A DNA Genetic Algorithm for Beam Angle Selection in Radiotherapy Planning

Jie Lei, Yongjie Li
School of Life Science and Technology
University of Electronic Science and Technology of China
Chengdu, China
E-mail: liyj@uestc.edu.cn

***Abstract*—There are few of evolutionary algorithms (EAs) considering the influence of bit positions when mutation operation is implemented. A DNA genetic algorithm (DNA-GA) with a novel bit mutation strategy is presented in this paper. "Hot spots" and "cold spots" are set in DNA individuals with different mutation probabilities, and three structure mutation operations are designed to replace those bad individuals with better ones. DNA-GA uses DNA encoding method which borrows the intelligence from the biological DNA encoding mechanism to encode the solutions. The presented DNA-GA is applied to automatically select the beam angles for intensity-modulated radiotherapy (IMRT) planning, which uses a triplet code to represent a beam angle. The preliminary results show that DNA-GA is feasible and effective for the beam angle optimization (BAO) problem in IMRT planning and faster to obtain the optimal plan than GA.**

Keywords*—Beam angle optimization, DNA computation, intensity-modulated radiotheropy*

I. INTRODUCTION

For tumor treatment, intensity-modulated radiotherapy (IMRT) is a powerful clinical technique to potentially improve the therapeutic radio [1]. By using intensity-modulated beams from multiple spatial directions, IMRT can obtain highly conformal doses for target volumes while sparing organs at risks (OARs) and normal tissues as much as possible. The conventional IMRT planning starts with the selection of suitable beam angles, followed by an optimization of beam intensity maps using inverse optimization methods under the guidance of an objective function.

During the past several years, many efforts have been made for IMRT to increase the automatization of beam set-up and shorten the optimization time of inverse planning. Many researchers have found that the selection of suitable beam angles is most valuable for a plan with a small number of beams (<=5) [2]-[5], and is also important for plans with lager number of beams (>=9) in some complicated cases [6]-[9].

To date, many optimization algorithms have been introduced into the radiotherapy area. Ezzell used genetic algorithm (GA) to find an optimal combination of external beams [10]. Langer *et al*. used GA to optimize the beam weights for treatment of abdominal tumours [11]. In [12], Yu and Schell chose GA for the optimization of prostate implants. Wu and Zhu proposed a technique to optimize the beam directions and weights using a mixed-encoding GA in [13]. Zhang *et al*. used a hybrid GA and simulated annealing (SA) together, to optimize the gamma knife treatment planning [14]. Rowbottom *et al*. used fast simulated annealing (FSA) to select the beam angles and adopted down-hill simplex algorithm to set beam weights [15]. Li *et al*. used GA to select the beam angles and used conjugated gradient (CG) to optimize intensity maps for each selected beam combination based on a dose objective function [16]-[17]. Yang *et al*. used an algorithm based on the technique of mixed integer linear programming in which binary and positive float variables are employed to represent candidates for beam orientation and beamlet weights in beam intensity maps [18]. Craft locally refined 100 random beam angle sets in a continuous manner using gradient-based optimization and got optimal plan using a global search in these beam angle sets [19].

Despite these excellent works mentioned above, the computation time of optimizing beam angles is still expected to be further improved especially for the clinical practice.

In recent years, DNA computing has been proposed for many applications, such as Hamilton path problem [20], knapsack problem [21]-[22], traveler salesman problem (TSP) [23], signal processing [24]-[25], image recognition in intelligent visual mechanics [26], *et al*. The GA, as one of the excellent global optimization algorithms for solving complex problems, borrows the intelligence of the biologic evolution. Accordingly, more DNA knowledge is introduced to the standard GA to enhance the evolving ability of the population.

The DNA genetic algorithm (DNA-GA) uses DNA encoding method stemmed from the structure of the biological DNA encoding method to encode the beam angles and some genetic operators based on the DNA genetic operations are adopted. The basic elements of biological DNA are four nucleotides, i.e., Adenine (A), Guanine (G), Cytosine (C) and Thymine (T). In the artificial DNA model, we use a four-letter alphabet $\sum${A, G, C, T} to encode DNA strands, i.e., the individuals of DNA-GA population [27]-[30].Furthermore, there exist 'hot spots' and 'cold spots' in the DNA sequence model [31]-[32], i.e., the larger feasible region is explored when the spots in high bit positions mutates and local region is explored when the spots in low bit positions mutates. This mutation strategy could enhance the evolving ability of the GA

to some extent in that the uniform mutation of the standard GA is not the best way to search for the real best individual.

