

DIGITAL AMPLITUDE CONTROL FOR INTERFERENCE SUPPRESSION USING IMMUNITY GENETIC ALGORITHM

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Abstract—In this paper, we propose a novel genetic algorithm (GA) called immunity GA (IGA) for array pattern synthesis with interference suppression using digital amplitude only control. The IGA is based on crossover evolution where the crossover operator is a variant of the known GA operator. A new formulation of the array factor transform for a specific number of elements N is expressed by a discrete cosine transform (DCT) with pre-computed DCT matrix. Evaluating thousands of candidate solutions generated by the IGA using the precomputed DCT matrix will result in a high speed computation. This high performance allows us to find a good approximation of the absolute minimum SLL of synthesized arrays with digital amplitude control. Simulation results show the effectiveness of this new algorithm for pattern synthesis with low SLL and null steering.

1. INTRODUCTION

Antenna-based signal processing that suppress the interfering signals from prescribed directions while receiving the desired signal from a chosen look direction are still a challenging problem to date [1–4]. Through array antenna signal processing algorithms, sidelobe jammers can be attenuated by modifying some of the array-element amplitude

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weights to cause deep pattern nulls in the jamming or interfering signal direction. The determination of the appropriate set of amplitudes is the main role of the anti-jam signal processing algorithms. These amplitudes (weights) must be determined adaptively, since a jammer may move from one part of the sidelobe region to another, and therefore the amplitudes must be readapted. The cost of carrying out the amplitude-adaptation algorithm depends sensitively on the number of amplitudes being determined. The computational cost is proportional to the number of elements and thereby the computation time depends on the number of multiplications and additions. Reducing these later is very critical and hence a good algorithm should be based on fast computation technique to allow instant interference suppression. Since large antenna size is needed to obtain narrow main beam width, it requires a cumbersome procedure to calculate the current excitations which will be very sensitive to the relative errors.

Also, to simplify the feeding network, the constituent antennas in a linear array which possess identical characteristics, are uniformly spaced with identical current excitations. Furthermore, the array hardware complexity can be significantly reduced by turning off some elements in a uniformly spaced or periodic array to produce low side lobes [5]. In the on-off approach, the problem can be reformulated as an array pattern synthesis with digital amplitude weighting control where the elements amplitude weights can be 1 (on) or 0 (off). In this approach, the problem of finding the best combinations of the active array elements to obtain minimum side lobe level (SLL) with interference suppression involves checking a large number of possibilities which is only practical for small array size. To take advantage of previous research works, the problem of array elements digital amplitude weights control can be considered as a dynamic array thinning to produce an active elements density across the aperture in order to create the desired nulls while minimizing the SLL array pattern. More recent researches for designing thinned antenna arrays are oriented towards new algorithms to produce the lowest SLL, such as genetic algorithms (GA) [5–7], simulated annealing (SA) [8, 9], neural networks [10], evolutionary programming [1–13]. Mahanti et al. proposed a real-coded GA with elitist strategy for thinning a large uniformly array [6]. The SLL obtained was about -20.5 dB with thinning of 22% and 24% of 100 array elements. Evolutionary programming (EP), a multi-agent stochastic search method, is proposed for optimizing thinned phased arrays with a large number of elements [11]. Also, recently, a pattern search (PS) algorithm was proposed by Razavi and Forooghi as a tool for array thinning [12]. Moreover, differential evolution algorithm (DE) and

a binary-coded GA are jointly applied to the minimization of SLL problem in planar arrays [13]. The most prominent advantage of DE is its low computation time compared to that of GA, particularly in large antenna arrays. Also, recently, pattern synthesis with minimum SLL and null control based on particle swarm optimization (PSO) was presented [2, 3]. Moreover, a bacterial foraging algorithm (BFA) for null steering of linear antenna arrays by controlling only the element amplitudes was proposed [4].

