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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 aims at array thinning and optimization of element positions and weights by minimizing the side-lobes level. 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.

I. 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 $\lambda/2$-equispaced. Moreover, in [6] and in [7] a binary genetic algorithm was applied in order to deal with isophorical array thinning, and a stochastic approach aimed at optimizing isophorical arrays with a fixed number of elements was proposed in [8]. Unfortunately, all of these papers consider symmetrical 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' positions asymmetry and arbitrary weighting. To this end, an optimization method based on a simulated annealing (SA) process was applied to simultaneous weights' and positions' optimization in [4] and to global array synthesis and beam pattern shaping in [9].

In this framework, the aim of this paper is to present 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.

II. 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 $x_k, k = 0,...,M-1$. 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 fulfilling some constraints (e.g., side lobes level (SLL) lower than a fixed threshold) or reproducing a desired shape ($p^{ref}(u)$), an array configuration must be synthesized. First of all, it is necessary to define a measure of the difference between desired and synthesized beam pattern. To this end, let us define a function called *fitness function*, *f*, as follows

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

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

$$f_{SLL}\left(\overline{\zeta}\right) = \frac{Q}{\max_{u_{start} \leq u \leq 1}\{p_{dB}(u)\}}$$

$$f_{BP}\left(\overline{\zeta}\right) = \int_{u \in S}\left(\frac{p_{dB}(u)}{Q} - p_{dB}^{ref}(u)\right)du$$

$$f_N\left(\overline{\zeta}\right) = M$$

$$f_D\left(\overline{\zeta}\right) = D$$

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

The fitness function defined in (2) results highly non-linear with a large number of local maxima, where deterministic procedure 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.

III. 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., trial solutions for the 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 don't need to use derivatives;
- SGAs use random transition rules, not deterministic ones.

According to [10], SGA must be customized for each application in order to give optimal results. To this end, an IGA is proposed for some class of antenna synthesis problems. The flow chart of the IGA is shown in Figure 2. The main features of the algorithms are:

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

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

A. Parameters Representation

Generally, 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. On the other side, if discrete parameters are taken into account, a coding procedure is necessary. Each parameter is represented by a string of q bits, where $q = \log_2(L)$, being L the number of values that the discrete variable can assume [11]. However, when real unknowns are considered, binary

coding is unpractical and disadvantageous because of quantization noise and time consuming coding/decoding procedures [12]. In order to overcome these problems, a real-valued representation should be used [13].

As far as the antenna synthesis of linear $\left(\lambda/2\right)$ 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 $\{w_k; k = 0,...,M-1\}$. In order to effectively address this problem by means of a GA-based procedure, a hybrid coding is used. The chromosome assumes this structure

$$\overline{\xi} = \{M; b_0,...,b_k,...,b_{N-1}; w_0,...,w_k,...,w_{N-1}\} \tag{4}$$

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 $\left(\lambda/2\right)$ intervals separating the kth element of the non-uniform array to the left array extremity ($x_k = k\dfrac{\lambda}{2}$), w_k is the corresponding excitation coefficient, and N is the number of intervals ($\dfrac{\lambda}{2}$ 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 possibly enhance the convergence process. However, mutation must remain a mean for exploring new regions of the solution space and crossover must again constitute a way to mix at the best the genes of the current population. In our implementation some innovative choices have been applied.

B. 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

$$f_i' = (f_{i-1} - f_{i-1}^{avg})^n - (f_{i-1}^{worst} - f_{i-1}^{avg})^m \tag{5}$$

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, being i the generation index. The values of m and n are heuristically defined in order to avoid premature convergence and speed up the search when the population approaches convergence [15].

- *Crossover*

  The basic concept in crossover is to exchange gene information between chromosomes, and it is clear that the use of the crossover technique to improve the offspring production is undoubtedly problem oriented. An effective design of crossover operation greatly increases the convergence rate of the maximization procedure. 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 $\overline{\xi}^{(b)}$, a randomly selected crossover point k_s.

$$\overline{\xi}^{(a)} = \left\{ M^{(a)}; b_0^{(a)}, \dots, b_{k_s-1}^{(a)}, b_{k_s}^{(a)}, b_{k_s+1}^{(a)}, \dots, b_{N-1}^{(a)}; w_0^{(a)}, \dots, w_{k_s-1}^{(a)}, w_{k_s}^{(a)}, w_{k_s+1}^{(a)}, \dots, w_{N-1}^{(a)} \right\}$$

$$\overline{\xi}^{(b)} = \left\{ M^{(b)}; b_0^{(b)}, \dots, b_{k_s-1}^{(b)}, b_{k_s}^{(b)}, b_{k_s+1}^{(b)}, \dots, b_{N-1}^{(b)}; w_0^{(b)}, \dots, w_{k_s-1}^{(b)}, w_{k_s}^{(b)}, w_{k_s+1}^{(b)}, \dots, w_{N-1}^{(b)} \right\}$$

