

A Novel Quantum Evolutionary Algorithm And Its Application

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Abstract- In this paper, a novel algorithm-the quantum evolutionary algorithm(QEA) is introduced. It is characterized by a representation of quantum chromosomes, quantum mutation and quantum crossover. Its advantages lies on better diversity of individuals, effective guidance of mutation and the avoidance of prematurity by crossover. Some simulations are given to illustrate its efficiency and better performance than its counterpart. Finally we applied it to the multi-user detection in DS-CDMA, and good results are attained.

I. INTRODUCTION

Evolutionary algorithm(EA) is an effective algorithm which simulates the natural evolution. The best-known examples are genetic algorithm(GA)^[1], evolutionary programming (EP)^[2] and evolutionary strategy (ES)^[3-4]. EA simulates the principles of evolution(survival of the fittest) and begins with a population of random individuals, then it maintains a population of potential solutions (individuals) through repeated application of some genetic operators(crossover, mutation and selection). They give each individual the chance of optimization and encourage the survival of the better simultaneously, so EA can yield individuals with successively improved fitness, and hopefully, converge to the fittest individual representing the optimum solutions. It has been proved in theory that EA is convergent from the viewpoint of probability^[5].

Because of the great robustness, parallelism and easy application of EA, it has been applied to the combinational optimization^[6-7], structure designing^[8], machine learning rule-based classify systems^[9-10] and some other engineering problems^[11-13]. However, it has some disadvantages such as torpid convergence and prematurity for the randomness of evolution. So looking for new methods to improve the efficiency of searching has become urgent and necessary in the study of EA.

Recently the quantum mechanism has been proved to offer a new paradigm for information processing^[14-15]. The quantum computing has inspired many interests and made rapid developments, two paramount examples being Shor's factoring algorithm^[16] and Grover's searching algorithm^[17]. As a consequence of these developments, many efforts have gone into both the search for a physical realization of quantum computers^[18] and the establishment of a complete quantum information theory, especially its penetrating into other classical methods^[19-20]. In the spirit of the latter line, we introduce a novel EA-quantum evolutionary algorithm (QEA), in which quantum concept

and principles are used to inform and inspire more efficient EA.

Instead of binary, numeric, and symbolic coding, QEA adopts a quantum chromosome which can represent many classical chromosomes, so it has better diversity. Moreover, the quantum mutation can speed up the evolution easily. Additionally, a quantum-inspired crossover is put forward to avoid the prematurity in the anaphase of the evolution.

This paper is organized as follows. In Section 2, some preliminary knowledge about QEA is expounded, then we give a full description of QEA in Section 3. Two evolution operators-quantum mutation and quantum crossover, and the framework of QEA are given. In Section 4, a series of examples about QEA's application are given. The paper is then concluded in Section 5.

II. PRELIMINARY KNOWLEDGE FOR QEA

A. Physical Foundation

As far as we know today, all matter is composed of atoms-nuclei and electrons. Landauer reveals that all information is physical in nature^[21]. Quantum computation(QC) takes full advantage of the superposition and interference of quantum states, as well as the entanglement of each other, so it has powerful capacity of parallel processing^[22].

The power of QC lies on its replacement of classical bit by quantum bit(qubit), so we first introduce the concept of qubit. In quantum informatics, the carrier of information is not a bit but a quantum system with two states such as an atom, an ion or a photon with two polarize directions that is called qubit. It is in a linear superposition state and the complex numbers α, β are used to specify the amplitudes of two states. The magnitudes of any two qubits can interfere with each other, which is called the quantum interference. Moreover, the transformation on each part of the superposition state can be fulfilled in an operation which is called the quantum parallelism.

B. Quantum Bit

A qubit can be represented as

$$|\Psi\rangle = \alpha|0\rangle + \beta|1\rangle \quad (1)$$

where $|\alpha|^2$ gives the probability that the qubit will be found in state "0" and $|\beta|^2$ gives the probability that the qubit will be found in state "1". Normalization of the state to unity guarantees:

$$|\alpha|^2 + |\beta|^2 = 1 \quad (2)$$

If there is a system of m -qubit, the system can represent 2^m states at the same time, on the other side, after observing a quantum state; it collapses to a single state.