In this paper, a novel Immunity Genetic Algorithm based on stochastic crossover evolution is introduced to find an optimal set of active array elements by turning off some elements of a uniformly spaced array to produce low side lobes with null steering. Our crossover operator based on the swapping of two-points selected on the parent unduplicated chromosome (DNA) is a variant of the known GA crossover operator. These chromosomes are spread all over the solution space. Furthermore, a new expression of the array factor is presented based on precomputed array factor transform matrix. The array factor is remodeled in a form similar to the Discrete Cosine Transform (DCT). The array factor for a specific number of elements N is expressed based on a precomputed DCT matrix and a linear transform is used to achieve a high speed computation of the array factor. The new expression of the array factor achieves a high speed up factor which allow us to push the search process to new borders in stochastic search for optimum solutions. Determining the side lobe level accurately is based on finding the nulls of the first lobe; the deactivation process of some elements of the array causes the nulls to move, to resolve this problem a technique for dynamically finding the exact position of the antenna main beam is presented. With 20% deactivated elements our algorithm achieves a side lobe level of about -20 dB and -23 dB SLL for 100 and 200 elements, respectively, which agree with the fact that relative, mean SLL is $1/N$. The effectiveness of our technique is also demonstrated with null control while minimizing the SLL of the array pattern. The results show that the null steering with optimum SLL using the digital amplitude control of array elements is very efficient.

2. DIGITAL AMPLITUDE CONTROL USING IGA ALGORITHM

Consider a linear array model of $2N$ equispaced isotropic elements placed along the x -axis. A digital amplitude controlled antenna array and the corresponding weights (digital control sequence) is shown in Figure 1. Dynamically controlling the activation and deactivation of elements allows future array reconfiguration which provides high

flexibility antennas. Elements at the center of the array play an important role on the SLL, and hence they are kept turned on (active) as shown in Figure 1 (indicated as array core). With Centro-symmetric array configuration, the array factor is given by

$$AF(\theta) = 2 \sum_{n=1}^N a_n \cos[n k d \sin(\theta)] \quad (1)$$

where, a_n represent n th amplitude weights of array elements with ($a_n = 0$ if the element is disabled and $a_n = 1$ if the element is enabled or active), d represent the interelement spacing, and θ represents angle from broadside.

Figure 1 shows that the elements with white color are turned on (active elements) and are indicated by the bit 1, and black elements are disabled or nonactive elements and are indicated by the bit 0. The digital amplitude control sequence of the array is considered to be the chromosome of the genetic algorithm.

In genetic algorithms (GA), crossover is a genetic operator used to vary the programming of a chromosome or chromosomes from one generation to the next. It is analogous to reproduction and biological crossover, upon which genetic algorithms are based. Many crossover techniques exist for organisms which use different data structures. Our crossover algorithm is a variant of these algorithms, based on the swapping of two-points which are selected on the parent unduplicated chromosome; these two genes (bits) are swapped to produce a child unduplicated chromosome (evolution). It is similar to a DNA immunization process through generations against chronic viruses. The swapping is based on the generation of two random variables.

In this work, the digital amplitude sequence of the array is similar to a chromosome, where the immunity to diseases evolves from parent

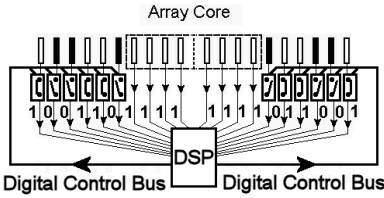


Figure 1. Centro-symmetric antenna array and the corresponding digital amplitude control sequence.

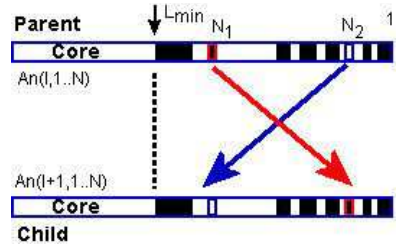


Figure 2. DNA Immunity Evolution from parent to child.

to child by crossover evolution, hence the name immunity GA (IGA). In order to find how this chromosome will evolve from generation to generation by changing a part of its genes (bits), we tried to generate large number of the chromosomes and then searching for the best one in term of acquired immunity (SLL). The core of the chromosome (Array core) which contains the main genetic properties is not affected through generations, and it is estimated to be 40% of the number of genes (bits), the rest of the chromosome genes are changed by evolution except the last element. This evolution from parent to child is performed by swapping individual bits in the chromosome (digital amplitude sequence). The selection of bits to be swapped (crossed over) is based on a stochastic process controlled by two variables. The immunity of the chromosome to viruses, which represents the SLL of the array pattern, is measured and the best chromosome with high immunity is kept (array factor with lowest side lobe level).