The purpose of this paper is to introduce a hybrid algorithm named DNA-GA to solve the BAO problem in IMRT planning. The rest of this paper is organized as follows. Section II describes in details the structure of the DNA-GA. In section III, a clinical chest cancer is employed to demonstrate the feasibility and effectiveness of DNA-GA. Finally, some conclusions are made in Section IV. Also, some further research directions are suggested about the BAO problem in IMRT planning.

II. THE DNA GENETIC ALGORITHM

The genetic algorithm (GA), as one of the excellent global optimization algorithms for solving complex problems, borrows the intelligence of the biologic evolution. Accordingly, more DNA knowledge is introduced to the standard GA to enhance the evolving ability of the population in recent years. In this paper, a novel bit mutation strategy and three structure mutation operations are introduced into DNA-GA as two independent parts of DNA-GA. The details are described in this section.

A. The Procedure of DNA-GA

Procedure of DNA-GA

Begin

i). Initialization

ii). Evaluating the fitness of the individuals in the initial population

While (not termination-condition) do

Begin

iii). Selection

iv). Crossover

v). Bit mutation

vi). Structure mutation (deletion, insertion and inversion)

vii). Evaluating the fitness of the individuals in the new population

End

End

Although the structure of DNA-GA is similar with GA, the mutation operations are quite different from that of GA. The details of DNA-GA are described in the following sub-sections.

B. The details of DNA-GA

1) Initialization

The basic elements of biological DNA are four nucleotides, i.e., Adenine (A), Guanine (G), Cytosine (C) and Thymine (T). In the artificial DNA model, a four-letter alphabet $\sum${A, G, C, T} is used to encode DNA strands, i.e., the individuals of DNA-GA population. For the convenience of mathematical operations, a quaternary alphabet $\sum${0, 1, 2, 3} is used to represent the characteristics of DNA nucleotide bases and the population space for a DNA sequence is $S = \{0, 1, 2, 3\}^L$, i.e., sequences of length L.

2) Evaluating the fitness of the individuals in the population

Each quaternary solution is evaluated to give a level of its fitness. The method of evaluating the fitness is same as that of GA.

3) Selevtion

The selection probability of the ith individual, i.e., P_i, is determined according to the strategy of proportional assignment expressed as [16]

$$P_i = \frac{Fitness_i}{\sum_{j=1}^{N} Fitness_j} \tag{1}$$

Where N is the size of the population. A scheme called Roulette Wheel selection is used to determined which individual will be selected after all the fitness values are calculated.

4) Crossover

The crossover operation is very important for the entire search process and the two-point crossover operation shown in Fig. 1 is adopted in this paper [27]~[28]. The crossover points, pc_1 and pc_2, are randomly selected and the middle parts of the chromosomes are exchanged with each other. Normally, the crossover probability is in (0.5~0.9) [16].

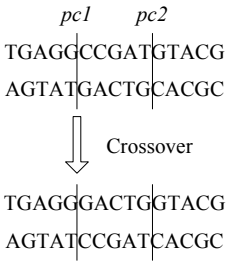

Figure 1. An example of the two-point crossover operation.

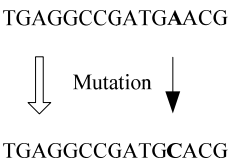

Figure 2. An example of mutation operation (A→C).

5) Crossover

This operation is applied to a randomly selected basic nucleotide of the individual according to the mutation probability. Simply, A is randomly replaced with G, T, or C, G randomly replaced with A, T, or C, T randomly replaced with A, G, or C, and C randomly replaced with A, G, or T. The 12th nucleotide A of the former individual is randomly selected shown in Fig. 2, in which A is randomly replaced with C.

Furthermore, there exist 'hot spots' and 'cold spots' in the DNA sequence model [31]-[32], i.e., the nucleotide bases in the 'hot spots' mutate faster than those in 'cold spots'. The larger feasible region is explored when the spots in high bit positions mutate and local region is explored when the spots in low bit positions mutate. We set the first $L/3$ nucleotide bases of each DNA individual as the hot spots with larger mutation probability at the beginning stage of evolution. As the population evolves, the mutation probability decreases. While the region of the global optimum is found, the mutation probability of these bases decreases down to a small number in order to prevent better solutions from disrupting. Then these hot spots are converted into cold spots with smaller mutation probability.

