

## USING A REAL CHROMOSOME IN A GENETIC ALGORITHM FOR WIRE ANTENNA OPTIMIZATION

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### INTRODUCTION

A GA is composed of several elements: the chromosome representation of a design, the mating and mutation methods that generate new designs from existing populations, the cost function, selection and replacement schemes, and runtime parameters like population size. The first two of these elements, which determine in large part the effectiveness of the algorithm, are the main subject of this paper. The reader is referred to [1] for a complete treatment of the GA process.

The most common type of chromosome representation is the binary string, which codes all design variables into a series of binary numbers. The most common mating operator for such chromosomes is the simple single-point crossover. In this operation, a child is created from two parents by randomly selecting a crossover point, and copying the genes from the part of the first parent's chromosome before the crossover point, and the part of the second parent's chromosome beyond the crossover point into the child chromosome. The mutation operator is also simple, requiring merely a randomly-chosen bit to flip.

The binary GA requires that all continuous problems be approximated by discrete ones. Unknowns are found by appropriately translating several binary genes, however, there is nothing in the GA operators that takes this into account. The chromosome, then, becomes longer the more accurately one wishes to specify the variables. The longer the chromosome, the more difficult the search becomes. To give a hypothetical situation, let a problem have one unknown that can span the range from  $0.01 - 1\lambda$ , with a desired minimum resolution of  $0.01\lambda$ . A binary chromosome would require 7 genes to allow this kind of resolution ( $7 \text{ bits} = 128 \text{ steps}$ ). If one could use real numbers in the chromosome, one would need only a single gene to go to an almost arbitrary resolution. Thus, the use of a real chromosome can significantly decrease the number of genes needed to specify a design over a binary chromosome.

In addition, binary mating and mutation operations do not make use of numerical relationships between different values of genes, because they are modeled after biological processes. This quality is not important in situations where there is no mathematical relationship between two different design values, like the difference between different materials or different items selected from a list. However, most problems in electromagnetics have variables whose values are related mathematically, like distances or diameters.

It is more natural to use this kind of information when using real chromosomes. The mating and mutation schemes presented here use methods like interpolation which can predict the effectiveness of combinations that have not been seen by the GA and allow the GA to make full use of the power and compactness of the real chromosome.

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## THE METHOD OF USING REAL CHROMOSOMES

The following method [2] allows the GA to interpolate and extrapolate from the data provided by the parents' genes and fitnesses the most likely gene values to produce superior children. Since it only considers two or three parents at a time, its predictions will often be wrong. However, over a large number of matings, its predictions will be correct enough to move the population toward an optimum.

The first step is to choose three parents from the population. While in biological situations choosing three parents would be unviable, this form of mating is mathematical in nature rather than true to its biological counterpart.

Once parents are chosen, the following steps are then performed for each gene separately:

1. Perform Quadratic crossover on the genes.
2. If 2 fails, due to lack of the desired extremum in the feasible gene range, perform heuristic crossover with the best and the worst parents of the three.
3. If 3 fails to produce a child gene in the feasible range, randomly choose one of the three parents to have its gene copied into the child's gene.

Quadratic crossover fits a quadratic curve relating parents' gene values to fitness. If the desired extremum exists inside the feasible range, that value is chosen for the child's gene value, as shown in Figure 1. The equations to produce this curve and associated expressions for its extremum and tests to show its existence are given by standard 2<sup>nd</sup> order linear regression.

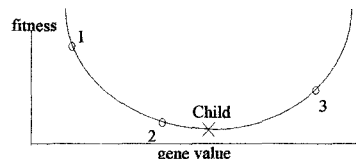


Figure 1. Quadratic Crossover. In this case, the fitness is desired to be minimized.

Heuristic crossover involves extrapolating from only two parents the most likely region for a superior child's gene value, as shown in Figure 2.

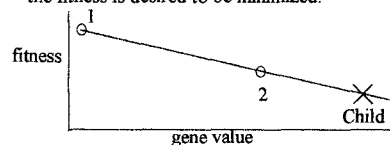


Figure 2. Heuristic Crossover. In this case, the fitness is desired to be minimized.

The following procedure is used for Heuristic Crossover [3]. Given two parents:  $P1 = \{p_{11}, p_{12}, \dots, p_{1n}\}$ ,  $P2 = \{p_{21}, p_{22}, \dots, p_{2n}\}$ , let  $P2$  have a better fitness level than  $P1$ , and let the child  $C = \{c_1, c_2, \dots, c_n\}$ . The child's genes are given by  $c_i = \text{rnd}(p_{2i} - p_{1i}) + p_{2i}$  where  $\text{rnd}$  is a random number between 0 and 1.

Mutation methods are less critical in most cases than mating methods. Commonly used in real-valued chromosomes are the uniform probability mutation, where the new, mutated gene has a value that is drawn from a uniform probability density within the feasible range, and the Gaussian probability mutation, where the mutated gene is drawn from a Gaussian distribution centered around the current gene value [2].