Consequently, our IGA algorithm is given by the following steps:

Algorithm

- 1- Initialization; the array size ($2N$), the number of generated chromosomes (K) of length N , the evolutions index (I), the dynamic thinning range $[L_{\min}+1, N-1]$ ($L_{\min}$ represents the index of the last element of the array core), dynamic thinning efficiency (Th_{eff}) (the element deactivation ratio), and initial DNA given by $\mathbf{a}_N$.
- 2- Generate two random indexes N_1, N_2 within dynamic thinning area.
- 3- Crossover the two bits (genes) indexed by N_1 and N_2 : $\mathbf{a}_N(N_1) = \mathbf{a}_N(N_2)$ and $\mathbf{a}_N(N_2) = \mathbf{a}_N(N_1)$
- 4- Add this new unduplicated chromosome evolution (digital amplitude sequence) to the IGA population.
- 5- Increment index I .
- 6- If $I < K$ GOTO step 2 else GOTO step 7.
- 7- Save the IGA population and exit.

The K evolutions, generated stochastically, are spread all over the total number of possible evolutions given by

$$C_J^{N-L_{\min}-1} = \frac{(N - L_{\min} - 1)!}{(N - J - L_{\min} - 1)! \cdot J!} \quad (2)$$

where J is the number of active elements in the dynamic thinning area given by

$$J = N(1 - Th_{eff}) - L_{\min} - 1 \quad (3)$$

When the number of active elements, J , is variable, then the total number of all possible chromosomes will be $2^{(N-L_{\min}-1)}$. For $N = 50$ (actual array size is $2N$) and $L_{\min} = 19$ this means that for a deactivation ratio of 40% there will be 30,045,015 possible evolutions. The K evolutions generated by the stochastic crossover although are very limited compared to the whole evolutions space; they are spread on all possible evolutions values and not concentrated in a limited area. This is a type of spread spectrum evolution where the search for lowest SLL is performed with fixed deactivation ratio. The evolution from parent to child is illustrated by Figure 2.

Each evolution by the IGA is stored for later analysis. The core of the chromosome is not affected by the evolutions. In genetic organism, this means that the global characteristics inheritations are conserved from parent to child through generations. Figure 3 shows the similarity between a biological chromosome (single molecule of DNA) and the digital amplitude sequence. The evolutions of genes in the biological chromosome are similar to the evolutions of bits in the digital amplitude sequence. The bit is 1 (white) when the array element is active and is 0 (black) when the element is deactivated.

After generating thousands of possible chromosomes, a sample of evolutions is shown in Figure 4, where the array core representing the unchanged genes (bits) is in the middle. Each row represents a possible solution with white pixels denote active elements and black

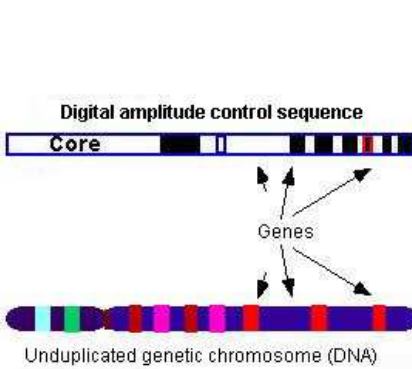


Figure 3. Similarity between biological unduplicated chromosome (DNA) and digital amplitude control sequence.

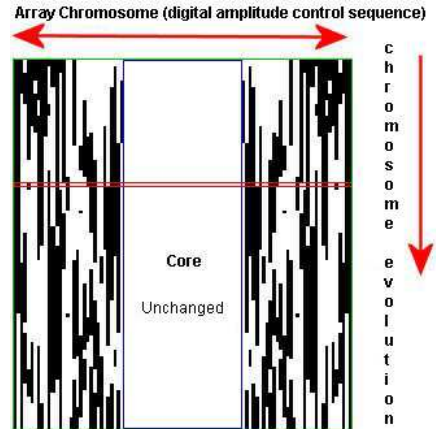


Figure 4. Sample of the symmetric (duplicated) chromosome evolution generated by immunity genetic algorithm (IGA).

pixels denote disabled elements. A sample of evolutions is represented by an image which is the top view of the IGA population matrix. The process of generating the array digital amplitude sequence and measuring their SLL in order to increase their rejection to interferences is similar to a DNA immunization process against chronic viruses.

The array core of the chromosomes do not change, the chromosome evolution from parent to child is performed by a 2 bits crossover until a desired SLL is obtained. All identical chromosomes are removed (Hamming distance $d = 0$). Experiments show that about 50% of the chromosomes are repeated. As the population of possible solutions is large, a fast computation technique is needed to evaluate the SLL of all chromosomes.

