experience value determined by a large number of test, the number of experiments and iteration each condition is 20 and 300 respectively. The statistical average results from all obtained data each condition is shown in Table III.

As shown in Table III, we can obtain a feasible route when the smaller size of population is chosen. Furthermore, when the number of gene is same, 'F_Route' not only substantially reduces with increasing the size of population, but 'A_J' gradually decreases and converges. Based on the large diversity of the population derived from the introduction of gradient-field and quantum operators, it is demonstrated that the proposed method has the stronger capabilities of the searching and convergence

In addition, when the size of population is same, 'F_Route', describing the average number of iterations, in which first feasible route is found, firstly decrease and then increase with increasing the number of iterations, and then the average optimal cost value 'A_J' increase. These are caused by the location of the selected start-point and end-point. Moreover, the excessive nodes (namely, the number of genes) will increase the risk of failure in route planning.

TABLE III
RESULTS COMPARISON AMONG DIFFERENT PARAMETERS IN GQGA

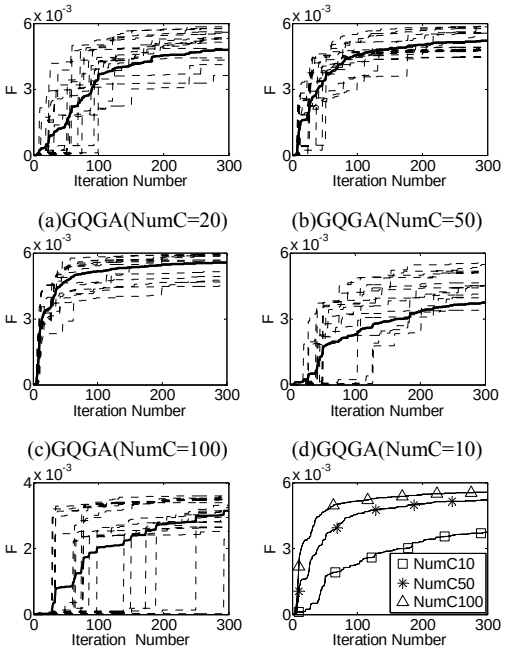
Gene number	Proformance index	Population number			
		6	10	20	50
6	F_Route	99.1	74.4	41.5	15.4
	A_J	180.6	169.6	168.4	165.8
10	F_Route	117.1	56.4	27.5	11.7
	A_J	183.8	180.8	171.2	167.6
20	F_Route	189.7	132.7	43.5	23.4
	A_J	368.8	256.4	235.3	203.0

B. Results comparison with traditional QGA

1) Convergence capabilities

When the gene number is 10 in Table III, Fig. 1(a)-(d) show the fitness curves for routes obtained from different chromosome number in a population (namely, NumC is 10, 20, 50 and 100) in our method, while Fig. 1(e) shows the fitness curves when NumC is 10 in traditional QGA. Every fitness curve in 20 experiments are represented as the dashed lines in Fig. 1(a)-(e), while the average fitness curve from the 20 experiments are represented as the real lines. The average fitness curves are represented in Fig. 1(f) when the number of chromosome is chosen as 10, 50 and 100 respectively.

As can be seen in Fig. 1(a)-(d), with increasing the number of chromosome in a population, the intensity of fitness curves increases gradually, and the number of iteration finding first feasible route is substantially reduced. Compared with traditional QGA, fitness curves shown in Fig. 1(d)-(e) in the proposed GQGA has more intensity with increasing the number of iterations, and first feasible route is found earlier. The difference of the fitness function value F in Fig. 1(d)-(e) is caused by using different cost function (only the obstacle cost and the distance cost are used, and its corresponding weight coefficient is 0.5). Therefore, it further demonstrates our method has stronger convergence capabilities.



(a)GQGA(NumC=20) (b)GQGA(NumC=50)

(c)GQGA(NumC=100) (d)GQGA(NumC=10)

(e)QGA(NumC=10) (f)Average fitness curve in GQGA

------ represent every fitness curve; —— represent average fitness curve

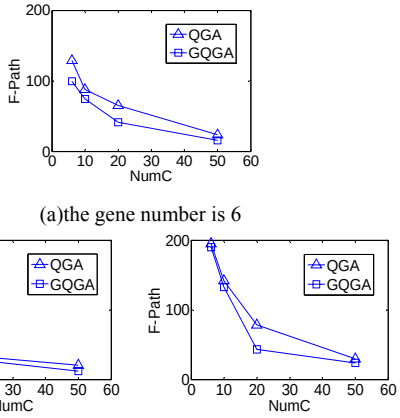
Figure 1. Fitness curves from different parameters (The gene number is 10).

