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LINEAR ANTENNA SYNTHESIS WITH A HYBRID GENETIC ALGORITHM

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Abstract—An optimization problem for designing non-uniformly spaced, linear arrays is formulated and solved by means of an improved genetic algorithm (IGA) procedure. The proposed iterative method is aimed at minimizing the side-lobes level and thinning the array by optimizing the element positions and weights. Selected examples are included, which demonstrate the effectiveness and the design flexibility of the proposed method in the framework of electromagnetic synthesis of linear arrays.

1. INTRODUCTION

The global synthesis of antenna arrays that generate a desired radiation pattern is a highly nonlinear optimization problem. Many analytical methods have been proposed for its solution. Examples of analytical techniques include the well-known Taylor method and the Chebishev method [1]. However, analytical or calculus-based methods are generally unable to optimize both positions and weights of the array elements. To this end, stochastic methods are necessary [2, 3] in order to efficiently deal with large nonlinear search spaces and to extend the analysis also to the elements placement.

In the literature, problem-tailored Genetic Algorithms (GAs) have been largely applied to various test cases [4]. As far as symmetrical array synthesis is concerned, a real-coded GA-based procedure was proposed in [5] for the optimization of the array weights when the sensors are $\lambda/2$-spaced. Moreover, in [6] and in [7] a binary genetic algorithm was applied in order to deal with isophorical array thinning, and in [8] a stochastic approach was proposed aimed at optimizing isophorical arrays with a fixed number of elements. Unfortunately, these approaches consider symmetric arrays in order to reduce the computational time.

On the other hand, in [4, 9] the array optimization has been investigated by considering a higher number of degrees of freedom such as elements position and weighting. Toward this end, an optimization method based on a simulated annealing (SA) process was applied in [4] to the simultaneous weights and positions optimization, and in [9] to the global array synthesis and beam pattern shaping.

In this framework, this paper is aimed at presenting a modular method, based on a Genetic Algorithm, able to synthesize linear, real-weighted arrays according to different constraints, such as side lobes peak minimization, array thinning, linear dimension minimization, and beam pattern (BP) shape modeling. Several successfully investigated test cases seem to confirm the effectiveness, but also the flexibility and suitability of the proposed GAs-based procedure for the antenna array optimization.

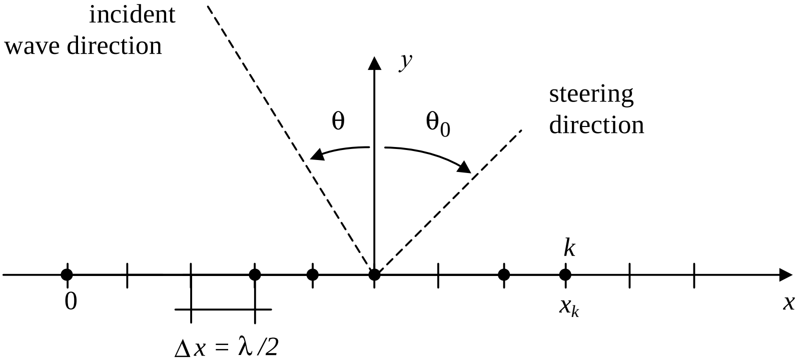


Figure 1. Linear array geometry.

2. MATHEMATICAL FORMULATION

Let us consider the linear array shown in Fig. 1, where M non-uniformly spaced elements are located along a straight line (L) at the positions $x_k,\ k = 0, \dots, M-1$. The beam pattern function of the array, $p(u)$, is defined as follows

$$p(u) = \sum_{k=0}^{M-1} w_k e^{j\frac{2\pi}{\lambda}x_k u} \tag{1}$$

where w_k is the weight coefficient of the k-th element, λ is the background wavelength, $u = \sin\theta - \sin\theta_0$, being θ and θ_0 the incident angle of the impinging plane wave and the steering angle of the array, respectively.

In order to generate a BP that fulfills some constraints (e.g., side lobes level (SLL) lower than a fixed threshold) or reproduces a desired shape ($p^{ref}(u)$), it is necessary to synthesize an array configuration. Firstly, a measure of the difference between desired and synthesized beam pattern should be defined. Toward this end, let us define a function called *fitness function, f*, as follows

$$f(\overline{\zeta}) = \frac{1}{k_1 f_{SLL}(\overline{\zeta}) + k_2 f_{BP}(\overline{\zeta}) + k_3 f_N(\overline{\zeta}) + k_4 f_D(\overline{\zeta})} \tag{2}$$

where $\overline{\zeta} = [M; x_0, \ldots, x_k, \ldots, x_{M-1};\ \ w_0, \ldots, w_k, \ldots, w_{M-1}]^t$ is the unknown array and

$$\begin{aligned} f_{SLL}(\overline{\zeta}) &= \frac{Q}{\max\limits_{u_{start} \leq u \leq 1} \{p_{dB}(u)\}} \\ f_{BP}(\overline{\zeta}) &= \int\limits_{u \in S} \left(\frac{p_{dB}(u)}{Q} - p_{dB}^{ref}(u) \right) du \\ f_N(\overline{\zeta}) &= M \\ f_D(\overline{\zeta}) &= D \end{aligned}$$

u_{start} being a value that allows excluding the main lobe from the calculation of the SLL. Moreover, D is the array aperture, Q is a normalizing constant, and S is the range of values for which $\{p_{dB}(u)/Q\} > p_{dB}^{ref}(u)$, $p_{dB}^{ref}(u)$ being the desired BP shape. Finally, k_1, k_2, k_3, and k_4 are normalizing coefficient chosen according to the optimization strategy.

The resulting fitness function defined in (2) is highly non-linear with a large number of local maxima, where deterministic procedures can be trapped. Consequently, a stochastic method able to avoid local maxima and effective in exploring highly non-linear search spaces should be used to solve the maximization problem at hand. GAs have already proven their effectiveness in optimizing antenna arrays and seem to be a reasonable choice.

3. GA-BASED COMPUTATIONAL TECHNIQUE

GAs are optimization methods based on Darwinian theory of evolution. They simulate the evolution of a population of individuals (i.e., a set of trial solutions for the addressed problem dealt with) over time favoring the improvement of individual characteristics (i.e., the fitting with some constraints evaluated by means of a fitness function).