C. Quantum Chromosome

QEA uses a novel representation based on qubit. An m -qubit system can be defined as:

$$\begin{bmatrix} \alpha_1 & \alpha_2 & \dots & \alpha_m \\ \beta_1 & \beta_2 & \dots & \beta_m \end{bmatrix} \quad (3)$$

where $|\alpha_i|^2 + |\beta_i|^2 = 1 (i=1, \dots, m)$. If there is a 3-qubit system with such three pairs of complex numbers:

$$\begin{bmatrix} \frac{1}{\sqrt{2}} & \frac{\sqrt{3}}{2} & \frac{1}{2} \\ \frac{1}{\sqrt{2}} & \frac{1}{2} & \frac{\sqrt{3}}{2} \end{bmatrix} \quad (4)$$

The states of the system can be represented as:

$$\frac{\sqrt{3}}{4\sqrt{2}}|000\rangle + \frac{3}{4\sqrt{2}}|001\rangle + \frac{1}{4\sqrt{2}}|010\rangle + \frac{\sqrt{3}}{4\sqrt{2}}|011\rangle + \frac{\sqrt{3}}{4\sqrt{2}}|100\rangle + \frac{3}{4\sqrt{2}}|101\rangle + \frac{1}{4\sqrt{2}}|110\rangle + \frac{\sqrt{3}}{4\sqrt{2}}|111\rangle \quad (5)$$

It means the appear probabilities of the states $|100\rangle, |101\rangle,$

$|110\rangle, |111\rangle, |000\rangle, |010\rangle, |011\rangle$ are $\frac{3}{8}, \frac{9}{8}, \frac{1}{8}, \frac{3}{8}, \frac{9}{8}, \frac{1}{8}$ respectively, i.e.,

we can get the information of 8 states from a 3-qubit system. Additionally, along with the convergence of the quantum chromosomes, the diversity will fade away little by little and the algorithm converges.

III. THE QUANTUM EVOLUTIONARY ALGORITHM

Research on the merging of EA with quantum algorithm (QA) has been started since later 1990's, some focused on constructing new QAs^[23] and some devoted to quantum-inspired computations which is characterized of quantum mechanics^[24]. In this section we deal with QEA in detail.

A. Quantum Evolution Algorithm (QEA)

QEA is a probabilistic algorithm that is similar to EA. It maintains a population $Q(t) = \{q'_1, q'_2, \dots, q'_n\}$ at generation t , where n is the size of the population, and q'_j is a quantum chromosome which is defined as:

$$q'_j = \begin{bmatrix} \alpha'_1 & \alpha'_2 & \dots & \alpha'_m \\ \beta'_1 & \beta'_2 & \dots & \beta'_m \end{bmatrix}, j = 1, 2, \dots, n \quad (6)$$

where m is the chromosome's length. Compared with EA, two steps "observe $Q(t)$ " and "update $Q(t)$ " are added. In the first step, binary solutions $P(t)$ is formed by observing $Q(t)$, the procedure can be described as: For each bit of the chromosome, generate a random real number $p \in [0, 1]$, if $p > |\alpha'_i|^2$, the corresponding bit in $P(t)$ takes "1"; else "0".

In the "update $Q(t)$ ", one can use different methods to evolve $Q(t)$, for example, generate $Q(t)$ in a random way, and generate $Q(t)$ by evolutionary operator, or apply some suitable quantum gates to produce $Q(t)$. If a quantum gate is designed, the transform matrix must be a unitary matrix. The most commonly used matrixes are Control-not gate, Rotation and Hadamard gate. The QEA is described as: begin

```

t ← 0
initialize Q(t)
make P(t) by observing Q(t) states
evaluate P(t)
store the best solution among P(t)
while (not termination-condition) do
begin
t ← t + 1
crossover and mutate to update P(t) (omissible)
evaluate P(t)
store the best solution among P(t)
update Q(t) to get Q'(t)
make P'(t) by observing Q'(t) states
select in {P(t) ∪ P'(t)} to get new P(t)
end
end

```

B. Advantage of the QEA

An EA should balance between using the evolution history and exploring the new individuals, i.e., it should search the current space as well as the unknown space. In addition, it should converge rapidly and avoid prematurity. How can QEA solve them?

Firstly, QEA saves the best individual at each epoch and uses observation to produce new individuals. Secondly, QEA adopts a quantum chromosome, by which QEA has better diversity and can perform a wise mutation with ease.