2) The number of iteration finding first feasible route

Comparison test for the number of iteration finding first feasible route 'F_Route' between GQGA and QGA was implemented in our experiments by choosing different number of gene and chromosome in a population (Shown in Table IV). 'Inc(%)' represents the growth rate of 'F_Route', namely $Inc=(F\_Path\_QGA-F\_Path\_GQGA)\times 100\%/F\_Path\_QGA$, when selecting the same number of gene and chromosome in GQGA and QGA. 'A_Inc(%)' represents the average value of the growth rate 'Inc(%)' when selecting the different number of gene in the condition of same chromosome. Furthermore, Fig. 2 shows the comparison for the number of iteration finding first feasible route between GQGA and QGA. As can be seen in Table IV and Fig. 2, the proposed GQGA is better than QGA, and the number of iteration finding first feasible route 'F_Route' has an average increase of nearly 25%. Therefore, it further demonstrates our method has the stronger searching capabilities.

TABLE IV
RESULTS COMPARISON AMONG DIFFERENT PARAMETERS BETWEEN GQGA AND QGA

Gene number	Proformance index	Population number			
		6	10	20	50
6	QGA	128.8	87.9	65.2	23.7
	GQGA	99.1	74.4	41.5	15.4
	Inc(%)	23.1	15.4	36.3	35.0
10	QGA	118.5	102.4	32.7	20.2
	GQGA	117.1	56.4	27.5	11.7
	Inc(%)	1.2	44.9	15.9	42.1
20	QGA	195.0	141.8	78.3	29.8
	GQGA	189.7	132.7	43.5	23.4
	Inc (%)	2.7	6.4	44.4	21.5
A_Inc (%)		9.0	22.2	32.2	32.9



(a)the gene number is 6

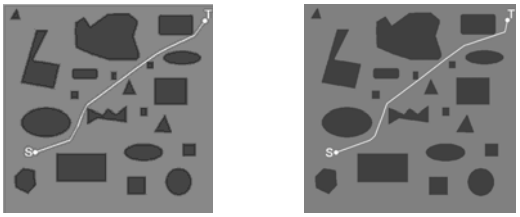
(b) the gene number is 10 (c) the gene number is 20

Figure 2. Results comparison about F_Route in Table 4 between GQGA and QGA.

3) The obtained optimal route

When the gene number (defined as NumG) is 10, the optimal route obtained from different chromosome number in a population (namely, 50 and 100) in our method and QGA respectively are showed in Fig. 3. As can be seen in Fig. 3, the smaller chromosome number in our method has a similar route with the larger chromosome number in QGA. Moreover, the obtained optimal route in our method is further away from the obstacles by introducing the gradient field. This further illustrates that a more feasible route can be obtained in our method, and can greatly reduce the computational consumption.

C. Results Comparison with Traditional GA



(a)QGA (NumC=100, NumG=10) (b) GQGA (NumC=50, NumG=10)

Figure 2. Results comparison about the obtained optimal route between GQGA and QGA.

Comparison experiments between GQGA and QGA was implemented in our experiments. Here, the number of gene is 10; the start-point and end-point of each route are chosen as the point S and point T in Fig. 3, and the number of experiments and iteration each condition is 20 and 300 respectively. The statistical average results from different methods were shown in Table V. 'Time' represents the time-consuming of every generation in iterative process.

As can be seen in Table V, compared with traditional QGA and GA, the number of iteration finding first feasible route 'F_Route' in the proposed GQGA is better than traditional QGA when chromosome number is 20, and is close to the result in GA when chromosome number is 50. Furthermore, the obtained 'F_Route' in the proposed GQGA is far superior to the result in GA when chromosome number is 50, while the two method have a

similar time-consuming. Therefore, it further demonstrates the smaller size of population in our method has a similar result with the larger size of population in traditional QGA and GA, and our method has the stronger capabilities of searching convergence.

TABLE V
RESULTS COMPARISON AMONG GA, QGA AND GQGA

	GQGA			QGA		GA
NumC	10	20	50	10	20	50
F_Route	56.4	27.5	11.7	102.4	32.7	18.2
Time	0.19	0.33	0.75	0.15	0.28	0.73

V. CONCLUSIONS

By introducing the gradient field of a grid map to QGA model and using QGA to optimize the cost function of route planning, a route planning method based on GQGA model is presented in this paper. Based on quantum characteristics with the capabilities of the large diversity of the population, fast convergence rate and high global searching, the proposed method guides and realizes the optimization of route by using the genetic operators with the essential characteristics of quantum and the gradient information of a grid map, in which quick convergence and the capability of searching the optimal route are further improved effectively. Experimental results demonstrate that our method has important reference value in route planning.

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