

**Application of Genetic Algorithms in Array synthesis  
for Linear Phase Array Antenna**

*Ass.Prof. Dr. Waleed K. Abid Ali\**

*Ass.Lecturer Zaid A.Abed Al-hussein\**

**ABSTRACT**

**This paper demonstrates the application of genetic algorithms (GA) in array synthesis. This approach directly represents the array excitation weighting vectors as real number chromosomes. This approach has some advantages, such as giving a clearer and simpler representation of the problem, simplifying chromosome construction, and totally avoiding binary encoding and decoding so as to simplify software programming.**

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\* Electrical Engineering Dept./ College of Engineering / Al-Mustansiriya University, Baghdad, Iraq.

## **1. Introduction to Genetic Algorithm (GA)**

From the practical view points, several things are desired of broadside antenna arrays. The beam should be as narrow as possible, the gain should be a maximum and side lobes if any should be at a low level. It is often a difficult matter to reconcile these demands. To illustrate, the gain may be made a maximum by feeding all elements of equal magnitude and phase. Unfortunately, although it true that this current distribution results in high side lobes of the order of -12 dB down of the main lobe. In many applications it is more important to sacrifice some gain and beam width in order to achieve low side lobe levels [1,2].

Various analytical and numerical techniques have been developed to meet the challenge. Examples of analytical techniques include the well-known Taylor and Chebyshev methods. In recent years, numerical approaches have become more popular as they are applicable not only to regular arrays (such as linear arrays and circular arrays) but genetic algorithms have very wide applications [3].

Genetic algorithm is inspired by Darwin's theory about evolution. Algorithm started with a set of solutions (represented by chromosomes) called population. Solutions from one population are taken to form a new population. This is motivated by a hope, that the new population will be better than the old one. Solutions which are selected according to their fitness the more suitable they are the more chances they have to reproduce. This is repeated until some condition is satisfied [3,4].

Genetic algorithm may be used as a simple and flexible alternative to achieve the same objective, which other methods can do, and more importantly, it has unique features to treat some complicated problems (arbitrary geometric layout, including mutual coupling), which can not be done by other methods [3].

Conventional GA's with binary coding and binary genetic operation are non-convenient and inefficient for array pattern synthesis problem to optimize real or complex numbers. This approach avoids coding and directly deals with real weighting vector [3]. The details of this approach will be discussed in the following sections.

## 2. Construction of Chromosomes

Using genetic algorithms for array pattern synthesis, radiation patterns corresponding to living beings and array-weighting vectors correspond to chromosomes. Genetic algorithms were invented to manipulate a string of binary coding. Conventional genetic algorithms encode the parameters in binary chromosomes and perform binary genetic operation. In this approach, chromosomes are represented directly by real weighting vector [3].

$$a_1 = [A_1 A_2 A_3 \dots A_n \dots A_N] \quad \dots(1)$$

Where  $A_n$  (known as a genetic material in a GA) represents the excitation of the  $n$ th radiator and  $a_1$  is set of real numbers.  $N$  is the length of the weighting vector. This simple representation explicitly shows the relation between chromosomes in genetic algorithm and array- excitation weighting vector [3].

### 3. Initial Population

For fast convergence of genetic algorithm iteration, the initial population can include approximate excitations by other simple techniques (minimization of mean square errors (MMSE) method and Taylor (one-parameter) method), and excitations by guess based on experience and/or at random [3]. In this work Taylor (one-parameter) method can be used with the excitation values as given by [1].

$$A_n(x') = J_0 \left[ j\pi B_1 \sqrt{1 - \left( \frac{2x'}{Nd} \right)^2} \right] \quad \dots(2)$$