$$(6)$$

After crossover operation, the offspring result equal to

$$\left[\overline{\xi}^{(a)} \right]' = \left\{ M^{(a)}; b_0^{(a)}, \dots, b_{k_s-1}^{(a)}, b_{k_s}^{(a)}, \left[b_{k_s+1}^{(a)} \right]', \dots, \left[b_{N-1}^{(a)} \right]'; w_0^{(a)}, \dots, w_{k_s-1}^{(a)}, w_{k_s}^{(a)}, \left[w_{k_s+1}^{(a)} \right]', \dots, \left[w_{N-1}^{(a)} \right]' \right\}$$

$$\left[\overline{\xi}^{(b)} \right]' = \left\{ M^{(b)}; \left[b_0^{(b)} \right]', \dots, \left[b_{k_s-1}^{(b)} \right]', b_{k_s}^{(b)}, b_{k_s+1}^{(b)}, \dots, b_{N-1}^{(b)}; \left[w_0^{(b)} \right]', \dots, \left[w_{k_s-1}^{(b)} \right]', w_{k_s}^{(b)}, w_{k_s+1}^{(b)}, \dots, w_{N-1}^{(b)} \right\}$$

$$(7)$$

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

$$\left[w_k^{(a)} \right]' = r \left[w_k^{(a)} \right] + (1-r) \left[w_k^{(b)} \right]$$

$$\left[w_k^{(b)} \right]' = (1-r) \left[w_k^{(a)} \right] + r \left[w_k^{(b)} \right]$$

$$(8)$$

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

$$w_k^{\min} \leq \left[w_k^{(a)} \right]' \leq w_k^{\max} \quad k = 0,...,N-1$$
$$w_k^{\min} \leq \left[w_k^{(b)} \right]' \leq w_k^{\max}$$

(9)

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

On the other hand, boolean positions obey to semi-probabilistic rules, equal sensors' states of the parents are preserved and unequal sensors' states are activated with probability r for one child and $1-r$ for the other

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

(10)

The crossover is performed with a probability p_c and the reproduction (i.e., duplication of selected chromosomes from old to new population) with a probability $(1-p_c)$.

- *Mutation*

The mutation is performed with probability p_m on a chromosome of the population. Then occasionally (with probability p_{bm}) a mutation operation occurs which alters the value of a string position so as to introduce variations into 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 standard *binary mutation* is adopted [16] by using different probabilities for death or birth of an array element

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$$[b_k]' = \begin{cases} not\{b_k\}|_{b_k=0} & \text{with probability } p_{birth} \\ not\{b_k\}|_{b_k=1} & \text{with probability } p_{death} \end{cases} \qquad (11)$$

To adopt the concept of introducing variations into the chromosome, a random mutation has been designed also for real-valued genes

$$[w_k]' = w_k + \eta \qquad (12)$$

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

- *Elitism*

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

C. GA-HYBRIDIZATION

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 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 gradient-descent algorithm into the evolution concept of the GA in order to provide a structured random search (Fig. 2). The proposed hybridization performs 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 SGA performing selection, crossover, mutation and elitism, then a "Modified G-Bit Improvement" (MGbI) is performed. A randomly selected chromosome, $\overline{\xi}$, is modified by sweeping each gene, $\xi_l; l = 0,...,2N$. Boolean-valued genes are changed $([\xi_l]^* \Leftarrow not\{\xi_l\})$ and real valued genes slightly updated $([\xi_l]^* \Leftarrow \xi_l + r\dfrac{\xi_l}{\sum_{k=0}^{N-1} w_k}; r \in [-1,1])$. At each step ($l = 0,...,2N$), the difference between the values

of the fitness function evaluated by using the new field configuration and the last accepted configuration is computed $\Delta f = f(\overline{\xi}^*) - f(\overline{\xi})$. If $\Delta f > 0$ then we accept the new chromosome configuration so that we set $\overline{\xi} = \overline{\xi}^*$. 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 $(M^{opt}; b_0^{opt}, ..., b_k^{opt}, ..., b_{N-1}^{opt})$) is frozen and a local search is performed by means of a standard Polak-Ribière conjugate-gradient algorithm [18] to further improve array weights ($w_0^{opt}, ..., w_k^{opt}, ..., w_{N-1}^{opt}$).

III. 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.

A. Optimization of Element 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 antenna synthesis procedure was applied to a linear array of 25 isotropic elements $D = 50\lambda$ in length. In order to compare 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 $N = 100$ $\left(\lambda/2\right)$-spaced steps by imposing equal to $M = 25$ the number of active elements. Then the structure of the chromosome results

$$\begin{aligned}
\overline{\xi} &= \{w_0, ..., w_k, ..., w_{N-1}\} \\
b_k &= 1 \quad k = 0, ..., N-1 \\
M &= 25
\end{aligned} \tag{13}$$

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 values suggested in related literature) resulted: population dimension, $J = 140$; $p_c = 0.6$; $p_m = 0.6$; gene mutation probability for boolean-values,

$p_{bm} = \left(\frac{1}{6 \cdot 10^3}\right)(i-1) + 0.06$;   gene   mutation   probability   for   real-values,

$p_{bm} = \left(\frac{7}{10^5}\right)(i-1) + 0.03$; maximum number of iterations, $I = 600$. MGbI was performed on $R = 4$ roulette-wheel selected individuals (this value represents a good choice allowing an effective trade-off between amount of computational load and convergence rate).