Standard GAs (SGA) differ from other optimization methods because of these characteristics [16, 17]:

- SGAs work with a coding of the parameters, not with the parameters themselves;
- SGAs are multiple-agent searching procedure (i.e., multiple sampling of the search space);
- SGAs do not need to use derivatives;
- SGAs use random transition rules, not deterministic ones.

According to [10], SGAs have to be customized for each application in order to give optimal results. Toward this end, an improved genetic algorithm (IGA) is proposed for some classes of antenna synthesis problems. The flow chart of the IGA is shown in Figure 2. The main features of the algorithm are:

- the use of an hybrid coding;
- the independence of the chromosome's genes (i.e., the genes representing the placement of the array elements and the weights coefficients are optimized at the same time);
- the design of *a-priori* knowledge-augmented operators;
- the definition of an adaptive evolution strategy;
- the hybridization with a local search algorithm.

In the following, a detailed analysis of the proposed maximization strategy is presented.

3.1. Parameters Representation

SGAs code an individual with a binary array (also called chromosome), so that pseudo-Boolean optimization problems (see for example [6, 8]) are accurately handled. If discrete parameters are taken into account, a coding procedure is needed. Each parameter is represented by a string of q bits, where $q = \log_2(L)$, L being the number of values that the discrete variable can assume [11]. Nevertheless, when real unknowns are considered, binary coding is unpractical and disadvantageous because of the quantization noise and time consuming coding/decoding procedures [12]. In order to overcome these drawbacks, a real-valued representation should be used [13].

As far as the antenna synthesis of a linear ($\lambda/2$) equally spaced array is concerned (to prevent grating lobes), different kinds of parameters have to be optimized: number of active elements, M, and weights of active elements $\{w_k; k = 0, \ldots, M-1\}$. In order to effectively address this problem by means of a GA-based procedure, a hybrid coding is used. The chromosome assumes the following structure

$$\overline{\xi} = \{M; b_0, \ldots, b_k, \ldots, b_{N-1};\ w_0, \ldots, w_k, \ldots, w_{N-1}\} \tag{3}$$

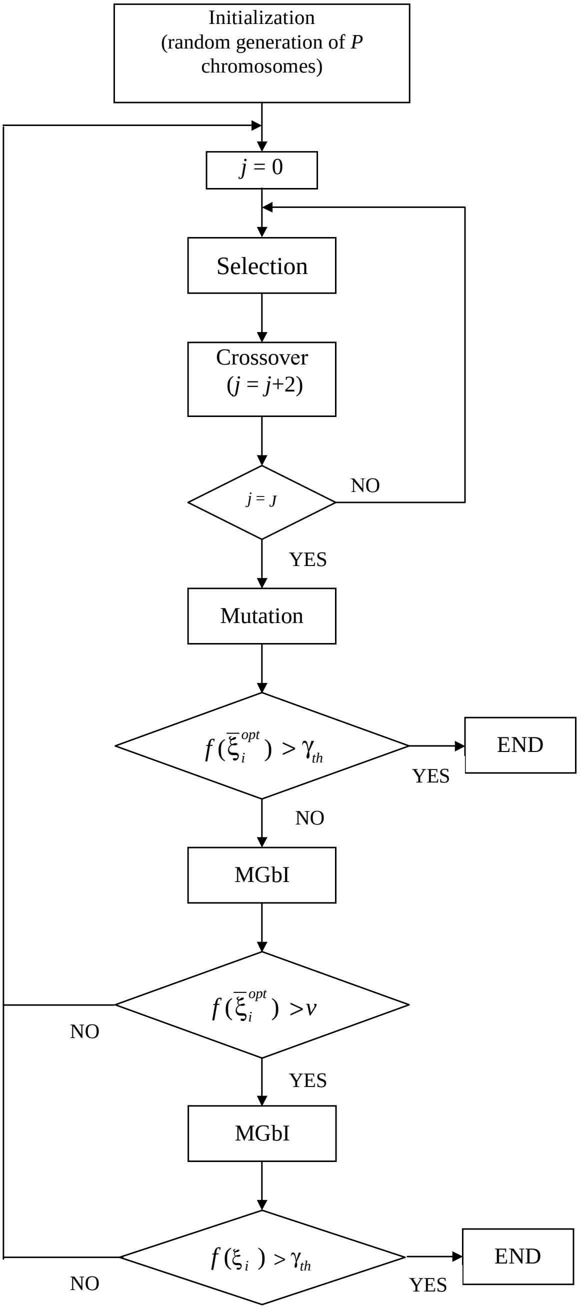


Figure 2. Flowchart of the improved genetic algorithm.

where b_k is a boolean value indicating the state (turned on or off) of the kth array element, k is the integer number of $(\lambda/2)$ intervals between the kth element and the left array limit ($x_k = k\frac{\lambda}{2}$), w_k is the related excitation coefficient, and N is the number of intervals ($\frac{\lambda}{2}$ in length) in which the array length has been discretized.

According to the adopted representation, suitable genetic operators have to be defined in order to obtain admissible solutions and to enhance the convergence process. In the proposed implementation, although the mutation remains a means for exploring new regions of the solution space and crossover constitutes the way to mix the best genes of the current population. In our implementation some innovative choices have been applied.

3.2. Genetic Operators

- *Selection*

A Roulette Wheel Selection [14] with fitness scaling is considered. As far as the scaling is concerned the following rule is applied

$$f_i' = \left(f_{i-1} - f_{i-1}^{avg}\right)^n - \left(f_{i-1}^{worst} - f_{i-1}^{avg}\right)^m \tag{4}$$

where f' is the scaled fitness function, f^{avg} is the average fitness value of the current population and f^{worst} indicates the lowest fitness value, i being the generation index. The values of m and n are heuristically defined in order to avoid premature convergence and to speed up the search when the population approaches convergence [15].