3. DIRECT ARRAY FACTOR TRANSFORM

The array factor expression given, by Equation (1) is similar to the discrete cosine transform (DCT), therefore, it can be written as linear transformation using matrix representation. With M the number of evaluation points of the array factor and N is half the array elements. The array factor expression for the Centro-symmetric array of Equation (1) is rewritten as

$$\begin{bmatrix} AF(\theta_1) \\ AF(\theta_2) \\ \vdots \\ AF(\theta_M) \end{bmatrix} = 2 \begin{bmatrix} W(1, \theta_1) & W(2, \theta_1) & \cdots & W(N, \theta_1) \\ W(1, \theta_2) & W(2, \theta_2) & \cdots & W(N, \theta_2) \\ \vdots & \vdots & \ddots & \vdots \\ W(1, \theta_M) & W(2, \theta_M) & \cdots & W(N, \theta_M) \end{bmatrix} \cdot \begin{bmatrix} a(1) \\ a(2) \\ \vdots \\ a(N) \end{bmatrix} \quad (4)$$

where $W(n, \theta) = \cos(kdn \sin(\theta))$. The above expression is called Direct Array Factor Transform (DAFT) and can be rewritten as

$$AF_M = \mathbf{W}_{(n, \theta)} \cdot \mathbf{a}_N \quad (5)$$

where, $\mathbf{a}_N$ is the amplitude weight vector of the N elements and $\mathbf{W}_{(n, \theta)}$ is the array factor transform (AFT) matrix of size (M, N) expressed by a non square matrix which has for consequence the inability to find its inverse using a linear transformation. Hopefully, the synthesis of antennas for relatively small size can be done with acceptable computation.

Since the AFT matrix does not depend on the array amplitude coefficients ($\mathbf{a}_N$), it can be precomputed to speed up the Transform computation process. This will push the computation process to new limits in the stochastic process where we search for a best solution among an astronomic number of combinations to satisfy the design requirements such as element deactivation ratio (dynamic thinning efficiency) and SLL. Note that the model of the array factor is written

using real values. This has a great effect on the computation speed since multiplications and additions are real. The DAFT is applied to a set of chromosomes generated by the IGA algorithm. After a set of thousands of chromosomes is generated, a search is performed within the array factor to satisfy given minimum SLL.

4. SIDE LOBE LEVEL ESTIMATION

When the Array Factor Transform is computed for all chromosomes generated by the IGA, a calculation of the SLL is performed on each array factor. This step is very critical because it is the key feature of a chromosome selection. In order to exactly measure the SLL an accurate estimation of the first lobe is needed. The nulls cannot be estimated correctly from analytical solution because the deactivation of some elements moves these nulls. Hence a good estimation is based on a good numerical method. To achieve this goal we considered the edges of the first lobe as an image processing edge detection problem and used the zero-crossing method to estimate their positions. The first derivative of the Array Factor normalized magnitude is computed. Figure 5, shows the array factor and its derivative where the dashed lines show that the main beam is located exactly at the zero crossing of the array factor derivative.

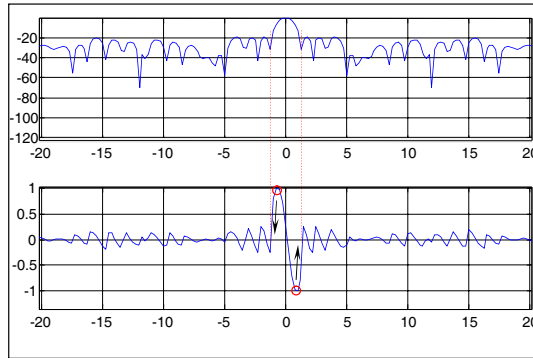


Figure 5. Main beam or first lobe edges detection using zero-crossing method. The upper graph is the array factor and the lower graph is its derivative.