Because the second $L/3$ nucleotide bases of each DNA individual have also great effect on the search of the optimum, the mutation probability of these bases should be assigned as that of hot spots. However, the effect is smaller than that of the first $L/3$ nucleotide bases, so the mutation probability of these bases should decrease more slowly. The rest bases of each DNA individual have only effect on the solution in the local range of the optimum, so the mutation probability of these bases could be a specific constant. Accordingly, these three mutation probabilities, i.e., P_h, P_m and P_l, are given by:

$$p_h = p_{cold} + \frac{p_{range}}{1+\exp[a_b(g-g_h)]} \tag{2}$$

$$p_m(g) = p_{cold} + \frac{p_{range}}{1+\exp[0.5a_b(g-g_m)]} \tag{3}$$

$$p_l(g) = p_{cold} + p_{range} \tag{4}$$

Where P_{cold} and P_{hot} are respectively the mutation probabilities of the cold and hot spots, P_{range} is the range of bit mutation probability, a_b is a slope parameter, g_h and g_m are delay parameters.

6) Structure mutation (deletion, insertion and inversion)

The deletion, insertion and inversion operations derived from biologic DNA evolution are actually the structure mutation operations to be applied to the individuals. The purpose of adopting these operations is to try to replace those bad individuals with better ones at the beginning stage of evolution. It should be noted that the probability of these operations should decrease fast as that of the hot spots because we could get not better but worse individuals if the global region of the optimum is found and these probability are still large. Different from [27], [28], the length of the individual is fixed in this paper.

When the deletion operation is implemented, new bases are randomly generated to make the individual unabridged (Fig. 3). The superfluous of the bases are deleted when the insertion operation is implemented (Fig. 4). Fig. 5 shows the process of the inversion operation with the inversion segment randomly selected. Considering the effectiveness of the structure mutation operations, the length of the deletion or insertion sequence containing only a few bases has enough ability to disrupt the individuals. The structure mutation probability is described as

$$p_s(g) = p_{sl} + \frac{p_{sr}}{1+\exp(a_s(g-g_s))} \tag{5}$$

Where P_{sl} is the basic structure mutation probability, P_{sr} is the range of change of structure mutation probability, a_s is a slope parameter, g_s is a delay parameter.

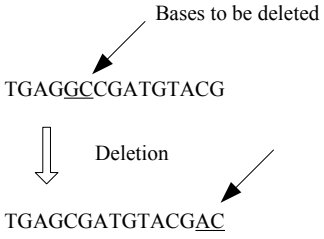

Figure 3. An example of the deletion operation.

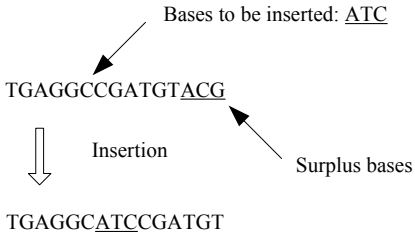

Figure 4. An example of the insertion operation.

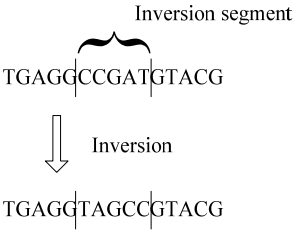

Figure 5. An example of the inversion operation.

7) The termination rule

The optimization process will be terminated if the predefined maximum iteration number is reached, or some other termination conditions are satisfied.

III. Application Of DNA-GA To BAO

We apply DNA-GA to the BAO problem of a clinical chest tumor. To test the robustness of the proposed algorithms, both of the GA-based and DNA-GA-based optimization tasks independently run 20 iterations. Both of the two algorithms are

coded in Borland C++, and run on an Intel Pentium III 2.4 GHz PC with 512 MB RAM.

A. The work flow of DNA-GA solving BAO

The flow chart of the DNA-GA solving BAO is shown in Fig. 6. Some steps in Fig. 6 are described as follow.