Where

**N** is the number of elements.

**d** is the distance between elements.

**x'** is the distance measured from the center of

$$\text{array} = \frac{d}{2} + (f' - 1) * d$$

$$f' = 1, 2, 3, \dots$$

**J<sub>0</sub>** is a Bessel function

**B<sub>1</sub>** is constant determined from side lobe level.

$$R_o = 4.603 \frac{\sinh(\pi B_1)}{\pi B_1} \quad \dots(3)$$

#### 4. Fitness Function

After producing the initial populations are produced, and their fitnesses correspond to side lobe levels for the selection of suitable chromosome to compete for next generation. The radiation pattern generated by an N-elements antenna array is given by [5].

$$E(q) = 2 \sum_{n=1}^{N/2} A_n \cos \left( \left( \frac{2n+1}{2} \right) \gamma \right) \quad \dots(4)$$

and relative side lobe level in dB is computed from the radiation pattern using [6]

$$SLL_{dB} = 20 \log \frac{\max |E_{rad.}(\theta)|}{E_{max.}} \quad \dots(5)$$

where

**SLL** is the side lobe level in dB.

$\max |E_{rad.}(\theta)|$  is the maximum value of the highest side lobe magnitude.

**E<sub>max</sub>** is the peak of main lobe.

From the equation (5), the objective function is obtained as:

$$\text{error} = |SLL_{desired} - SLL_{obtained}| \quad \dots(6)$$

Then

$$\text{The fitness function} = 1/\text{error} \quad \dots(7)$$

Where the objective function is the calculation of its associated fitness.

The fitness function is measure of the quality of a chromosome [7].

## **5- Selection**

There are many mating techniques available to pick two parent chromosomes to produce child chromosome [3].

### **1) Roulette Wheel selection**

Parents are selected according to their fitness. The better chromosomes are, the more chances to be selected they have. Imagine a roulette wheel where are placed all chromosomes in the population are placed every has its place big accordingly to its fitness function [4].

### **2) Rank Selection**

Rank selection first ranks the population and then every chromosome receives fitness from this ranking. The worst will have fitness 1, the second worst 2 etc., and the best will have fitness P (where P is the number of chromosomes in population). After this all the chromosomes have a chance to be selected [3].

## **6- Crossover**

Crossover is another process that involves exchange of genetic materials between two parent chromosomes to make child chromosome. The simplest way to do this is to choose randomly some crossover point and then everything before this point copies from the first parent and everything after a crossover point copies from the second parent. There are many types of crossover [3,4].

### 1) Single point crossover:

One crossover point is selected, string from the beginning of chromosome to the crossover point is copied from one parent and the rest is copied from the second parent [4].

### 2) Two points crossover:

Two points crossover are selected, string from the beginning of chromosome to the first crossover point is copied from one parent, the part from the first to the second crossover point is copied from the second parent and the rest is copied from the first parent [4].

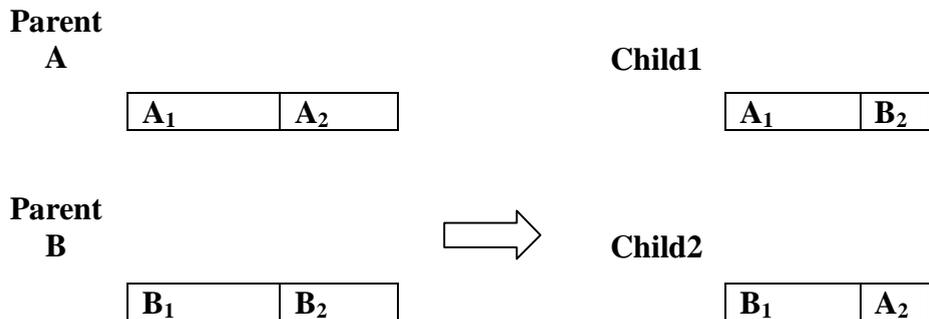


Fig.(1) One point crossover

### 3) Uniform crossover

Genes are randomly copied from the first or from the second [4].

### 4) Arithmetic crossover (linear crossover)

Some arithmetic operations are performed to make a new offspring (average, and extrapolation crossover from midpoint) [3,4].