The best result was an array with a side lobe peak $\Phi_{slp} = -14.77dB$. 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 $-14.45dB$ ($u_{ml} = 0.191$ being the half-beamwidth). Figure 3 compares the BP, the element weights and position layout of such arrays.

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

For completeness, in order to point out the achievable tradeoff between side-lobe peak and main-lobe width, a small collection of the best results obtained after some runs of the proposed algorithm have been reported in Fig. 4. For comparison, also the point given by the SA-based procedure is shown.

Finally, isophoric arrays [19] were considered as well. In this case the array element weights were fixed ($w_k; k = 0,..., N-1$) and the optimization dealt with array element positions. Figure 5 shows the BP and position layout in correspondence with best solutions, in term of minimum side-lobe level peak ($\Phi_{slp} = -13.06dB$ and $u_{ml} = 0.0170$; IGA (a)) as well as in term of optimal tradeoff between side-lobe level and main-lobe width ($\Phi_{slp} = -12.32dB$ 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 given ($\Phi_{slp} = -12.07dB$ and $u_{ml} = 0.0133$; SA [4]).

B. Optimization of Element 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 taken into account. The desired pattern was the same as in [9][19] and described in Table I.

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 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 $D = 16.5\lambda$ (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 disadvantage of the sharply reduced aperture is the increased main lobe width, which is 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, $f\left(\overline{\xi}_i^{opt}\right)$, versus the iteration number for the best array synthesis. For completeness, also single terms of the fitness function are given ($f_{BP}\left(\overline{\xi}_i^{opt}\right), f_N\left(\overline{\xi}_i^{opt}\right), f_D\left(\overline{\xi}_i^{opt}\right)$).

C. Optimization of Element 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 resulted

$$\overline{\xi} = \{M; b_0, ..., b_k, ..., b_{N-1}\}$$
$$w_k = 1 \quad k = 0, ..., N-1$$

(14)

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 $p_{birth} = 0.003$.

Due to the stochastic nature of the proposed method, some statistical parameters related to the collection of simulations were evaluated. Table II 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 generally the side-lobe peak value. The best result in terms of minimum Φ_{slp} ($\Phi_{slp} < -23.09dB$) (Fig. 8) was obtained with a 76% filled array ($M = 152$). On the other hand, the array with 73.5% filling presented a side-lobe peak $\Phi_{slp} < -22.60dB$ slightly worse than the best result in [10] ($-22.60dB$ versus $-22.79dB$), but with a reduced number of array elements (147 versus 154).

In conclusion, it should be pointed out that removing symmetry constraints resulted in better performances (symmetrical arrays are considered in [6][7]).

D. Optimization of Element Weights – Side Lobes Level

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

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 $\Phi_{slp} = -36.02dB$ and $u_{ml} = 0.0418$. The array configuration (Fig. 9(*a*)) - achieved with the IGA-based procedure - generated a BP shown in Figure 9(*b*), characterized by a side-lobe peak equal to $-40.418dB$ and a main-lobe width equal to 0.0417. As far as the optimum Dolph-Chebyschev weighted array is concerned, $u_{ml} = 0.0413$. Because of the slight difference between these values, we can conclude that the proposed method attained the global optimum of the fitness function.

Finally, side-lobe peak statistics given in Table III 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 best achieved.

V. Conclusions

An optimization method for the synthesis of linear array pattern functions has been proposed and assessed. Shaped beam pattern, constrained side-lobes level, 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. Many additional extensions of the proposed approach could be also easily implemented both in term of cost function definition, optimization methodology and applications and antenna types.

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<div align="center">**FIGURE CAPTIONS**</div>

- Figure 1

  Linear array geometry.

- Figure 2

  Flowchart of the Improved Genetic Algorithm.

- Figure 3

  Optimization of Element Weights – (*a*) BP with a side-lobe peak of $-14.77dB$; (*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).

- Figure 5

  Optimization of Element Positions and Weights – Optimal syntheses for isophoric arrays. (*a*) BPs; (*b*) array layouts.

- 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.