- *Crossover*

The crossover is aimed at exchanging gene information between chromosomes. The use of the crossover to improve the offspring production is undoubtedly problem-oriented. An effective design greatly increases the convergence rate of the maximization process. Due to the hybrid chromosome representation, a different strategy is considered for the real or boolean part of the chromosome. Let us consider two selected parents, $\overline{\xi}^{(a)}$ and $\overline{\xi}^{(b)}$, and a randomly selected crossover point k_s

$$\begin{aligned}
\overline{\xi}^{(a)} &= \Big\{M^{(a)}; b_0^{(a)}, \ldots, b_{k_s-1}^{(a)}, b_{k_s}^{(a)}, b_{k_s+1}^{(a)}, \ldots, b_{N-1}^{(a)};\\
&\qquad w_0^{(a)}, \ldots, w_{k_s-1}^{(a)}, w_{k_s}^{(a)}, w_{k_s+1}^{(a)}, \ldots, w_{N-1}^{(a)}\Big\}\\
\overline{\xi}^{(b)} &= \Big\{M^{(b)}; b_0^{(b)}, \ldots, b_{k_s-1}^{(b)}, b_{k_s}^{(b)}, b_{k_s+1}^{(b)}, \ldots, b_{N-1}^{(b)};\\
&\qquad w_0^{(b)}, \ldots, w_{k_s-1}^{(b)}, w_{k_s}^{(b)}, w_{k_s+1}^{(b)}, \ldots, w_{N-1}^{(b)}\Big\}
\end{aligned} \tag{5}$$

After crossover operation, the offspring result equal to

$$\begin{aligned} \left[\overline{\xi}^{(a)}\right]' &= \Big\{M^{(a)}; b_0^{(a)}, \dots, b_{k_s-1}^{(a)}, b_{k_s}^{(a)}, \left[b_{k_s+1}^{(a)}\right]', \dots, \left[b_{N-1}^{(a)}\right]'; \\ &\qquad w_0^{(a)}, \dots, w_{k_s-1}^{(a)}, w_{k_s}^{(a)}, \left[w_{k_s+1}^{(a)}\right]', \dots, \left[w_{N-1}^{(a)}\right]'\Big\} \\ \left[\overline{\xi}^{(b)}\right]' &= \Big\{M^{(b)}; \left[b_0^{(b)}\right]', \dots, \left[b_{k_s-1}^{(b)}\right]', b_{k_s}^{(b)}, b_{k_s+1}^{(b)}, \dots, b_{N-1}^{(b)}; \\ &\qquad \left[w_0^{(b)}\right]', \dots, \left[w_{k_s-1}^{(b)}\right]', w_{k_s}^{(b)}, w_{k_s+1}^{(b)}, \dots, w_{N-1}^{(b)}\Big\} \end{aligned} \tag{6}$$

For the real part of the chromosome, a real-crossover is performed according to a modified version (for variable length chromosomes) of the algorithm preliminarily proposed in [13], then

$$\begin{aligned} \left[w_k^{(a)}\right]' &= r\left[w_k^{(a)}\right] + (1-r)\left[w_k^{(b)}\right] \\ \left[w_k^{(b)}\right]' &= (1-r)\left[w_k^{(a)}\right] + r\left[w_k^{(b)}\right] \end{aligned} \tag{7}$$

$r \in [0,1]$ being a random number such that the resulting gene belongs to the acceptance domain defined according to the *a-priori* knowledge

$$\begin{aligned} w_k^{\min} &\leq \left[w_k^{(a)}\right]' \leq w_k^{\max} \quad k = 0, \dots, N-1 \\ w_k^{\min} &\leq \left[w_k^{(b)}\right]' \leq w_k^{\max} \end{aligned} \tag{8}$$

where $w_k^{\min}$ and $w_k^{\max}$ are fixed constants whose values are chosen to avoid mutual coupling effects arising in dense arrays.

On the other hand, boolean positions obey to a semi-probabilistic rule. The sensors states are preserved or changed with probability r for one child and $1-r$ for the other, respectively

$$\begin{cases} \text{if} \quad b_k^{(a)} = b_k^{(b)} & \begin{cases} \left[b_k^{(a)}\right]' = b_k^{(a)} \\ \left[b_k^{(b)}\right]' = b_k^{(b)} \end{cases} \\ \text{if} \quad \left[b_k^{(a)}\right] \neq \left[b_k^{(b)}\right] & \begin{cases} \left[b_k^{(a)}\right]' = \begin{cases} 1 & \text{with probability } r \\ 0 & \text{with probability } (1-r) \end{cases} \\ \left[b_k^{(b)}\right]' = \begin{cases} 1 & \text{with probability } (1-r) \\ 0 & \text{with probability } r \end{cases} \end{cases} \end{cases} \tag{9}$$

The crossover is performed with a probability p_c and the reproduction with a probability $(1-p_c)$.

- *Mutation*

The mutation is performed with probability p_m on a chromosome of the population. Then a mutation occurs, with probability p_{bm}. The value of a string position is changed in order to introduce some variations into the chromosome. The mutation is performed following different strategies according to the type of the gene to mutate. If the randomly selected gene is binary-valued, b_k, then a standard *binary mutation* is adopted [16] by using different probabilities for the death or the birth of the array element

$$[b_k]' = \begin{cases} not\{b_k\}\Big|_{b_k=0} & \text{with probability } p_{birth} \\ not\{b_k\}\Big|_{b_k=1} & \text{with probability } p_{death} \end{cases} \tag{10}$$

Otherwise, a random mutation has been designed for real-valued genes as well

$$[w_k]' = w_k + \eta \tag{11}$$

η being a random value such that the obtained solution be physically admissible.

- *Elitism*

To avoid losing the fittest individual from one generation to another, the elitism is applied [16]. At each generation the best chromosome obtained so far is reproduced in the new population.

3.3. GA-Hybridizaiton

Generally, a GA-based procedure is fairly slow to "fine tune" the optimum solution after locating an appropriate region (*attraction basin*) in the solution space. On the contrary, gradient-descent algorithm can do well in local optimization, but they can be trapped in local maxima of a highly nonlinear fitness function. To overcome these problems, a hybridization including the essence and merits of GA and gradient-descent methods is introduced. The idea is to embed a gradient-descent algorithm into the evolution concept of the GA in order to provide a structured random search (Fig. 2). The proposed hybridization works at different levels:

- basic level (i.e., at each iteration of the IGA);
- high level (i.e., during the evolution process).

At each generation (i), the procedure operates as a SGA performing selection, the crossover, the mutation and the elitism. Successively, a "Modified G-Bit Improvement" (MGbI) is performed. A randomly selected chromosome, $\overline{\xi}$, is modified by sweeping each gene, $\xi_l; l = 0, \ldots, 2N$. Boolean-valued genes are changed ($[\xi_l]^* \Leftarrow not\{\xi_l\}$) and real valued genes slightly updated ($[\xi_l]^* \Leftarrow \xi_l + r\frac{\xi_l}{\sum_{k=0}^{N-1} w_k}$; $r \in [-1, 1]$). At each step ($l = 0, \ldots, 2N$), a difference is computed between the values of the fitness function evaluated by using the new field configuration and the last accepted configuration, $\Delta f = f(\overline{\xi}^*) - f(\overline{\xi})$. If $\Delta f > 0$ then we accept the new chromosome configuration, thus setting $\overline{\xi} = \overline{\xi}^*$. Otherwise, the trial configuration is rejected.