III.B.1 Quantum mutation

The mutation is a stochastic disturbance, so it also leads to deterioration as well as improvement, on the other side, the best individual in the current generation is important, i.e., the communication among individuals is

needed to speed up the convergence. Quantum mutation focuses on a wise guidance by the current best individual.

①Consider such a quantum mutation matrix-rotation gate matrix:

$$U(\theta) = \begin{bmatrix} \cos(\theta) & -\sin(\theta) \\ \sin(\theta) & \cos(\theta) \end{bmatrix} \quad (7)$$

where θ is the rotation angle that can be seen in table I.

TABLE I

| x_i | $best_i$ | $f(x) > f(best)$ | $\Delta\theta_i$ | $s(\alpha_i\beta_i)$ | | | |
|-------|----------|------------------|------------------|-----------------------|-----------------------|----------------|---------------|
| | | | | $\alpha_i\beta_i > 0$ | $\alpha_i\beta_i < 0$ | $\alpha_i = 0$ | $\beta_i = 0$ |
| 0 | 0 | false | 0 | 0 | 0 | 0 | 0 |
| 0 | 0 | true | 0 | 0 | 0 | 0 | 0 |
| 0 | 1 | false | 0 | 0 | 0 | 0 | 0 |
| 0 | 1 | true | 0.01π | -1 | +1 | ± 1 | 0 |
| 1 | 0 | false | 0.01π | -1 | +1 | ± 1 | 0 |
| 1 | 0 | true | 0.01π | +1 | -1 | 0 | ± 1 |
| 1 | 1 | false | 0.01π | +1 | -1 | 0 | ± 1 |
| 1 | 1 | true | 0.01π | +1 | -1 | 0 | ± 1 |

In the table, $best_i$ and x_i are the i -th bit of the best solution $best$ and binary solution x , $f(x)$ is the fitness of x , $\Delta\theta_i$ is the rotation angle that controls the convergent speed, $s(\alpha_i\beta_i)$ is the sign of the angle that controls the direction of rotation. Why it can converge to a better solution? Looking into the figure, you may get some ideas.

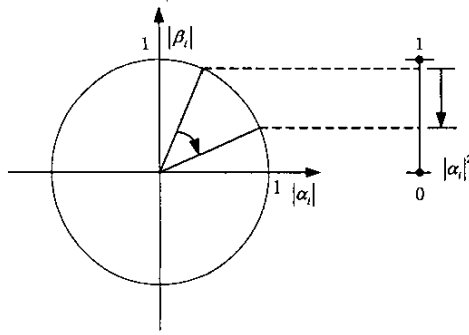


Fig. 1. Rotation of the quantum gate

For example, when $x_i=0$, $best_i=1$, $f(x) > f(best)$, the probability of current solution x_i be "0" should be larger to get a better chromosome, i.e., $|\alpha_i|^2$ should be larger, so if (α_i, β_i) is in the first or third quadrant, θ should rotate clockwise and else rotate counter-clockwise.

②Other matrixes can also be used as long as the uniformity is satisfied. For example a simple method can be described as:

$$\alpha(t+1) = [2 - best(t)] \times 0.5 \quad (8)$$

It means that the bits of the best individual will appear with a probability larger than 0.5 in the next generation.

③Another mutation method is given in the following. It deduces a probability distribution from the current best individual. Firstly define a guide quantum chromosome from the current best individual and spread the next generation with this guide chromosome being the center. It can be written as:

$$Q_{guide}(t) = \alpha \times p_{currentbest}(t) + (1-\alpha) \times (1 - p_{currentbest}(t)) \quad (9)$$

$$Q(t+1) = Q_{guide}(t) + b \times normrnd(0,1) \quad (10)$$

where $P_{currentbest}(t)$ and $Q_{guide}(t)$ are the current best individual and the guide quantum chromosome at the t -th generation respectively; a is the guide factor of Q_{guide} ; b is the spread variance. For easy of comprehending, an example is given. Obviously, we only need to let $Q=(0 \ 0 \ 1 \ 1 \ 0)$ to get $P=(1 \ 1 \ 0 \ 0 \ 1)$ with probability 1, i.e., $Q=\bar{P}$. If P is the optimum, the probability of getting the optimum becomes larger with a becoming smaller. When $a=0$, $Q_{guide}=\bar{P}$, one will get P with probability 1 after observing Q_{guide} . Often we let $a \in [0.1, 0.5]$, $b \in [0.05, 0.15]$.