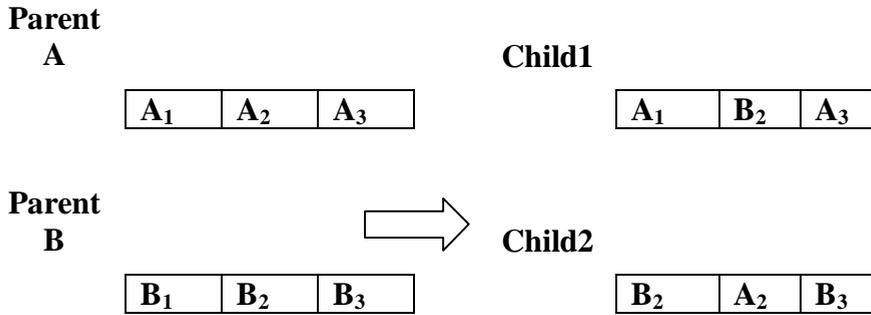


Fig.( 2) Two point crossover

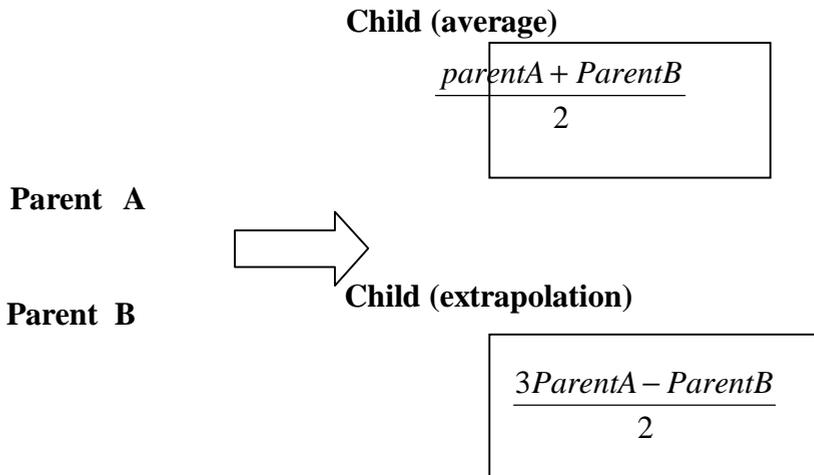


Fig.(3) Arithmetic crossover

## 7- Mutation

After a crossover is performed, mutation takes place. This is to prevent falling all solutions in population into a local optimum of solved problem. Mutation changes randomly the new offspring (children). There are many types of accomplishing mutation (binary mutation, and real mutation). Real mutation is used according to the following equation, as [4,8]:

$$d_i' = \begin{cases} r(L_o, U_p) & \text{if } z' \leq P_m \\ d_i & \text{otherwise} \end{cases} \quad \dots(8)$$

where

$z'$  is random number.

$r(L_o, U_p)$  is random number with limited range  $(L_o, U_p)$ .

$d_i$  is the value of gene before mutation.

$d_i'$  is the value of gene after mutation.

$P_m$  is probability of mutation equal to (0.5%-1%) .

## 8-Survival Selection

Once all the new child chromosomes are produced and their fitnesses are evaluated, the evaluation can be done by ideal pattern function. There are few selection techniques available. In this approach, Roulette Wheel selection is used. One can note that the competitors for survival selection include both parents (best parent) and their children so that the members of the next generation may include members of the previous generation. This guarantees

radian

...(9)

where that the newer generation performs no worse than ones [3].The progress of reproduction and survival selection continue until a satisfied result is obtained or maximum number of iteration is reached [3]. The half power beam width can be calculated from [9]:

$$HPBW = \frac{0.886I}{N * d_{eff}}$$

$d_{eff}$  is an illumination efficiency (or taper losses)