5. RESULTS AND DISCUSSION

The new digital amplitude controlled array method that utilizes the proposed IGA algorithm is demonstrated by many computer simulation examples in order to suppress interference signals while minimizing the SLL. The simulation is performed in three steps: 1) Generate an AFT matrix for a given number of array elements and store it for later usage, 2) generate thousands of unduplicated chromosomes (digital amplitude sequences). 3) Finally compute the SLL for all chromosomes population and select the best chromosome which gives the lowest SLL. The computing was achieved on a dual core 2 computer running at 1.8 GHz equipped with 2 GB of RAM. When generating a population of 300 thousands chromosomes about 50% of them are repeated, this is due to the fact that the probability to generate two numbers A and B is quasi the same as generating B and A in a large trials. The swapping of genes (bits) in the two cases will produce the same unduplicated chromosome. This also agrees with the fact that genetic chromosomes are also duplicated. After generating a given population a process of filtering duplicated chromosomes (equal bit patterns) is done and only the filtered population is stored for later analysis using DAFT.

The memory required by the DAFT analysis of the filtered population of chromosomes is given by:

$$\text{Memory Size} = P_F M C + P_F N C = P_F C [M + N] \quad (6)$$

where P_F is the filtered or unduplicated chromosomes, M is the number of points estimated in the range -90° to 90° , C is the number of bytes reserved for each value; N is half the number of array elements. The first term of equation (6) is the memory size of the array factor for all chromosomes and the second term is the memory size of the population. Using (6), a memory of 0.95 GB is required when P_F equal to 145 thousands chromosomes, M equal to 720 evaluation points, C is 64 bits (8 bytes) for double precision numbers, and 200 array elements ($N = 100$), neglecting all other computations. The computation speed is one of the key features of our technique since it is capable of computing the SLL of more than 145 thousands array chromosomes in less than 60 seconds for 100 array elements and for 200 elements the computation for all array patterns is achieved in less than 2 minutes. Therefore, the main limitation of the number of elements is due the available physical memory as the windows operating system denies the usage of more than 50% of the physical memory since itself uses 50%. This fast computation is performed using DAFT technique.

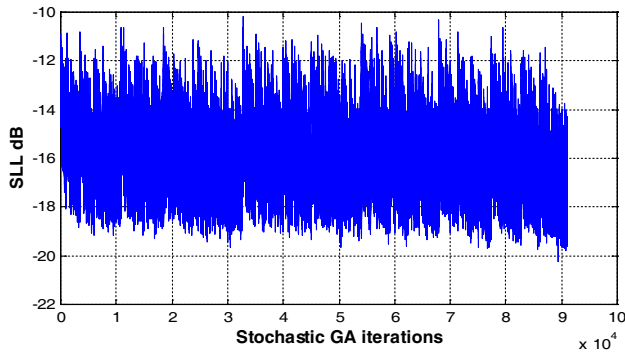


Figure 8. SLL versus IGA evolution index for an array of 100 elements ($N = 50$), 20% elements are deactivated, and 91 thousands chromosomes population size.

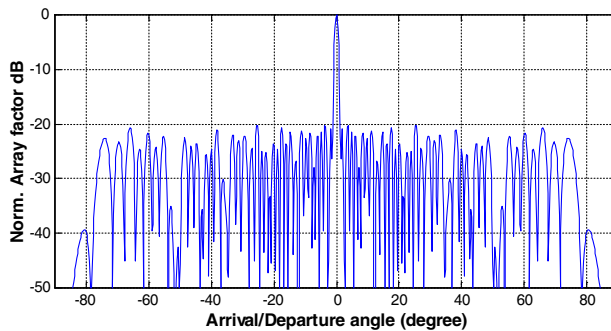


Figure 9. Array factor for best digital amplitude sequence given in row two of Table 1, $2N = 100$, only 80 elements are active. The SLL is -20.24 dB.

of a half wave interelement spacing for different deactivation ratios. In the following examples, different cases with different deactivation ratios are presented. Figure 6 shows the SLL of a population of about 100 thousands chromosomes for a 30% of deactivated elements. The lowest SLL is -19 dB as shown in Figure 7. The corresponding unduplicated chromosome is given in row one of Table 1. The lowest SLL of 20.24 dB is achieved for a population of 91 thousands chromosomes for 20% of deactivated elements as shown in Figure 8.

Figure 9 shows the array factor with the lowest SLL of the best unduplicated chromosome given in row 2 of Table 1. In the previous examples, the computation is achieved in less than 46 seconds since using DAFT, one array factor is computed in 0.35 ms, for N equal to

Table 3. SLL versus elements deactivation percentage for an array of 100 elements.