III.B.2 Quantum Crossover

Crossover is another searching method, some such as one-point, multi-points, and uniform crossover are often used in EA. However, most of them are limited within two individuals, which is local in some sense. In order to construct more robust crossover operators, we introduce a quantum crossover-global-interference crossover in light of the quantum interference, which allows more individuals involve in the crossover. Considering a population with 5 chromosomes of length 9. Table II is a global-interference crossover, chromosomes are recombined along diagonals and each new individual is labeled with one color.

This kind of crossover characters more individuals' participation in the operation, which aims to overcome the locality of its classical version. It is origin of quantum theory and can be used to prevent the prematurity. If two individuals are the same, the conventional crossover will not work while this new crossover is able to generate new individuals to impel the evolution. In the worst case when all the individuals in the population are identical, if such a global-interference crossover is used: generate an integer v in randomly the range of $[1, m]$ (m is the length of the chromosome) as the crossover point, then the v -th bit of the first chromosome is selected as the first bit of the new chromosome, continuing this operation on the chromosomes in turn until a string of length m , i.e., a new individual is got. It proves to be more powerful against prematurity in the practical experiments.

TABLE II

| chromosome (ABCDEFGHI) | | | | | | | | |
|------------------------|----|----|----|----|----|----|----|-------|
| 1 | A1 | A2 | D3 | C4 | B5 | A6 | | F1 C9 |
| 2 | B1 | A2 | B2 | D4 | C5 | B6 | A7 | H2 |
| 3 | C1 | B2 | A3 | H3 | D5 | C6 | B7 | A8 |
| 4 | D1 | C2 | B3 | A4 | H4 | D6 | C7 | B8 A9 |
| 5 | | D2 | C3 | B4 | A5 | C5 | D7 | C8 B9 |

IV. SIMULATIONS

A. Application in the Knapsack Problem

A typical combinational optimization problem-knapsack problem, is used to investigate the performance of QEA. Given a knapsack of load V and N items whose costs and weights are $C_i, W_i (i=1, \dots, n)$, our problem is: how to select the items to pack into the knapsack so that the total cost reaches maximum. In our test, $V=1000, N=50$, costs and weights of N items are:

$C=[220\ 208\ 198\ 192\ 180\ 180\ 165\ 162\ 160\ 158\ 155\ 130\ 125\ 122\ 120\ 118\ 115\ 110\ 105\ 101\ 100\ 100\ 98\ 96\ 95\ 90\ 88\ 82\ 80\ 77\ 75\ 73\ 72\ 70\ 69\ 66\ 65\ 63\ 60\ 58\ 56\ 50\ 30\ 20\ 15\ 10\ 8\ 5\ 3\ 1]$;
 $W=[80\ 82\ 85\ 70\ 72\ 70\ 66\ 50\ 55\ 25\ 50\ 55\ 40\ 48\ 50\ 32\ 22\ 60\ 30\ 32\ 40\ 38\ 35\ 32\ 25\ 28\ 30\ 22\ 50\ 30\ 45\ 30\ 60\ 50\ 20\ 65\ 20\ 25\ 30\ 10\ 20\ 25\ 15\ 10\ 10\ 10\ 4\ 2\ 1]$;

In the algorithm, each chromosome stands for a possible solution, its gene can be either 1 or 0, where 1 means the item is used and 0 means not. QEA can be described as:

1. Observing $Q(t)$ to get $P(t)$;
2. Evaluate the population and store the best individual;
3. Judge the termination-condition;
4. Quantum mutation: using rotation gate $U(t)$.

We investigate different algorithms' performance. In the greedy algorithm (GR), and get the result of the gross weight 996 and the gross cost 3036. In the SGA (simple GA) and HGA (hybrid GA), the size of population is 80 and the number of iterations is 500, the probabilities of crossover and mutation are 0.7 and 0.1. In QEA, a rotation quantum gate is used. Result of 50 tests is given in table III

TABLE III

| Algorithm | Generation of optimum appeared | Generation of a solution better than that of GR appeared | weight/cost |
|-----------|--------------------------------|--|-------------|
| SGA | 1379 | 132 | 3077/999 |
| HGA | 183 | 45 | 3103/1000 |
| QEA | 11 | 2 | 3103/1000 |
| GR | | 3036/996 | |

The convergent curves of QEA are shown in figure 2. In QEA, the optimum 3103/1000 appeared in the 11-th epoch and after 50 generations, the optimum has accounted for more than half in the population.