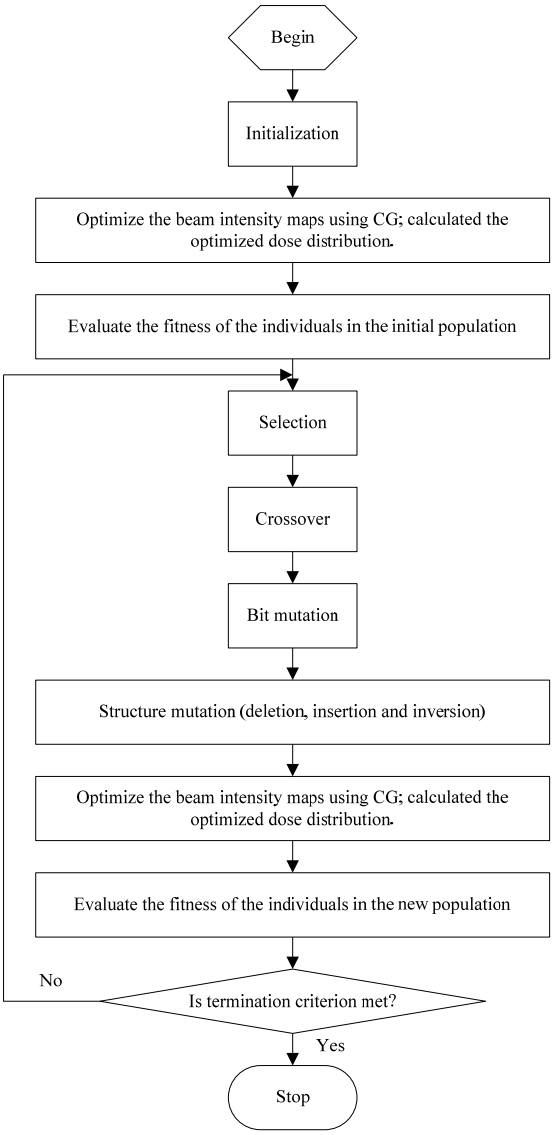

Figure 6. The flow chart of the DNA-GA.

1) Initialization

We use three nucleotide bases to represent a beam angle, and then the length of the individual is three times as the number of beams in IMRT plan. Mathematically, there are 64 possible triplet codes for DNA encoding, i.e., codons in biology, and the parameter values of codons are shown in table Ⅰ. The search space is discretized with an angle step of about 5.6°, which results in 64 candidates, a requirement of DNA coding scheme. The example of the DNA individual with 4 beams is shown in Fig. 7. The relationship between the values of codons and beam angle is described as:

$$V_{angle} = \frac{V_{codon}}{64} \times 360 \tag{7}$$

Where V_{angle} is the beam angle, V_{codon} is the parameter value of the codon.

TABLE I. THE PARAMETER VALUES OF CONDONS

First base	Second base				Third base
	A	*G*	*C*	*T*	
A	0	4	8	12	A
	1	5	9	13	G
	2	6	10	14	C
	3	7	11	16	T
G	16	20	24	28	A
	17	21	25	29	G
	18	22	26	30	C
	19	23	27	31	T
C	32	36	40	44	A
	33	37	41	45	G
	34	38	42	46	C
	35	39	43	47	T
T	48	52	56	60	A
	49	53	57	61	G
	50	54	58	62	C
	51	55	59	63	T

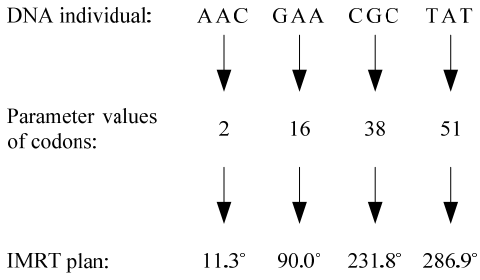

Figure 7. The relationship between a DNA individual and the IMRT plan with four beams.

2) Evaluating the fitness of the individuals in the population

The quality of each individual is evaluated by a fitness value, and the purpose of optimization is to find the individual with maximum fitness. For each new individual, an optimization of beam intensity maps is implemented using CG [16], [17]. The corresponding optimized dose distributions are calculated for the evaluation of the fitness of the individuals. The corresponding relationship between the DNA individual and the IMRT plan is described in Fig. 7. The beams with the angles contained in a plan $\vec{x} = (x_1, x_2, \cdots, x_D)$ are divided into pencil beamlets (also called rays), and all the rays are expressed as a vector $\vec{z}$. The fitness value of an individual is calculated by

$$Fitness(x) = F_{\max} - F_{obj}(x) \tag{7}$$

Where F_{max} is a rough estimation of the maximum value of the objective function, which makes sure that all the fitness values are positive, a requirement of the selection operation of GA.

The basic form of objective function used in this paper can be written as [16]

$$F_{obj}(\vec{z}) = \sum_{j=1}^{NT} \delta_j \cdot w_j \cdot [d_j(\vec{z}) - p_j]^2 \tag{8}$$

$$d_j(\vec{z}) = \sum_{m=1}^{Nray} a_{jm} \cdot z_m \tag{9}$$

Where NT is the number of sample point in the volume, δ_j=1 when point dose in the volume breaks the constraints, else δ_j =1. w_j is the weight of jth point, d_j is the calculated dose of the jth point in the volume, p_j is the prescribed dose of the jth point in the volume. N_{ray} is the total number of ray, a_{jm} is the dose deposition to the jth point from a unit weight of the mth ray, z_m is the intensity of the mth ray.