- Figure 8

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

- Figure 9

  Optimization of Element Weights – (*a*) Behavior of weight coefficient values; (*b*) BP with side-lobe peak equal to $-40.418dB$.
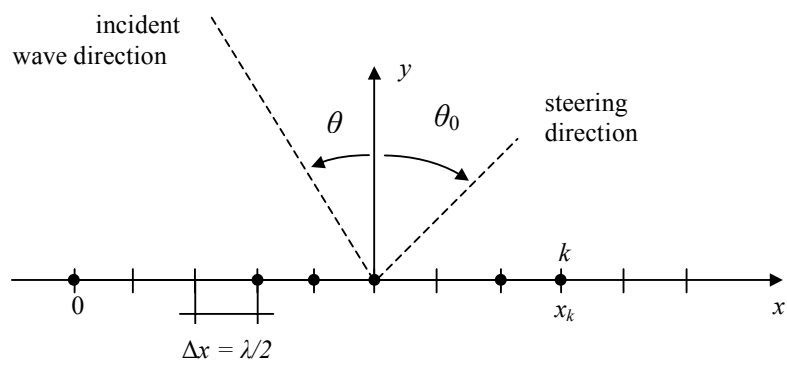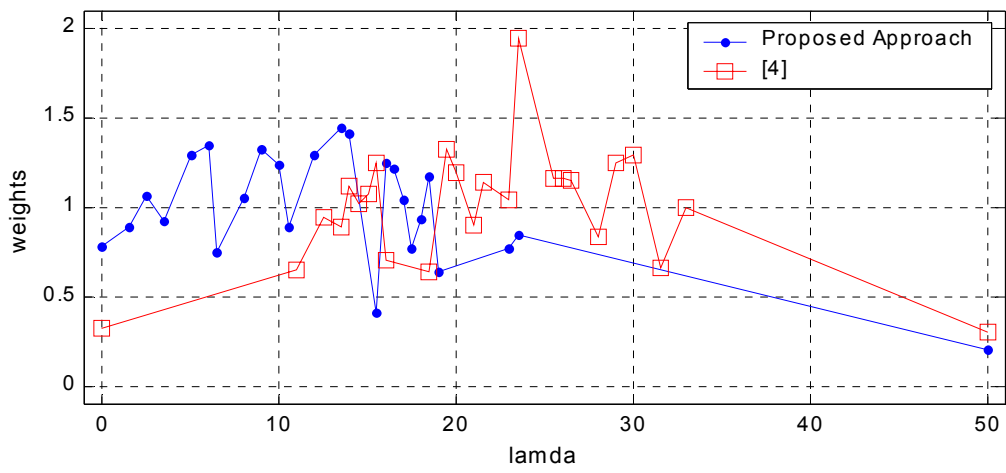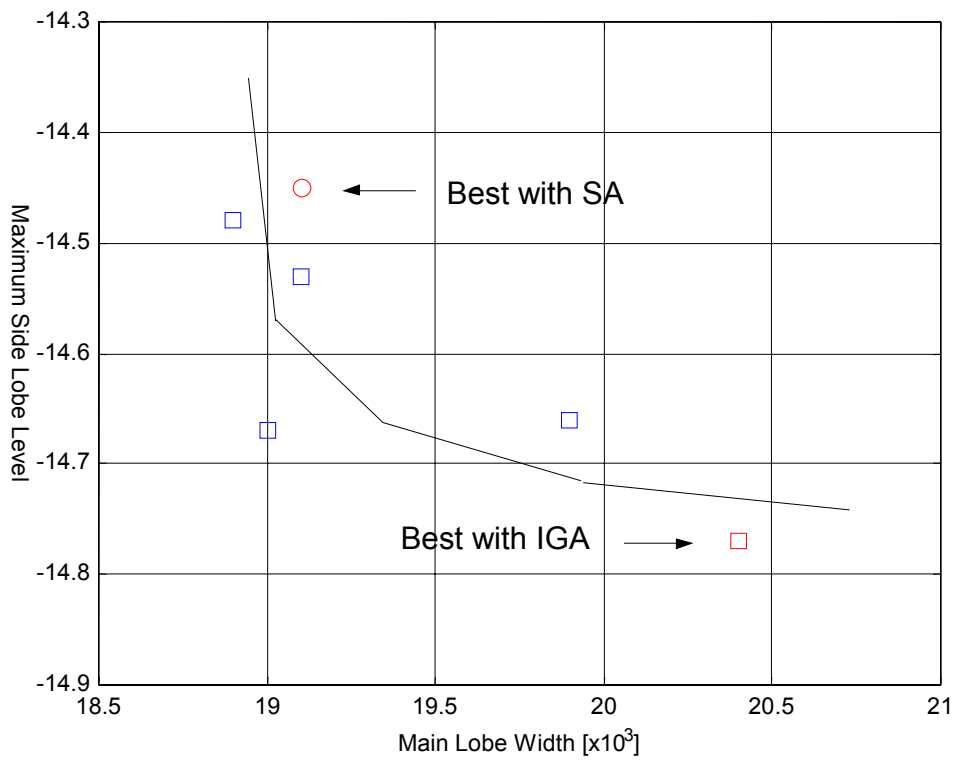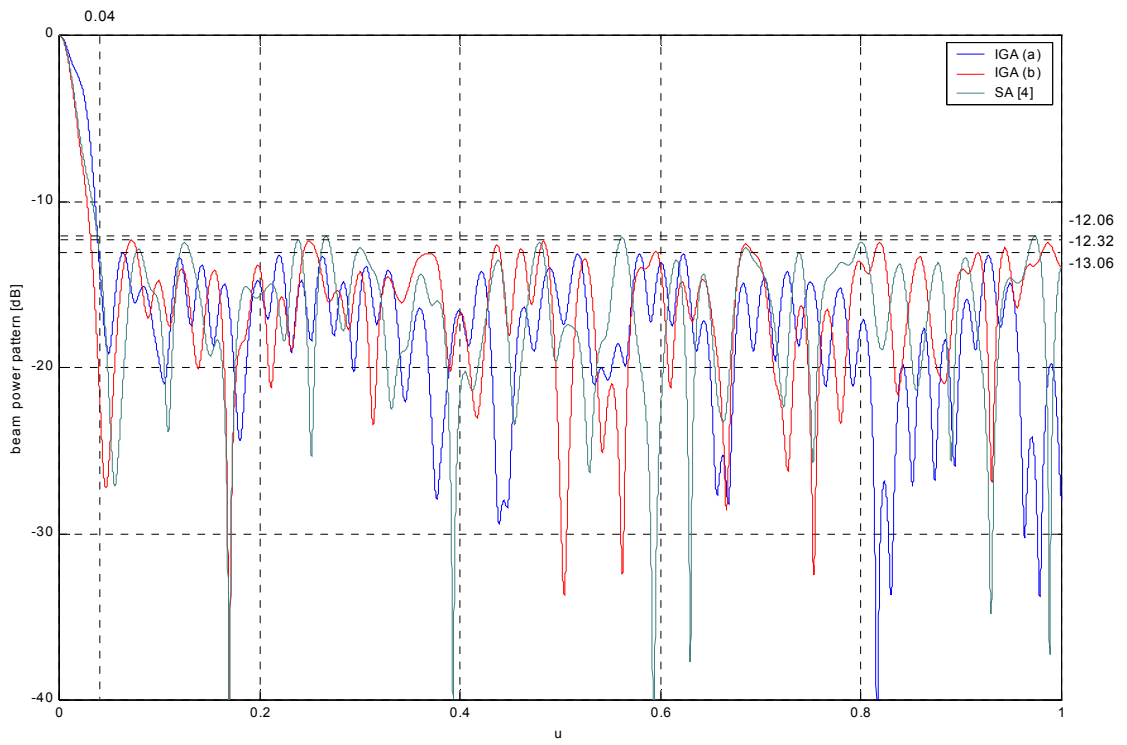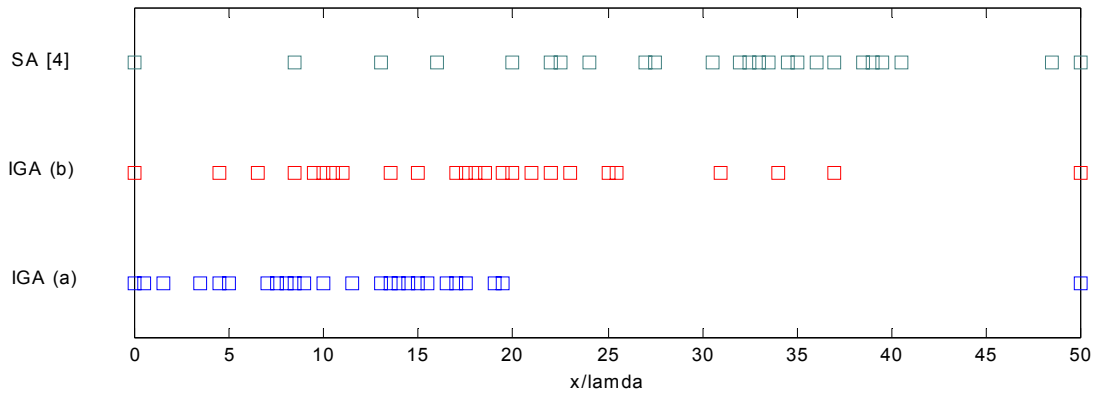