As far as the high-level hybridization is concerned, once a fixed threshold in the fitness function has been reached ($f(\overline{\xi}_i^{opt}) > \upsilon$), the geometry of the array (i.e., genes ($M^{opt}; b_0^{opt}, \ldots, b_k^{opt}, \ldots, b_{N-1}^{opt}$)) is frozen and a local search is performed by means of a standard Polak-Ribière conjugate-gradient algorithm [18] to further improve the array weights ($w_0^{opt}, \ldots, w_k^{opt}, \ldots, w_{N-1}^{opt}$).

4. NUMERICAL RESULTS

To assess the effectiveness of the proposed approach, different test cases were investigated. In this section, representative numerical results are presented and compared with reference solutions (available in literature) in order to assess the effectiveness and the flexibility of the proposed method.

4.1. Optimization of Elements Positions and Weights — Side Lobes Level Minimization

In the first example, the minimization of the maximum side lobes level (Φ_{slp}) by varying element weights is addressed. Concerning this problem, in [4] the synthesis procedure was applied to a linear array of 25 isotropic elements $D = 50\lambda$ in length. In order to compare the performances of the IGA-based optimization with the results achieved by Trucco et al. [4], the parameter u_{start} was set to 0.04 and weight coefficients were allowed to vary within the range [0.2,2.0].

For this application, the following hypotheses were considered: the array length was discretized in $N = 100(\lambda/2)$-spaced steps by imposing the number of elements M, equal to 25. Then, the structure of the chromosome results

$$\begin{aligned} \overline{\xi} &= \{w_0, \ldots, w_k, \ldots, w_{N-1}\}] \\ b_k &= 1 \; k = 0, \ldots, N-1 \\ M &= 25 \end{aligned} \tag{12}$$

The fitness coefficients were set as follows: $k_1 = 1$ and $k_2 = k_3 = k_4 = 0$. The other IGA parameters (chosen according to the values suggested in the related literature) turned out to be: population dimension, $J = 140$; $p_c = 0.6$; $p_m = 0.6$; gene mutation probability for boolean-values, $p_{bm} = (1/6 \cdot 10^3)(i-1) + 0.06$; gene mutation probability for real-values, $p_{bm} = (7/10^5)(i-1)+0.03$; maximum number of iterations, $I = 600$. The MGbI was performed on $R = 4$ roulette-wheel selected individuals (this value represents a good choice allowing an effective trade-off between computational load and convergence rate).

The best result was an array with a side lobe peak $\Phi_{slp} = -14.77\,\mathrm{dB}$. Let us consider that the threshold for side-lobes level achieved in [4], which to the authors' knowledge is the best in related literature, was of $-14.45\,\mathrm{dB}$ ($u_{ml} = 0.191$ being the half-beamwidth). Figure 3 compares the BP, the element weights and position layout of such arrays.

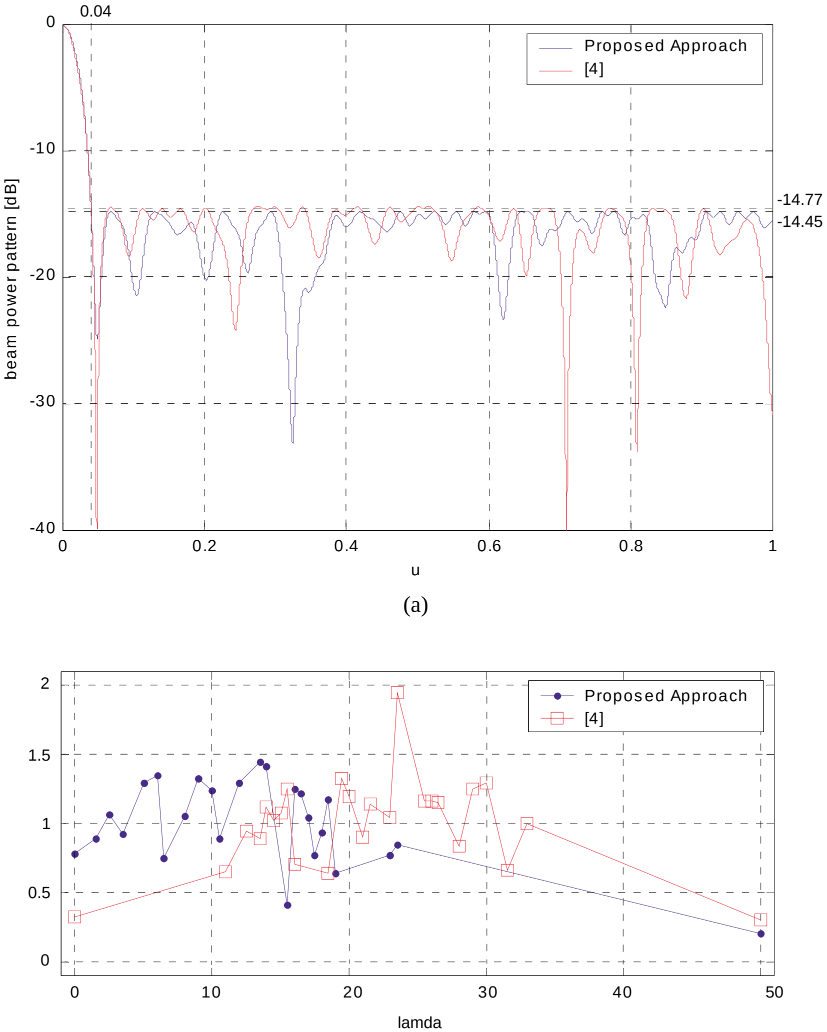
On the other hand, taking into account also the main lobe width, one of the best results was an array with a BP characterized by a side-lobe peak $\Phi_{slp} = -14.67\,\mathrm{dB}$ and a main-lobe width $u_{ml} = 0.0204$. In this case, the algorithm was able to synthesize an array with side-lobes level close to the optimal one ($-14.67\,\mathrm{dB}$ versus $-14.77\,\mathrm{dB}$) with a decrease in the main-lobe width (0.0190 versus 0.0204). As a comment, it should be pointed out that, even though a sidelobe reduction of about 0.2 dB could be lower than the error amount in real phased array, the achieved results are quite impressive due to the closeness to the theoretical optimal value [4].