I have applied the mating and mutation methods above to several wire antenna problems, and have found it to be highly effective. I will show how it has performed compared to traditional binary GAs for two very different wire antenna optimizations in the next section.

## EXAMPLES

The first example involves the Yagi antenna, which consists of a series of parallel wires, one of which is excited by the driving source. The design requires a value for every spacing and the length

of every wire. Following is a table comparing the outcome of 58 binary chromosome GA runs with the first run with a real chromosome. Each optimization was performed with the same cost function, which gave better scores for increased gain and decreased sidelobe and backlobe levels. The simulator used to evaluate all individuals was the Numerical Electromagnetics Code, Version 2 [4]. There were 36 unknowns in the design: 18 wire lengths, 17 spacings, and one for the wire diameter used throughout the antenna. Each variable, except wire diameter, was given 6 bits in the binary chromosome for adequate resolution; wire diameter was given 2 bits.

| 5.16 $\lambda$ , 18 elements | Binary Chromosome  | Real Chromosome                                |
|------------------------------|--------------------|--|
| # of GA runs                 | 58                 | 1  |
| NEC Sims. Needed             | 287,561            | 68,412<br>(99% in 18,994)<br>(99.9% in 45,439) |
| Best Gain                    | 16.7 dBi           | 17.4 dBi                                       |
| Sidelobe Level               | -18.2 dB from main | -18.0 dB from main                             |
| Backlobe Level               | -25.0 dB from main | -25.0 dB from main                             |

Table 1. Comparison of best individuals from binary and real chromosome GAs.

As shown in the table, the best individual from the real GA was somewhat better than the best individual from the binary GA. Notice that the average number of simulations for each binary GA run is less than that of the real-numbered GA, however, the real GA required only one optimization to beat every score attained by the binary GA.

With a binary GA, the population eventually converges to a single chromosome and stops improving, however, the real-numbered GA does not converge entirely, and the score tends to keep improving incrementally as it is allowed to run. However, the improvement in score eventually becomes very small as the run proceeds, as is shown by the above table.

The second example involves has been called the crooked-wire genetic antenna. This antenna consists of seven wires connected in series over a ground plane, with endpoints designated by the GA but restricted to be within a cube  $0.5\lambda$  on a side, as shown in Figure 3. The reader is referred to [5] for a more complete description of this antenna.

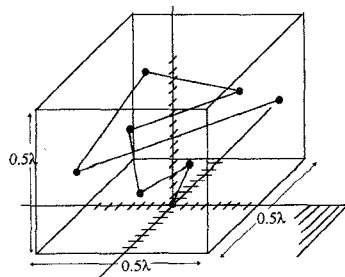


Figure 3. The design space of the crooked-wire genetic antenna.

The cost function involves attempting to produce an antenna pattern that is able to cover the hemisphere  $10^\circ$  above the horizon with a right-hand circularly polarized wave. This pattern is useful for satellite communications [5]. The cost function is the sum of the squares of the differences between each point in the pattern compared to the mean, which implies that a lower score is better.

The best antennas from the binary and real-numbered GAs were similar in fitness, though they are very different in shape. With a finely-tuned binary GA, which took many hundreds of runs and tens of thousands of simulations to tune, the best fitness score was 222. This is a very even coverage over the hemisphere. This result required 26,730 simulations and 6 separate GA runs to achieve, plus all the

runs to tune the GA, during which nothing appeared that was better. The real-numbered GA did not work well until a mating restriction was put in place. Once this was done, the GA did not require further tuning to produce a score of 185 on its first run, requiring 24,879 simulations.

This mating restriction was necessary because, as was previously noted, the mating process is applied gene-by-gene and produces children that may have little resemblance to its parents. But

because in this problem there is significant interdependence between genes, children created gene-by-gene often failed to work well. However, if similar parents are encouraged to mate, then the child will not be so dramatically different from its parents. The mating selection process was therefore modified. The first parent was chosen with the traditional fitness-weighted roulette wheel. The second and third parents were chosen using a distance-weighted roulette wheel, where distance was calculated to be the Euclidean distance (i.e. the root of the sum of squares of the difference between each of the unknowns) between the individual in question and the parent already chosen according to fitness. This is a method of speciation, a subject described in more detail in [1].

## CONCLUSION

The advantages of using a real-valued chromosome, then, are that the GA can use any continuity information inherent in the problem and decrease dramatically the number of genes required to specify a design, thus making the solution space easier to search. The real-numbered chromosome mating and mutation operators were outlined in detail, and examples that show their effectiveness were presented. A variant of the technique that requires atypical mating selection methods was shown in the last example.

Though the examples were in wire antenna design, this real-valued approach is more native to many other electromagnetics problems than the binary approach, and should be considered by the GA user. I recommend this method for those problems that are all or mainly real-numbered problems, and especially those that have difficult, "spiky" search spaces with many local minima. For those designs with highly inter-related variables, the mating restriction requirement is recommended, while those with more independent variables can probably use the conventional fitness-weighted mating selection with success.

## ACKNOWLEDGMENTS

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