Fig. 1 - M. Donelli et *al.*, "Linear Antenna Synthesis ..."
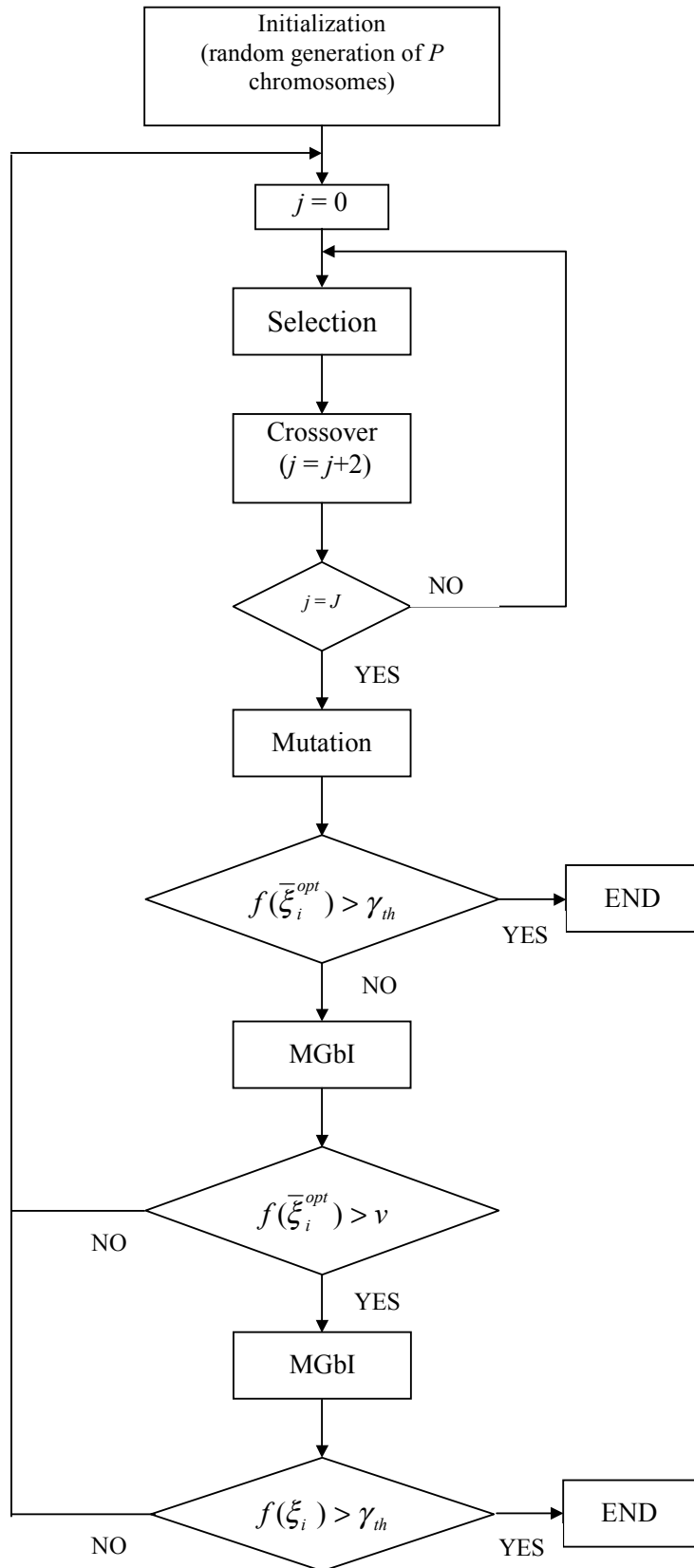
Fig. 2 - M. Donelli et *al.*, "Linear Antenna Synthesis ..."
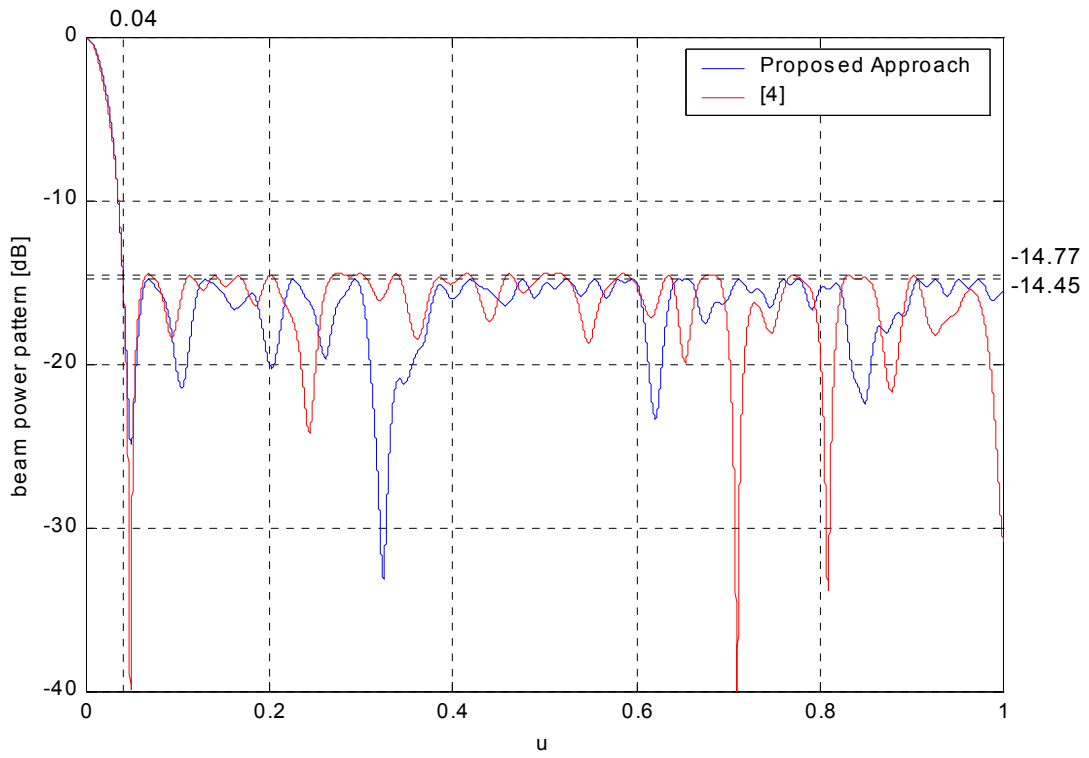
(*a*)