For the sake of completeness, in order to point out the achievable trade-off between side-lobe peak and main-lobe width, a collection of best results obtained after some runs of the proposed algorithm have been reported in Fig. 4. For comparison purpose, the result reached with the SA-based procedure is shown as well.

Finally, isophoric arrays [19] were considered as well. In this case the array element weights were fixed (w_k; $k = 0, \ldots, N-1$) and the optimization concerned the array element positions. Figure 5 shows the BP and position layout in correspondence with best solutions, in term of minimum side-lobe level peak ($\Phi_{slp} = -13.06\,\mathrm{dB}$ and $u_{ml} = 0.0170$; IGA (a)) as well as in term of optimal trade-off between side-lobe level and main-lobe width ($\Phi_{slp} = -12.32\,\mathrm{dB}$ and $u_{ml} = 0.0126$; IGA (b)), obtained by means of the IGA-based method. Also the features of the array synthesized with the SA-based procedure are provided ($\Phi_{slp} = -12.07\,\mathrm{dB}$ and $u_{ml} = 0.0133$; SA [4]).

4.2. Optimization of Array Layout and Weights — Beam Pattern Shaping

In the second test case, the optimization of the number of sensors and of the length of an array with a fixed BP shape was considered. The desired pattern was the same as in [9, 19] and described in Table 1.



(a)

(b)

Figure 3. Optimization of Element Weights — (a) BP with a side-lobe peak of $-14.77\,\mathrm{dB}$; (b) positions and weights of the array elements.

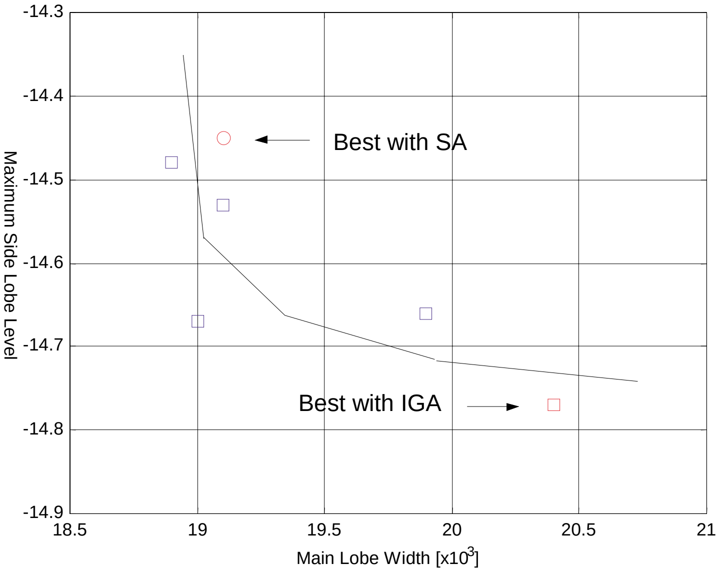


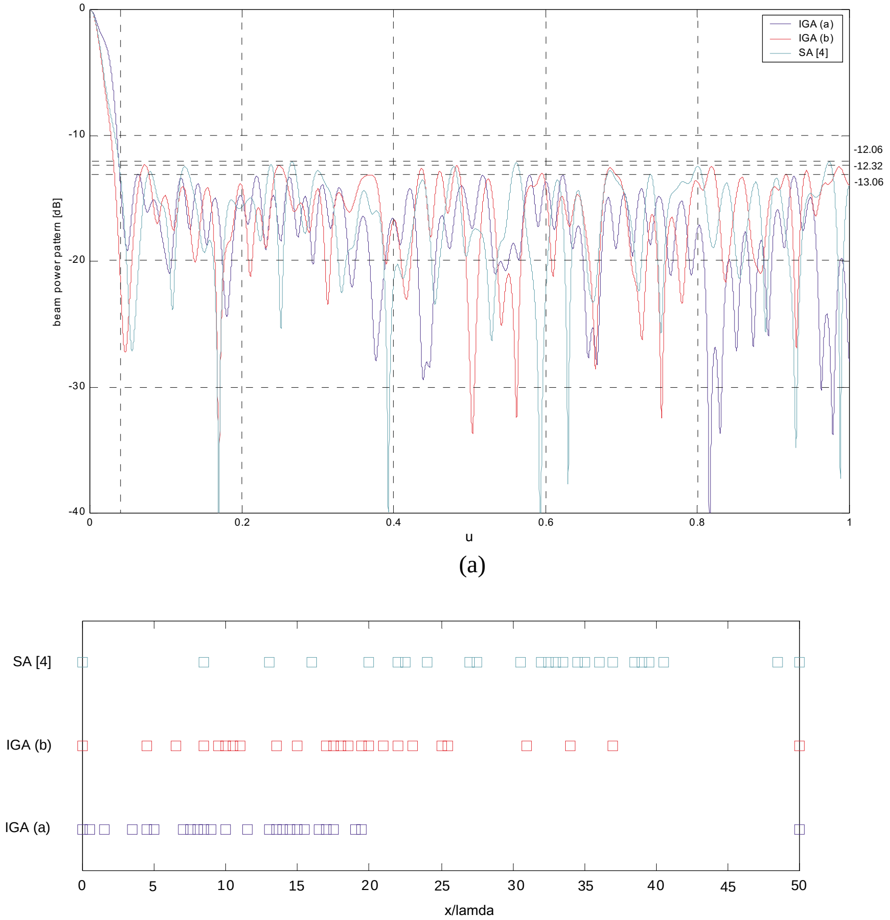
Figure 4. Optimization of Element Weights — Peak side-lobe level as a function of main-lobe width ([dB] units; - IGA simulation; O - SA simulation).

Table 1. Beam pattern constraints [9, 20].

Range	**Beam Pattern Amplitude**
$0 < u \leq 0.042$	0 dB
$0.042 < u \leq 0.31$	−13.4 dB
$0.31 < u \leq 0.45$	−26.9 dB
$0.45 < u \leq 0.80$	−13.4 dB
$0.80 < u \leq 1$	0 dB

As far as the IGA-based optimization procedure is concerned, the fitness coefficients were heuristically chosen: $k_1 = 0$, $k_2 = 6.5$, $k_3 = 4.3$, and $k_4 = 2.8$. The range of variation for array coefficients was fixed to $w_k \in [0.25, 1.75]$ and $I = 2000$ iterations were performed over a population of $J = 200$ individuals. The evolution strategy was defined by choosing $p_c = 0.5$, $p_{death} = 0.01$, and $p_{birth} = 0.003$.