$$= D_{taper} / D_{uniform} \cdot$$

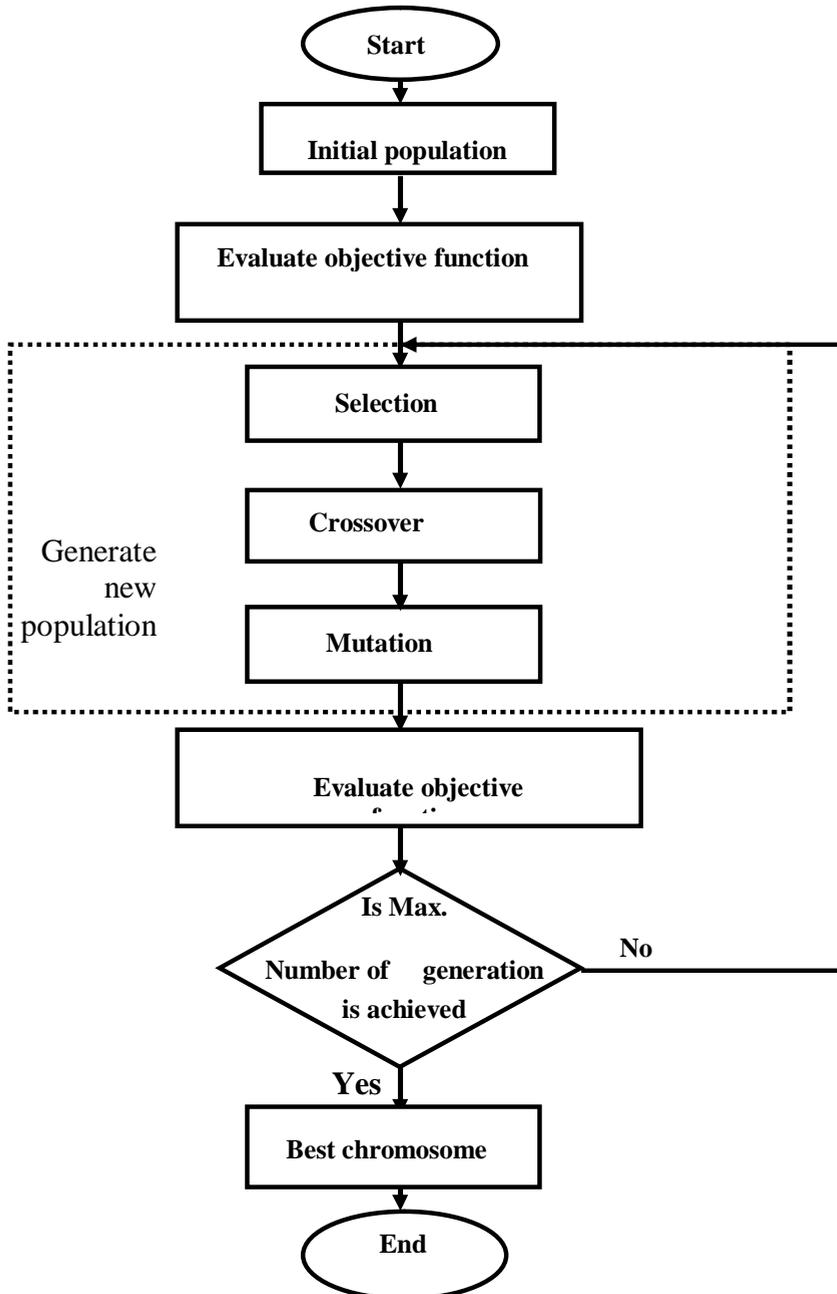
and the directivity can be calculated from.

$$D = \frac{\left( \sum_{k=0}^{N-1} A_k \right)^2}{\sum_{m=0}^{N-1} \sum_{p=0}^{N-1} A_m A_p \frac{\sin[(m-p)bd]}{(m-p)bd}} \quad \dots(10)$$

## 9- Implementation of the algorithm and results

The genetic algorithms are carried out in 13 runs of 200 iterations. The initial parent population consists of 20 sets of positive excitation amplitudes. This size is chosen such that be not small in order to cover the search space, and it is not large to prevent the increase of computation time. Symmetric excitation is assumed. The crossover is done on half of the chromosome followed by coping it to the other half in the mirror image format (using two points crossover). In this paper the Roulette Wheel selection and real mutation are used.