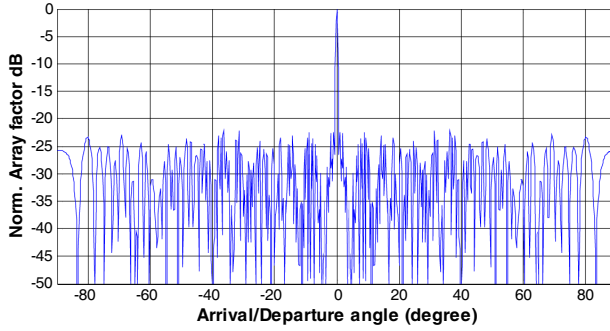
deactivation ratio (%)	SLL (dB)	Gain (dB)
16	-19.2	38.5
20	-20.0	38.0
22	-20.25	37.8
24	-19.8	37.6
26	-19.4	37.4
30	-19.0	37.0
40	-18.0	35.5
46	-17.0	35.0

which controls the total length of the array. Also, it was observed that the deactivation ratio with the lowest SLL is attained at 22% as given by Table 3. To confirm this observation we tried to study small array with size less than 28 elements. For these arrays, we first excluded the core from the amplitude control process, then we generated all possible chromosomes. While for array sizes greater the 28 elements we managed to concentrate the search within the last 17 elements. Table 4 shows that the best deactivation ratio increases for small arrays and settles at approximately 22%, where SLL_R is the real SLL searched within all possible chromosomes and SLL_S is the SLL obtained by stochastic search. Increasing N from 15 to 30, the two estimated SLL values match perfectly. Starting from N equal to 30 up to 50, we estimate SLL_R by searching the best deactivation ratio within last 17 elements (bits). From the table, excellent approximation is obtained. However, crossing the border of N equal to 50 the array synthesis based on stochastic search is the only way to perform a good SLL estimation.

To demonstrate the capability of the IGA algorithm, we consider an array of 200 elements with deactivation ratio of 20% where a SLL of -22.4 dB is obtained as shown in Figure 10. The corresponding chromosome is given in row two of Table 2(b). In order to increase the computation efficiency, and due to symmetry of the array factor, the computation can be performed in the range from 0° to 90° instead of -90° to 90° ; this will save 50% of the computation time. Using this feature we can computer 145 thousands array factors and extract the best digital amplitude sequence for 200 elements array in less than one minute. Note that with 20% deactivated elements, the SLL results agree with the fact that relative mean SLL is $1/N$.

Table 4. Variation of the best deactivation ratio versus array size.

N	Best deactivation ratio(%)	SLL_R (dB)	SLL_S (dB)
15	13	-13.56	-13.56
20	15	-15.54	-15.54
25	16	-17.16	-17.16
30	17	-17.99	-17.99
35	20	-18.68	-18.58
40	22.5	-19.39	-18.90
45	22.2	-19.77	-19.22
50	22.0	-20.11	-20.05

**Figure 10.** Array factor for best chromosome given in row two of Table 2(b), $2N = 200$, only 160 elements are active. The SLL is -22.4 dB.

5.2. Synthesis with Minimum SLL and Null Steering

In this section, the digital amplitude control is used to synthesize the array pattern with null steering for interference suppression. The search for the best chromosome that gives suppressed levels at the prescribed angular directions with the lowest possible SLL is based on the following fitness function

$$\text{Fitness} = w_1 AF(\theta_{null}) + w_2 SLL \quad (7)$$

where w_1 , w_2 are two weight parameters chosen experimentally to define the importance of each term and $AF(\theta_{null})$ is the array factor value at the imposed null angle. It is known that when the angle of arrival of the interference is close to the main beam, then imposing nulls at the array factor will deteriorate the SLL. Therefore, the direction of

arrival of the interference has been chosen at the peak of the 6th side lobe. Figure 11 shows the array factor (solid) in the range -20° to 20° for 50 elements ($N = 25$) with the imposed null at 8° and with 20% deactivation ratio. The array factor of the uniform array (dashed) is also shown in the figure. The interference rejection of less than -60 dB with -15 dB SLL was achieved with $w_1 = 3$ and $w_2 = 1$.