Figure 6 shows the BP of the best obtained array, in which 15 elements are located over a linear length equal to $D = 16.5\,\lambda$



(a)

(b)

Figure 5. Optimization of element positions and weights — Optimal syntheses for isophoric arrays. (a) BPs; (b) array layouts.

(Fig. 6(b)). To the best of the authors' knowledge, the most optimized result for this test case was reported in [9], where the authors synthesized an array with 16 elements and 19.5λ in length. However, the sharp reduction of the array aperture cause an increase of the main-lobe width, which turns out to be greater than the one in [9] ($u_{ml}^{(IGA)} = 0.0249$ versus $u_{ml}^{(SA)} = 0.0228$).

In order to give some indications about the iterative process, Figure 7 shows the behavior of the fitness function, $f(\overline{\xi}_i^{opt})$, versus

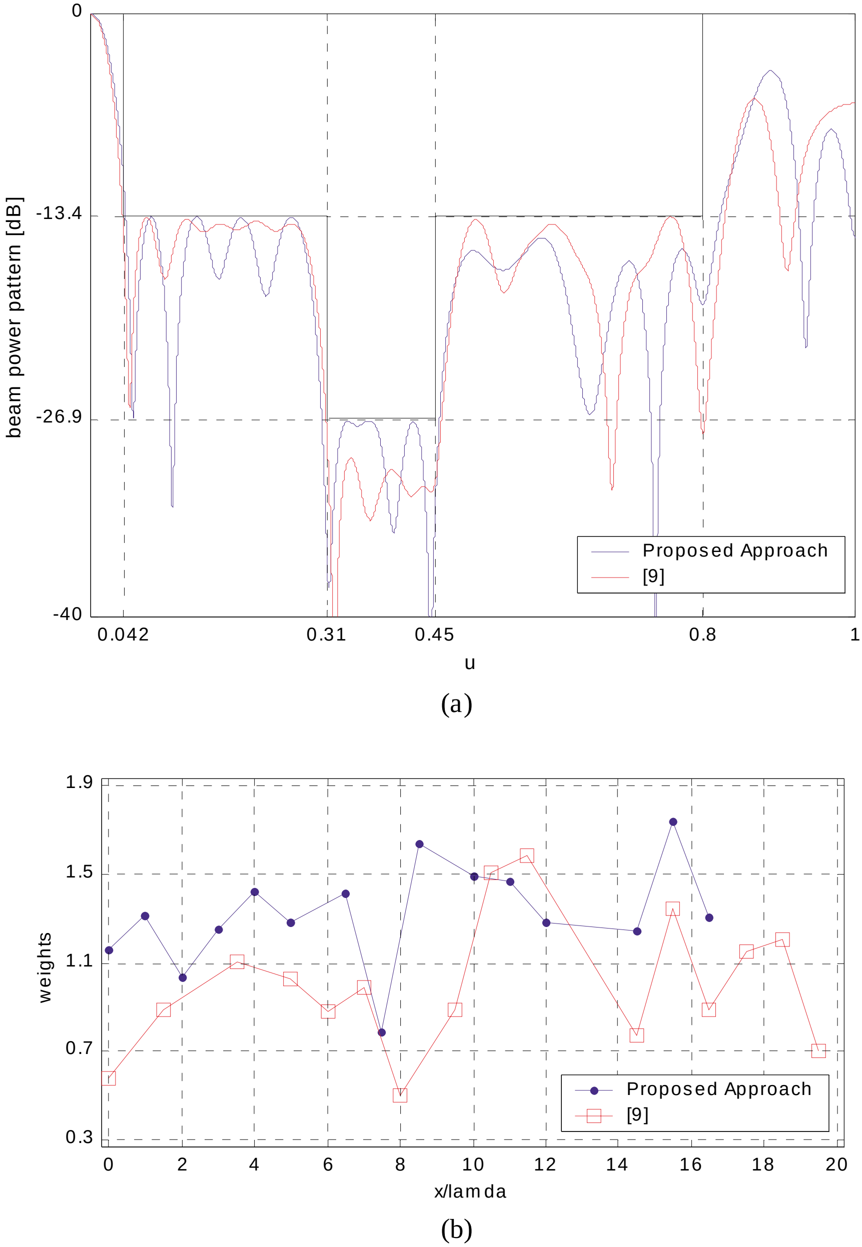


Figure 6. Optimization of element layout and weights — (a) BP of the 15-elements array with $D = 16.5\lambda$; (b) positions and weights of the array elements.

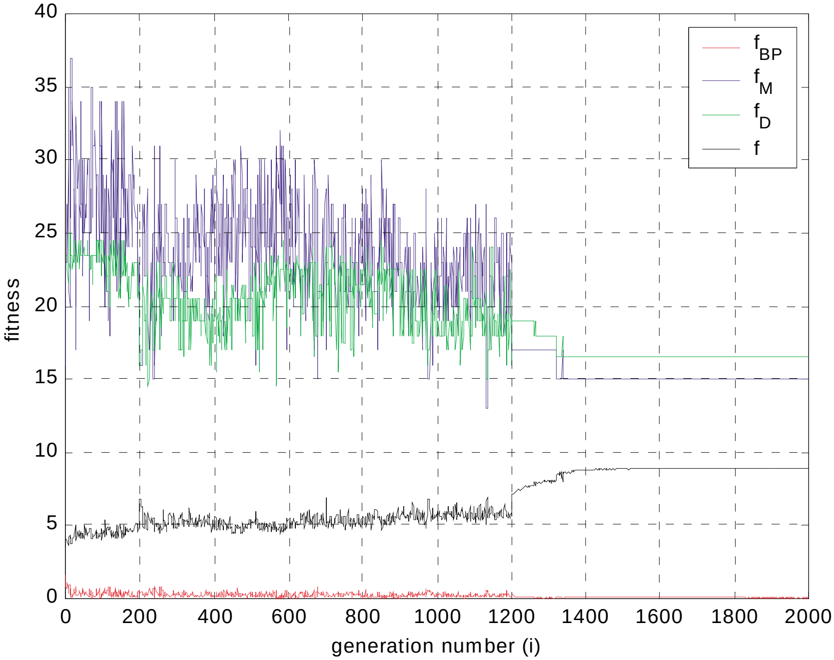


Figure 7. Optimization of element layout and weights — Behaviour of the fitness function versus the number of iterations.

the iteration number. For the sake of completeness, also single terms of the fitness function are provided $(f_{BP}(\overline{\xi}_i^{opt}), f_N(\overline{\xi}_i^{opt}), f_D(\overline{\xi}_i^{opt}))$.