(*b*)

Fig. 3 - M. Donelli et *al.*, "Linear Antenna Synthesis ..."

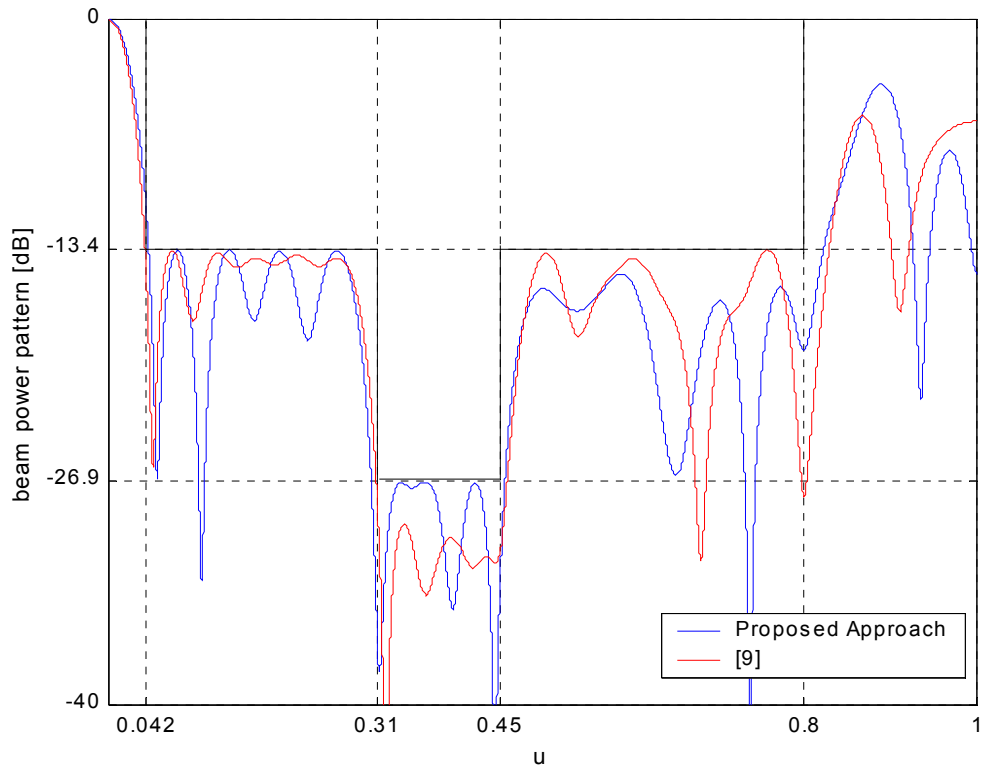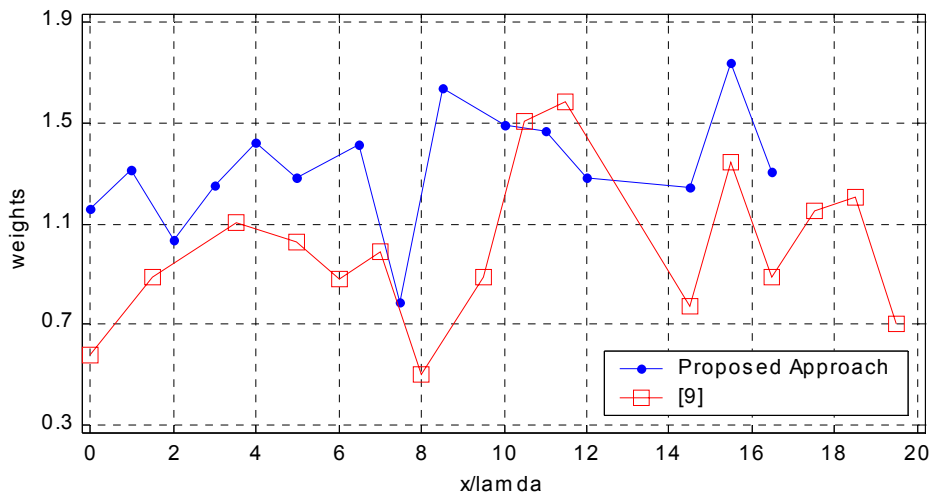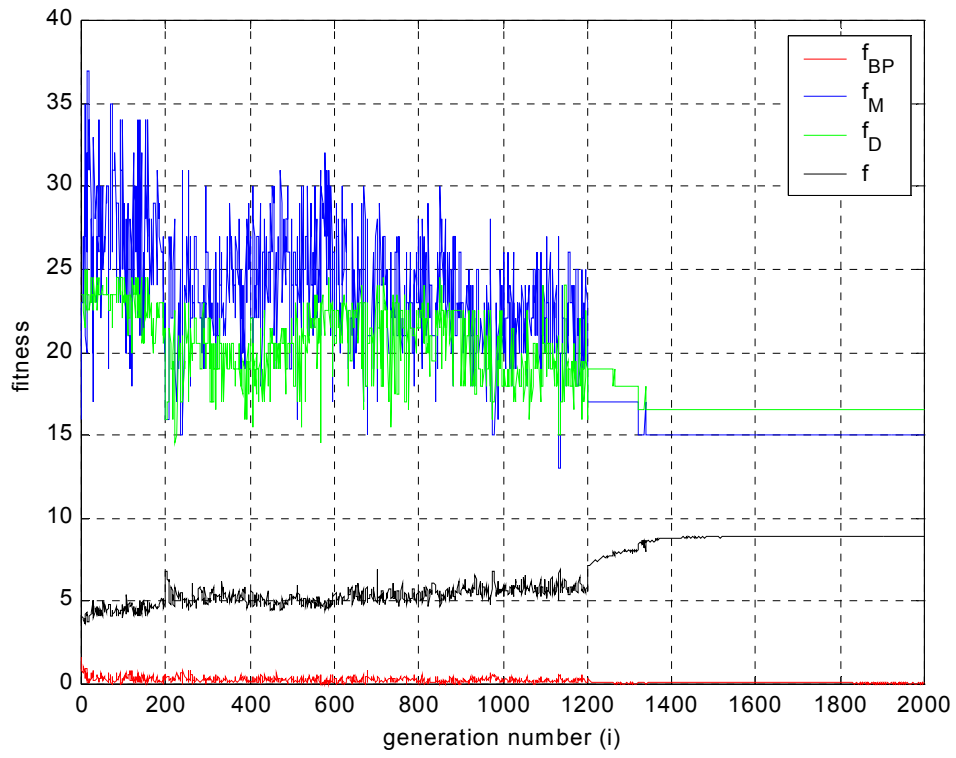**Fig. 4 - M. Donelli et *al.*,** "Linear Antenna Synthesis ..."