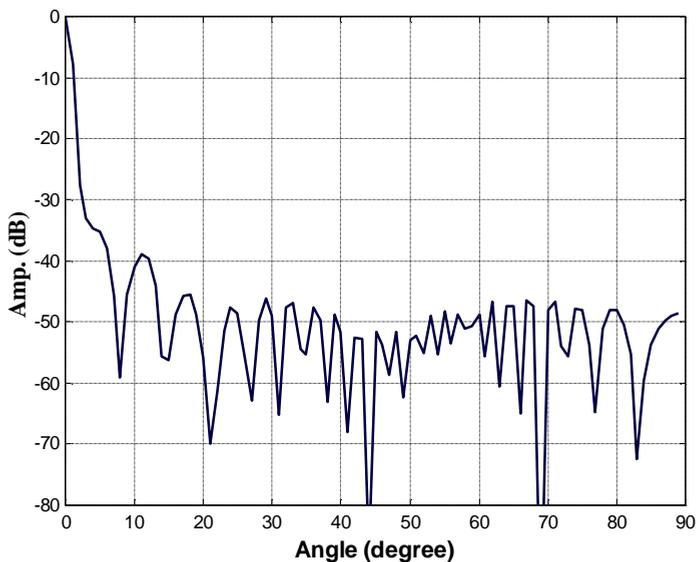
The relative side lobe levels are obtained between -27.8 and -35 dB, as shown in table (1). Fig.(4) shows Algorithm for the computation of current distribution of genetic algorithm. Fig.(5) shows pattern of array factor using genetic algorithm with elements equal to 72 at distance equals to  $0.5\lambda$  . Fig.(6) shows current distributions for half-number elements obtained by genetic algorithms, and table (2) shows current distributions for half-number elements for side lobe level of -35 dB. The directivity is equal to 19.2582 dB for array factor and half-power beam width of 1.0569 degree. Fig.(7-8-9-10) show far field pattern for array factor at distance equals to ( $0.4\lambda$ ,  $0.9\lambda$ ,  $1\lambda$  and  $1.2\lambda$ ) respectively. Fig.(11) shows the array factor of linear phase array at broadside using Dolph Chebyshev Distribution at distance is equal to  $0.5\lambda$  for different side lobe level. The directivity is equal to 18.5372 dB for array factor using Dolph Chebyshev Distribution.



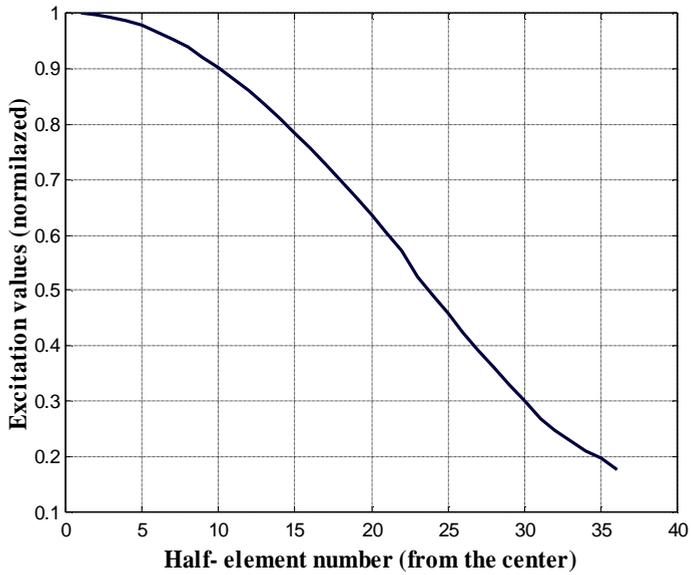
Fig(4) Algorithm for the computation of current distribution for genetic algorithm