4.3. Optimization of Array Layout — Thinning

The effectiveness of the IGA-based approach in array thinning was further assessed in the third scenario. The array pattern was optimized for the lowest maximum side-lobe level. A 200-elements isophoric array with half-wavelength spacing was considered to compare the results obtained by the proposed method with those presented in the literature [6, 7].

For this application, the chromosome structure was

$$\overline{\xi} = \{M; b_0, \dots, b_k, \dots, b_{N-1}\} \qquad w_k = 1 \; k = 0, \dots, N-1 \qquad (13)$$

and a suitable fitness function was considered by setting $k_1 = 2$, $k_2 = k_4 = 0$, $k_3 = 10^{-5}$. The parameters of the maximization algorithm were fixed as follows: $I = 1000$, $J = 200$, $p_c = 0.5$, $p_{death} = 0.01$ and $p_{birth} = 0.003$.

Table 2. Statistical behavior of the number of active elements, side-lobe peak and main-lobe width after some tens of process realizations.

Number of active elements (M)			
Best	***Worst***	***Average***	***Std. Dev.***
147 (73.5%)	153 (76.5%)	149.6 (74.8%)	1.0368
Side-Lobe Peak (Φ_{slp}) [dB]			
Best	***Worst***	***Average***	***Std. Dev.***
-23.09	-22.59	-22.82	0.2312
Main-Lobe Width (u_{ml})			
Best	***Worst***	***Average***	***Std. Dev.***
0.0050	0.0052	0.00508	~ 0

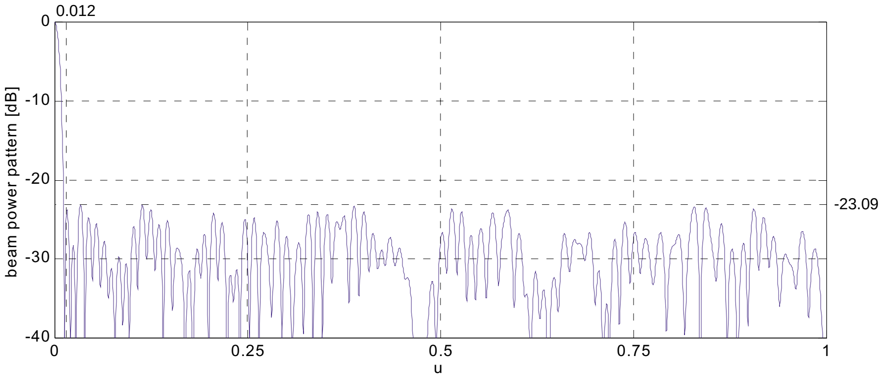
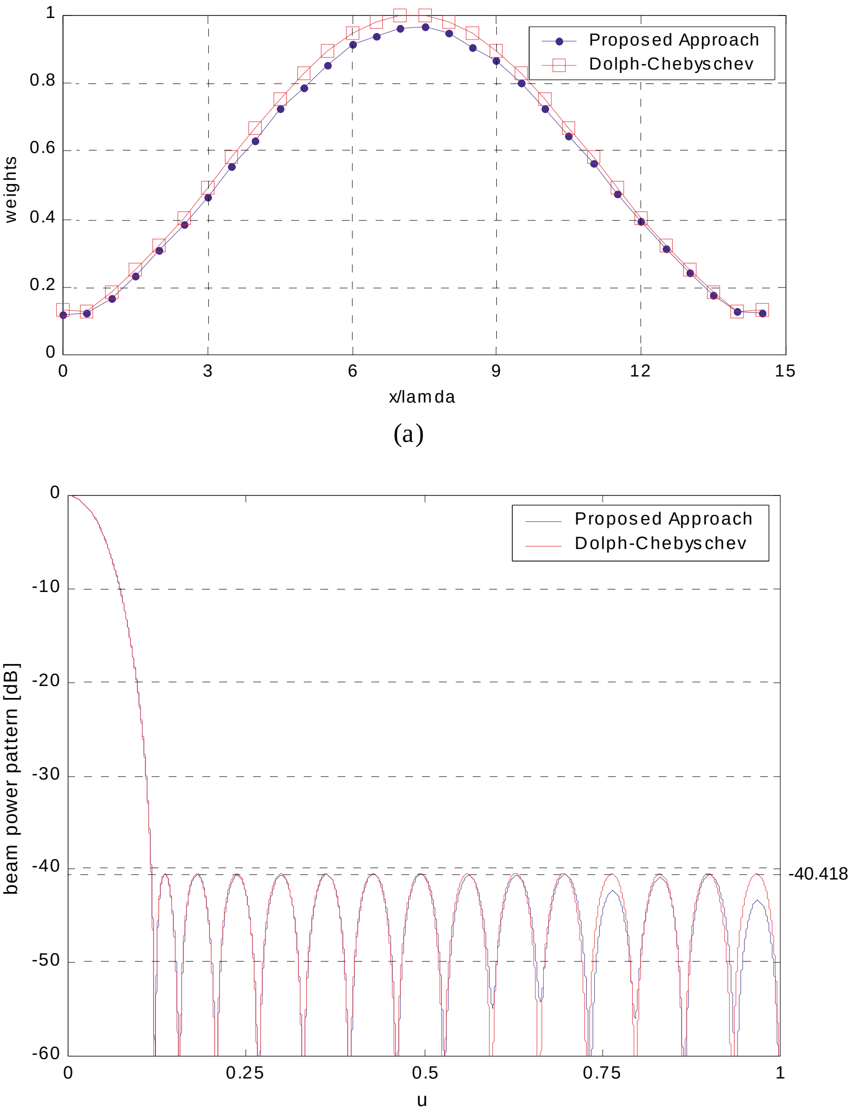


Figure 8. Optimization of Element Layout — BP generated by using $M = 152$ elements with side-lobe peak $\Phi_{slp} = -23.09\,\mathrm{dB}$.