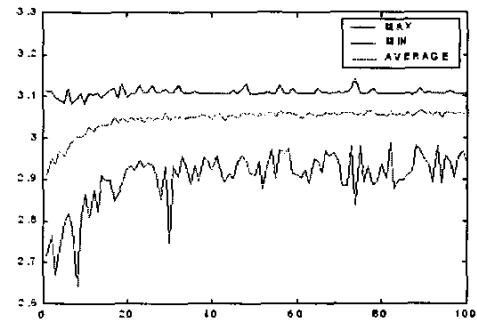


Figure 2 The convergence of QEA

B. Application in Solving Morbid Equations

Solving morbid equations often appears in the estimation of the parameters. For the large condition value of morbid equations, a small variation of the original data will cause deterioration of the solution. To avoid the difficulty to determine the best iteration times in the gradient algorithm and the sensibility to the truncation position in the strange value decomposition, GA has been introduced in solving this problem. Suppose such a morbidity linear equations:

$$\sum_{j=-N}^N a_{ij} x_j = b_i \quad i = 0, \pm 1, \pm 2, \dots, \pm M \quad (11)$$

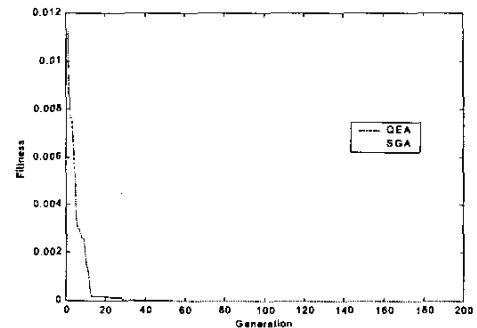
where $a_{ij} = \frac{\sin[\Omega T(i-j)]}{[\pi(i-j)]}$, $M=N=4$, $T=0.25$, $\Omega=2\pi \times 0.47$.

The solutions of the equations are $x_j = 1 (j=0, \pm 1, \dots, \pm N)$ and the maximum strange value $\sigma_{\max} = 0.987559$ and minimum $\sigma_{\min} = 9.26903 \times 10^{-10}$, so it is a high morbid equation with the condition value $K = \frac{\sigma_{\max}}{\sigma_{\min}} = 1.06544 \times 10^9$.

The fitness is:

$$F(x) = \left(\sum_{j=-N}^N a_{ij} x_j - b_i \right)^2 \quad x_j \in [-2, 2] \quad (12)$$

We use QEA and GA to solve it. The population size is 10 and the probabilities of crossover and mutation are 0.7, 0.1.



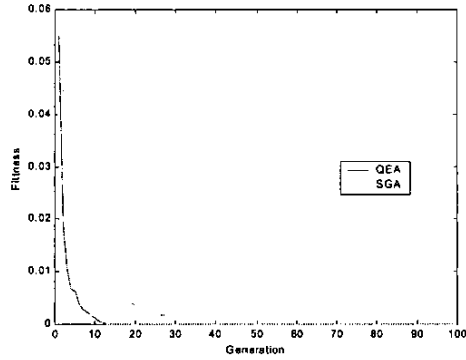


Figure 3 The convergence of GA and QEA

Result is shown in Fig 3 with the variation of the fitness of the best individual and the average.

C. Application in the CDMA

As we all know, CDMA is an effective method of personal wireless communication, it is characteristic of high rate of utilization of the resource and good security. In the model of a DS(direct sequence)-CDMA system with K users, the receive signal of the base station is:

$$r(t) = \sum_{i=-\infty}^{\infty} \sum_{k=1}^K A_k(i) b_k(i) s_k(t - iT - \tau_k) + n(t) \quad (13)$$

where $t \in [0, T]$ and $s_k(t)$ is the characteristic sequence of the k -th user; $b_k(i) \in \{-1, 1\}$ is the i -th transmit bit of the k -th user; T is the interval of the transmit sequence, $n(t)$ is the Gauss noise, ρ_{ij} is the correlation coefficient of the i -th user and j -th user. Then the output of the matching filter is:

$$y_k(i) = \int_{-\infty}^{\infty} r(t) s_k(t - iT - \tau_k) dt = A_k(i) b_k(i) + \sum_{j \neq k} A_j(i) b_j(i) \rho_{jk} + n_k(i) \quad (14)$$