Figures 12 and 13 show the array factor (solid) in the range -20° to 20° for 100 and 200 elements with imposed nulls at 8° and 4° , respectively, for 22% deactivation ratio. The nulls are chosen at the peak of the third and sixth side lobe of the uniform array factor, respectively. The array factor of the uniform array (dashed) is also

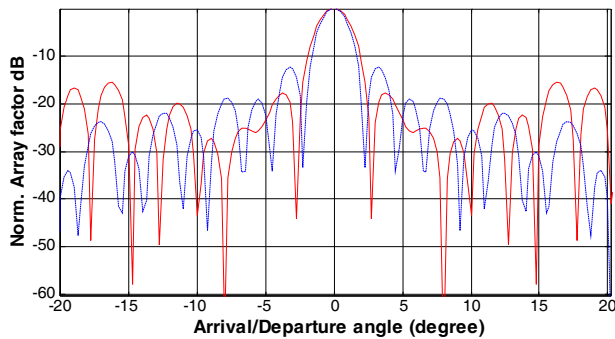


Figure 11. (Solid) Array factor with imposed null at 8° and 20% deactivation ratio. The null depth is -60 dB with -15 dB SLL. (Dashed) Uniformly array factor, $2N = 50$, $d = \lambda/2$.

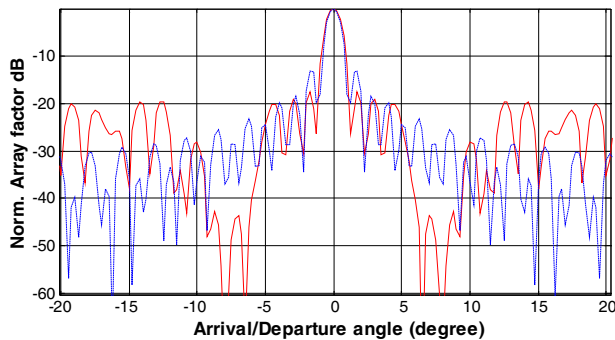


Figure 12. (Solid) Array factor with imposed null at 8° and 22% deactivation ratio. The null depth is -70 dB with -17.6 dB SLL. (Dashed) Uniformly array factor, $2N = 100$, $d = \lambda/2$.

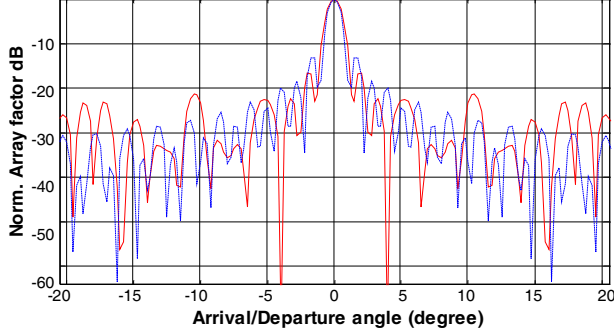


Figure 13. (Solid) Array factor with imposed null at 4° and 22% deactivation ratio. The null depth is -70 dB with -16.6 dB SLL. (Dashed) Uniformly array factor, $2N = 200$, $d = \lambda/2$.

shown in the figures. The interference rejection of less than -70 dB for both cases was obtained with -17.6 dB SLL for Figure 12 and -16.6 dB SLL for Figure 13. Moving the null towards the main beam will degrade the SLL as expected, but we still have an excellent SLL for background noise suppression.

6. CONCLUSION

This paper presents an Immunity Genetic Algorithm (IGA) for array pattern synthesis using digital amplitude control. The digital amplitude control can be considered as a dynamic thinning. Our IGA algorithm is based on the swapping of two genes (bits) which are selected on the parent unduplicated chromosome (DNA) represented by the digital amplitude control sequence. Several examples are presented in order to show the effectiveness of our proposed technique. Our main objective is to find the best SLL with fixed percentage of deactivated elements. Since the nulls of the array factor moves depending on elements deactivation ratio, we proposed a very fast method to determine the main beam nulls and hence compute the SLL with high accuracy. The method is based on the zero-crossing of the array factor derivative. With our proposed IGA algorithm we were capable of finding the best array chromosome for 200 elements by performing a search within a stochastic population of chromosomes of about 100 thousands extracted from 200 thousands. All computations of the extracted population are done within 40 seconds. Since the array factor is expressed as a linear transform based on a pre-computed DCT matrix, a huge reduction in computation time is obtained. This

allows us to find a good approximation of the absolute minimum SLL of synthesized arrays.

Results for array digital amplitude control of different sizes have illustrated the performance of our proposed technique. By studying the dynamic thinning percentage of different array sizes, it was found that the best percentage of deactivated elements is 22% for array size above 100 elements. Simulation results show the effectiveness of this novel algorithm for pattern synthesis with low SLL and interference suppression.

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