**Table (1) Side lobe levels of the 13 runs at the distance  $0.5 l$  .**

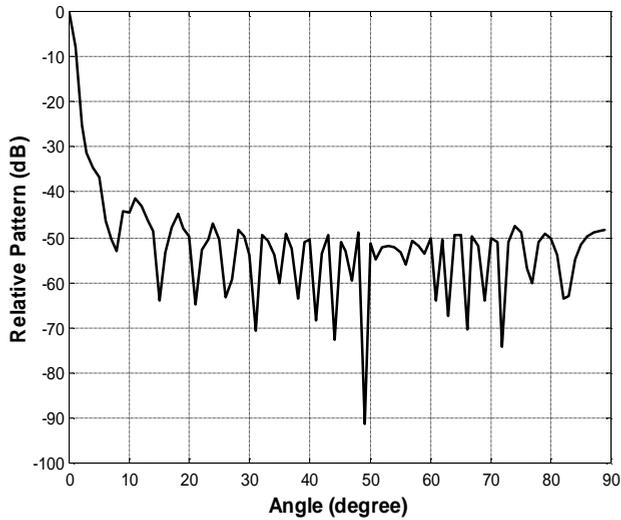
Side lobe level dB
-27.8
-28
-30
-31
-32
-32.5
-33
-33.3
-33.5
-34
-34.25
-34.4
-35



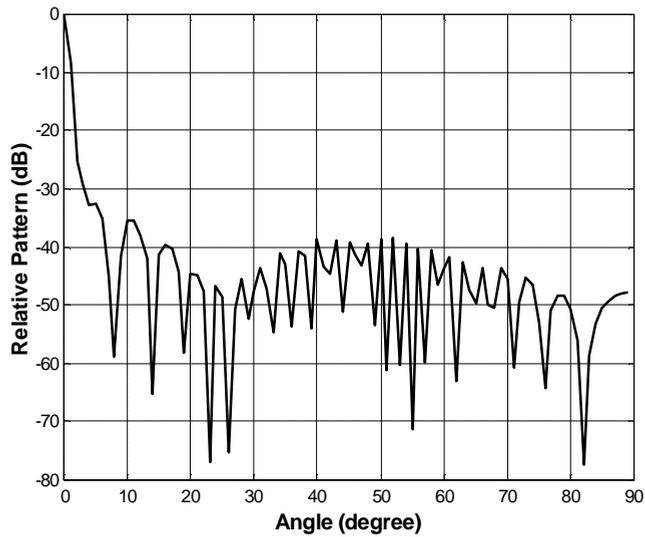
**Fig.(5) Far field pattern of array factor for linear phase array using Genetic algorithm at distance between elements is equal to  $0.5l$  with elements equal to 72**



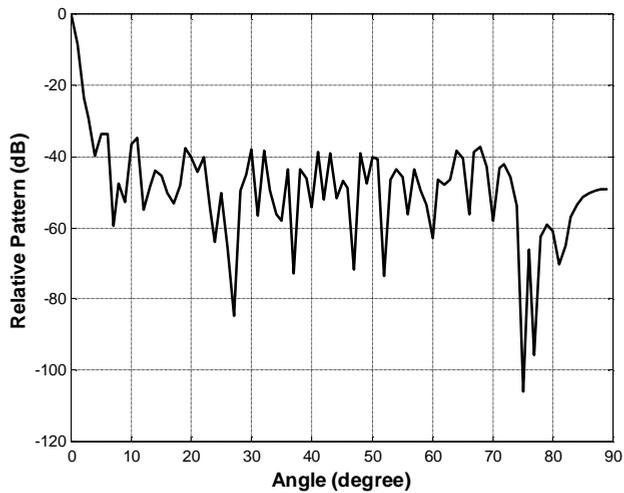
**Fig.(6) Excitation values for half-number elements for array using genetic algorithm(SLL=-35**