In the case of the multiple signal channels, the performance of classical matching filter declines remarkably, so *S.Verdu* advanced an optimal multi-user detection, which aims to find the input sequence b with the maximum likelihood function $J(b)$ of the output sequence:

$$\hat{b} = \operatorname{argmax} \left\{ \exp \left\{ 1/2\sigma^2 \times \left(\int_0^T y(t) - \sum_{k=0}^K b_k A_k s_k(t) \right)^2 dt \right\} \right\} \quad (15)$$

$$J(b) = 2b^T A b - b^T A R A b = 2b^T A b - b^T H b (H = A R A) \quad (16)$$

where R is the correlation matrix of all the users. Evidently it is an optimization problem with exponentially increased computation complexity with the increase of users. The exhaustive algorithm will meet "exponential expansion" when there are too many users, so it can hardly applied in the CDMA. In the following, we used QEA to solve it. It can be divided into some steps:

1. The description of the problem

For simplicity, we use a quantum chromosome with the fixed length, and each individual in the population represents a possible solution, the gene of the chromosome can be 1 or 0, which is corresponding to the transmit bit of the users.

2. The initialization of the population

Generally speaking, we select chromosomes randomly in the defined space. Here specially we take the output of the classical detector as the initial input.

3. Fitness function

In the multi-user detection, we want to maximum the likelihood function $J(b)$, we set the fitness function $f(b) = J(b) - J(b)_m$ to make $J(b)$ positive, where $J(b)_m$ is the minimum fitness function in the present population. The results are tabulated in table IV and V. A is the power of the signal and An is the power of the noise. In the test, we can see that QEA performs better. Although the algorithm is executed once a bit is received, it is of the high accuracy.

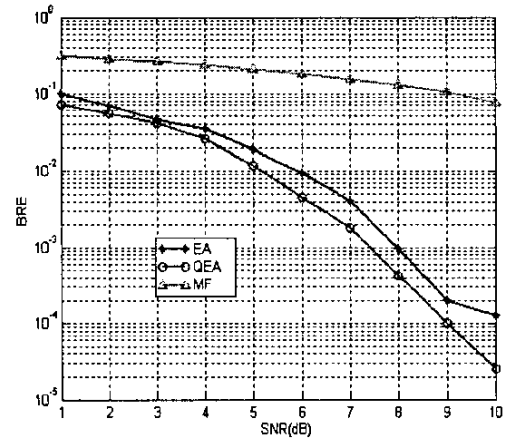
TABLE IV

| The number of error bit in 1000 bits (a CDMA system with 10 users) | | | | | | | | |
|--|-----|-----|-----|-----|----|----|---|----|
| An | 4.8 | | | | | | | |
| A | .1 | .5 | 1 | 2 | 4 | 6 | 8 | 10 |
| MF | 469 | 365 | 265 | 113 | 96 | 54 | 0 | 0 |
| QEA | 28 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |

TABLE V

| The number of error bit in 1000 bits (a CDMA system with 15 users) | | | | | | | | |
|--|-----|-----|-----|-----|-----|-----|-----|-----|
| An | 4.8 | | | | | | | |
| A | .1 | .5 | 1 | 2 | 4 | 6 | 8 | 10 |
| MF | 477 | 390 | 352 | 289 | 149 | 192 | 173 | 262 |
| QEA | 149 | 101 | 99 | 69 | 17 | 31 | 22 | 0 |
| A | 12 | 14 | 16 | 18 | 20 | 22 | 24 | |
| MF | 150 | 56 | 60 | 13 | 5 | 1 | 0 | |
| QEA | 0 | 0 | 0 | 0 | 0 | 0 | 0 | |

In the synchronous and asynchronous CDMA with $K=8$, figure 4 and 5 gives the results after the evolution of 10 and 20 epoches respectively.