Due to the stochastic nature of the proposed method, some statistical parameters related to the collection of simulations were evaluated. Table 2 gives the values of the best, worst, average results and standard deviation values in terms of number of elements, minimum side-lobe peak and main-lobe width. It is interesting to observe that the filling percentage is always lower than the one achieved in [6, 7] as well as the side-lobe peak value.

In conclusion, it should be pointed out that the removal of symmetry constraints significantly performances (symmetrical arrays are considered in [6, 7]).



(a)

(b)

Figure 9. Optimization of Element Weights — (a) Behavior of weight coefficient values; (b) BP with side-lobe peak equal to $-40.418\,\text{dB}$.

4.4. Optimization of Array Weights — Side Lobes Level

In the last test case, the optimization of weight coefficients (whose range was set to (0.05,1)) of $M = 30(\lambda/2)$-spaced elements in order to minimize the side-lobe peak of the resulting BP was addressed.

The IGA performed $I = 1000$ iterations with a fitness function characterized by $k_1 = 0.11,\ k_2 = k_3 = k_4 = 0$.

The same problem has been investigated in [5] yielding a BP with $\Phi_{slp} = -36.02\,\text{dB}$ and $u_{ml} = 0.0418$. The array configuration (Fig. 9(a)) — achieved with the IGA-based procedure — generated the BP shown in Figure 9(b), characterized by a side-lobe peak equal to $-40.418\,\text{dB}$ and a main-lobe width equal to 0.0417. For comparison purpose, the optimum Dolph-Chebyschev weighted array yields $u_{ml} = 0.0413$. Because of the negligible difference between these values, it can be assumed that the proposed method attained the global optimum of the fitness function.

Finally, the statistics given in Table 3 clearly point out the robustness of the results despite the stochastic nature of the suggested procedure. Many runnings of the proposed method (starting from random initial populations) gave results very close to the optimal one.

Table 3. Statistical characterization of the side-lobe peak value achieved after several process realizations.

Side-Lobe Peak (Φ_{slp}) [dB]			
Best	***Worst***	***Average***	***Std. Dev.***
−40.418 dB	−40.168 dB	−40.318 dB	0.118 dB

5. CONCLUSIONS

An optimization method for the synthesis of linear array pattern functions has been proposed and assessed. Shaped beam pattern, constrained side-lobes level, and main-lobe width are contemporarily taken into account by maximizing a suitable cost function by means of an innovative improved Genetic-Algorithm-based procedure. The proposed approach offers a great flexibility and an easy insertion of the *a-priori* knowledge within a low computational burden. Moreover, it should be pointed out that several extensions of the proposed approach could be also easily implemented without a significant increase of the algorithm complexity.

REFERENCES

1. Balanis, C., *Antenna Theory Analysis and Design*, second edition, John Wiley and Sons, Inc., 1997.
2. Ares-Pena, F., "Application of genetic algorithms and simulated annealing to some antenna problems," *Electromagnetic Optimization by Genetic Algorithms*, Y. Rahmat-Samii and E. Michielssen (Eds.), Wiley & Sons, New York, 1999.
3. Murino, V., A. Trucco, and C. S. Regazzoni, "Synthesis of unequally spaced arrays by simulated annealing," *IEEE Trans. Signal Processing*, Vol. 44, 119–123, 1996.
4. Rahmat-Samii, Y. and E. Michielssen, *Electromagnetic Optimization by Genetic Algorithms*, Wiley & Sons, New York, 1999.
5. Yan, K. and Y. Lu, "Sidelobe reduction in array-pattern synthesis using genetic algorithms," *IEEE Trans. Antennas and Propagation*, Vol. 45, No. 7, 1117–1122, 1997.
6. Haupt, R. L., "Thinned arrays using genetic algorithms," *IEEE Trans. Antennas and Propagation*, Vol. 42, No. 7, 993–999, 1994.
7. Weile, D. S. and E. Michielssen, "Integer coded Pareto genetic algorithm design of constrained antenna arrays," *Electron. Lett.*, Vol. 32, 1744–1745, Sept. 1996.
8. O'Neill, D. J., "Element placement in thinned arrays using genetic algorithms," *IEEE Int. Conf. Oceans 94 Osates, Brest (F)*, Vol. II, 301–306, September 1994.
9. Trucco, A. and V. Murino, "Stochastic optimization of linear sparse arrays," *IEEE Journal of Oceanic Engineering*, Vol. 24, No. 3, 291–299, 1999.
10. Wolpert, D. H. and W. G. Macready, "No free lunch theorems for optimization," *IEEE Trans. EVolutionary Computation*, Vol. 1, No. 1, 67–82, Apr. 1997.
11. Caorsi, S., A. Massa, and M. Pastorino, "A microwave procedure for NDT identification of a crack based on a genetic algorithm," *IEEE Trans. Antennas Propagation*, (in press).
12. Janikow, C. Z. and Z. Michalewicz, "An experimental comparison of binary and floating point representations in genetic algorithms," *Proc. 4th Conf. Genetic Algorithms*, 31–36, 1991.
13. Caorsi, S., A. Massa, and M. Pastorino, "A computational technique based on a real-coded genetic algorithm for microwave imaging purposes," *IEEE Trans. Geoscience and Remote Sensing*, Vol. 38, No. 4, 1697–1708, 2000.
14. Davis, L., *Handbook of Genetic Algorithms*, Van Nostrand

Reinhold, 1991.

15. Whitley, D., "The GENITOR algorithm and selection pressure: Why rank-based allocation of reproductive trials is the best," *Proc. 3rd Int. Conf. Genetic Algorithms*, 116–121, 1989.
16. Goldberg, D. E., *Genetic Algorithms in Search, Optimization and Machine Learning* Addison-Wesley, Reading, MA, 1989.
17. Haupt, R. L., "An introduction to genetic algorithms for electromagnetics," *IEEE Antennas and Propagation Magazine*, Vol. 37, 7–15, 1995.
18. Polak, E., *Computational Methods in Optimization*, Academic Press, New York, 1971.
19. Leeper, D. G., "Isophoric arrays — Massively thinned phased arrays with well-controlled sidelobes," *IEEE Antennas and Propagation Magazine*, Vol. 47, 1825–1835, 1999.
20. Leahy, R. M. and B. D. Jeffs, "On the design of maximally sparse beamforming arrays," *IEEE Trans. Antennas and Propagation*, Vol. 39, 1178–1187, 1991.

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