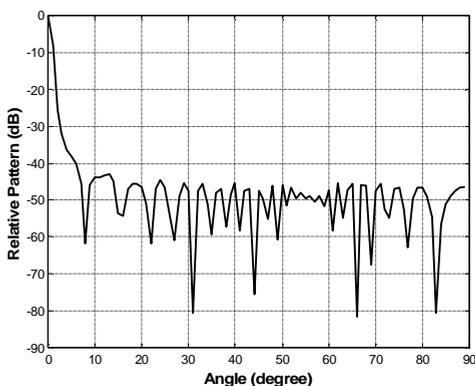
**Fig(7) Far field pattern for array factor at distance between elements is equal to 0.41 and SLL=-36.8dB dB) with**



**Fig(8 ) Far field pattern for array factor at distance between elements is equal to  $0.9l$  and  $SLL=-33.5dB$  with elements equal to 72.**



**Fig(9) Far field pattern for array factor at distance between elements is equal to  $1l$  and  $SLL=-33.73dB$**



Fig(10) Far field pattern for array factor at distance between elements is equal to  $1.2\lambda$  and SLL=-36.5dB with elements equal to 72.

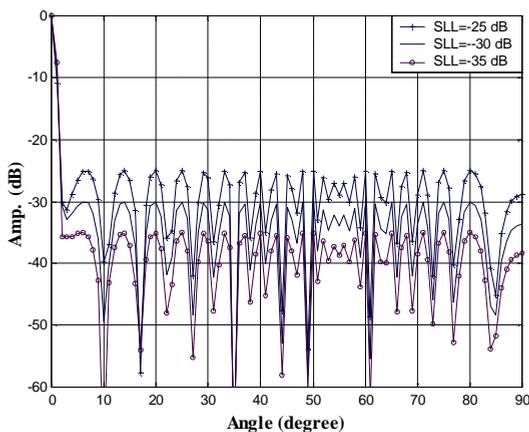


Fig.(11) Array factor pattern using Dolph Chebyshev method ( $N=72, d=0.5\lambda$ )

## 10- Conclusion

Simple and flexible GA's is proposed as a general purposed tool for current distribution at uniformly spaced linear array. Genetic algorithm may be used as alternative method to achieve the same objective, which other methods can do. Current distribution shape for genetic algorithms is monotonic decrease.

The directivity of genetic algorithms is greater than Dolph Chebyshev method for the same SLL. Genetic algorithm can solve the problem of element spacing for any value while Dolph Chebyshev is limited in the range  $[\lambda/2, \lambda]$ .

## Reference

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## تطبيق الخوارزمية الجينية لتشكيل مصفوفة هوائيات خطية

م.م. زيد اسعد عبد الحسين\* أ.م. د. وليد خالد عبدعلي\*

### المستخلص

إن هذا البحث يهدف إلى تصميم هوائي شريطي دقيق عريض الحزمة يعمل بتردد رنيني 2.9 GHz باستخدام هوائي شريطي دقيق ذو رقعة مستطيلة الشكل مربوط بفجوة مع رقع طفيلية. تم دراسة وتصميم عدة نماذج هندسية والتي تتركز على ربط تلك الرقع الطفيلية بالهوائي الشريطي المستطيل إما من الحافة المشعة للهوائي أو من الحافة الغير مشعة له أو من كلتا الحافتين. تم دراسة تأثير إضافة رقعة واحدة أو اثنين أو أربع رقع. تم تحليل هذا الهوائي باستخدام حقيبة برمجيات المايكروويف نسخة 7.5 الصادرة في عام 2007. وقد تم إثبات إن عرض الحزمة سوف تتضاعف بمقدار ستة أضعاف مقارنة مع هوائي شريطي دقيق مستطيل الرقعة.

\*قسم الهندسة الكهربائية/ كلية الهندسة/ الجامعة المستنصرية.