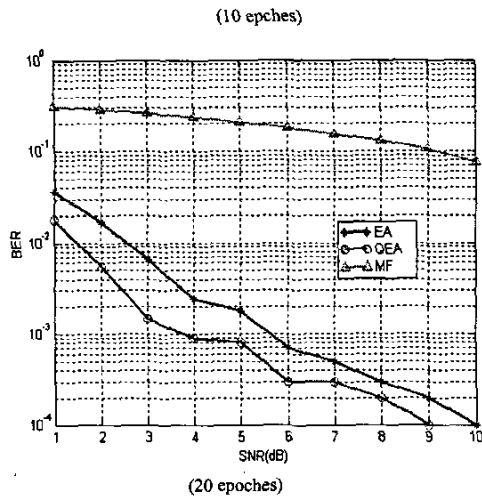


Figure 4 Synchronous CDMA

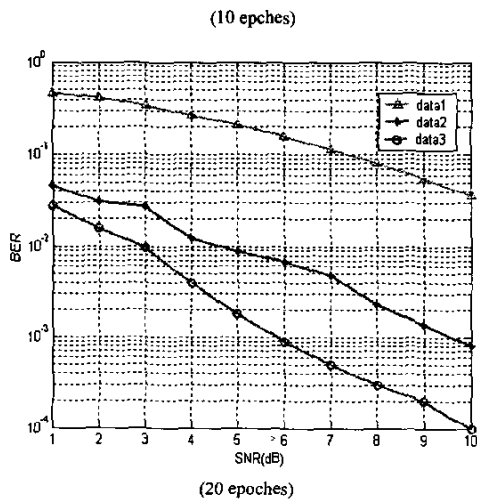
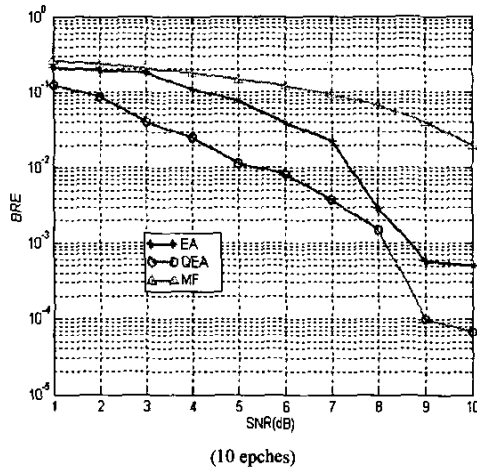


Figure 5 Asynchronous CDMA

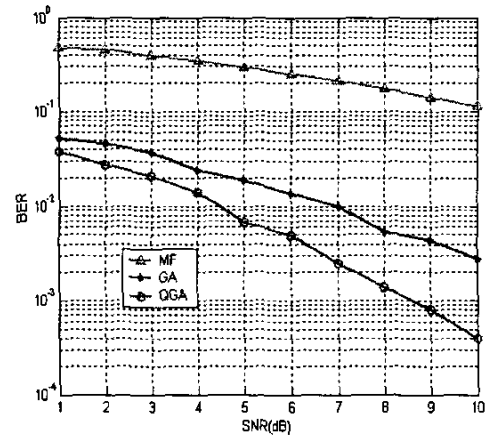


Figure 6 Synchronous CDMA(20 epoches)

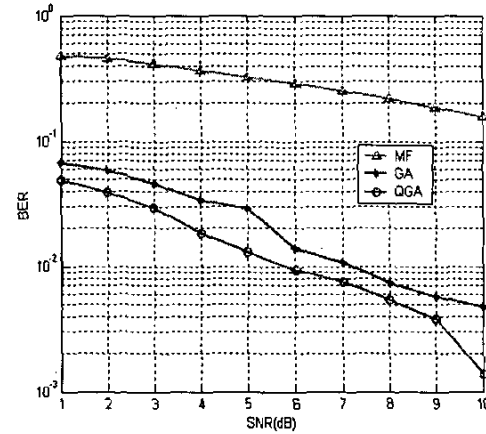


Figure 7 Asynchronous CDMA(20 epoches)

Then we investigate the case of a declined CDMA channel. Figure 6,7 gives the results of the synchronous and asynchronous CDMA with $K=8$ after 20 epoches.

V. CONCLUSION

In this paper, a novel kind of evolutionary algorithm, the quantum evolutionary algorithm-QEA, is proposed based on the combination of quantum theory with evolutionary algorithm. It is a kind of evolutionary algorithm with the form of quantum chromosome that provides more diverse individuals. On this basis, quantum evolution operators are advanced in light of some properties of the quantum mechanism. Then a lot of simulations are given to test this new algorithm, and rapid convergence and good global search capacity characterize the performance of QEA. The application in the CDMA also proves its superiority to its counterpart.

ACKNOWLEDGMENTS

The authors would like to thank the anonymous receives for their helpful suggestions, and also thank for Min Wang, who helped in editing the original manuscripts, and who has given many helpful suggestions on writing.

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