3) The termination rules

The optimization process will be terminated if the predefined maximum iteration number is reached, or the current best individual cannot be further improved after sufficiently large number of successive iterations. The angles contained in the current best individual will be regarded as the optimal set of beam angles.

The rest steps are the same as these described in section Ⅱ.The application of DNA-GA to BAO problem is shown in the following sub-section.

B. Application of DNA-GA to a clinical chest tumor

The clinical case of chest tumor is shown in Fig. 8. In this case, the planning target volume (PTV) is surrounded by three critical organs: spinal cord, left and right lungs. The dose prescription to the PTV is set to 5000 cGy, which is normalized to 100%. Three coplanar photon beams are used for the treatment.

We use a population of 24 individuals, and half of them are initialized with equi-spaced beam angles and the rest are stochastically initialized. Optimizations with the DNA-GA and GA-based algorithms are studied. DNA-GA and GA use the same encoding method described above.

Both DNA-GA and GA can obtain the optimal plan (5.6°, 112.5°, and 264.3°). Fig. 8 illustrates the dose distributions with three equi-spaced beams (0°, 120°, and 240°) and the optimal plan. We can see that the optimized plan spares the lungs with more volumes compared to the plan with equi-spaced beams.

Although DNA-GA and GA could get the same optimal solutions, the former is faster than the latter. Averagely, DNA-GA found the optimal results within about 35 iteration times; whereas, GA used far more than 50 times of iteration.

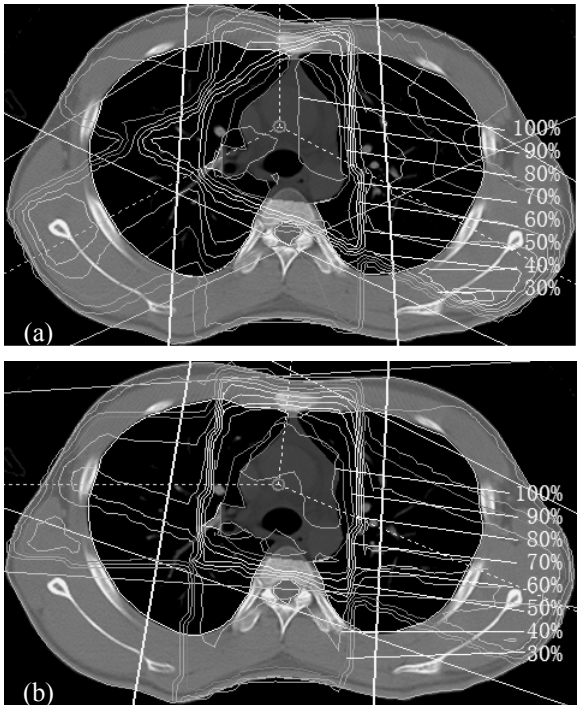

Figure 8. 1-PTV, 2-Right lung, 3-Left lung, 4- Spinal cord. The beam angles and dose distributions of equi-spaced (a) and optimized (b) plan.

IV. CONCLUSION

In this paper, a DNA genetic algorithm (DNA-GA) is introduced to optimize the beam angles for intensity-modulated radiotherapy (IMRT) planning. Some strategies borrowed from DNA computation are incorporated into the standard GA to enhance the evolving ability of the population. The preliminary result showed the feasibility of DNA-GA for the BAO problem, and the clinical case also demonstrated the importance to optimize the beam angles for IMRT planning. More importantly, the paper demonstrated that the proposed DNA-GA algorithm could solve the BAO problem more efficiently than the standard GA.

At the beginning stage of the evolution, the structure mutation operations, i.e., deletion, insertion and inversion, provide a higher probability to replace the bad individuals with better ones. Moreover, it is helpful to find the global optimal results by setting different bases of individuals with different mutation probabilities, i.e., P_h, P_m and P_l, so that it could be easier to find the region of global optima. A three-triplet code is used to represent a beam angle, which results in 64 possible discrete angle candidates among the continuous 360º degrees, and this meets the clinic requirements. Because of using the DNA encoding scheme, the code length of the individuals of DNA-GA is much shorter than that of GA. Accordingly, the cost of computer memory is lower that of GA. DNA-GA hybridizes the preferable encoding scheme and evolution operations of DNA and GA computation algorithm, which guarantees DNA-GA with faster convergence and higher probability to find the global optima.

In our future work, more clinical tumor cases, such as head-and-neck tumors and prostate tumors, would be employed to

test the efficiency and robustness of the proposed DNA-GA optimization algorithm. In addition, thorough comparisons would be made between DNA-GA and GA algorithm before the DNA-GA algorithm could be robustly and efficiently used in the IMRT routine practice.

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