(*a*)

(*b*)

Fig. 5 - M. Donelli et *al.*, "Linear Antenna Synthesis ..."

(*a*)

(*b*)

Fig. 6 - M. Donelli et *al.*, "Linear Antenna Synthesis ..."

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Fig. 7 - M. Donelli et *al.*, "Linear Antenna Synthesis ..."

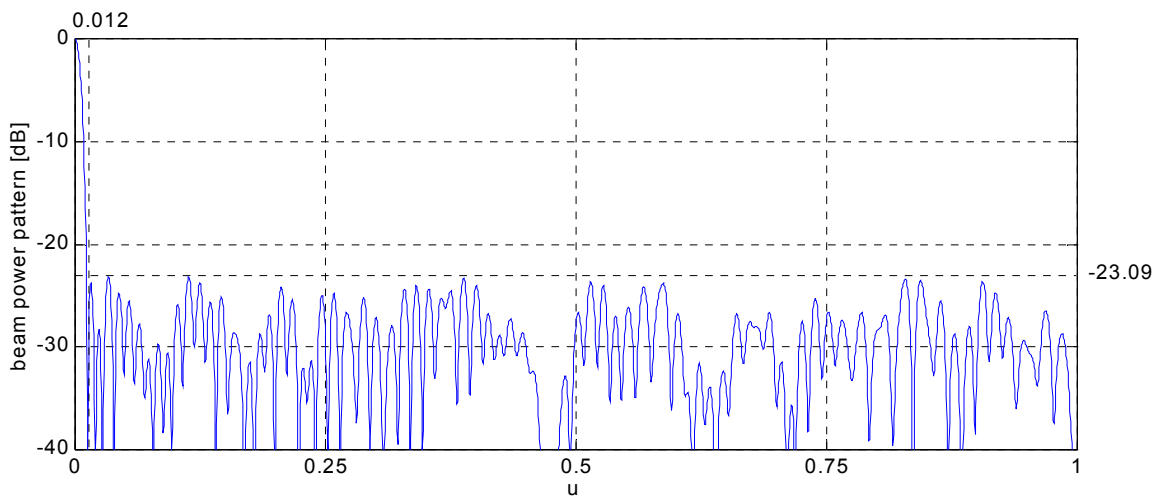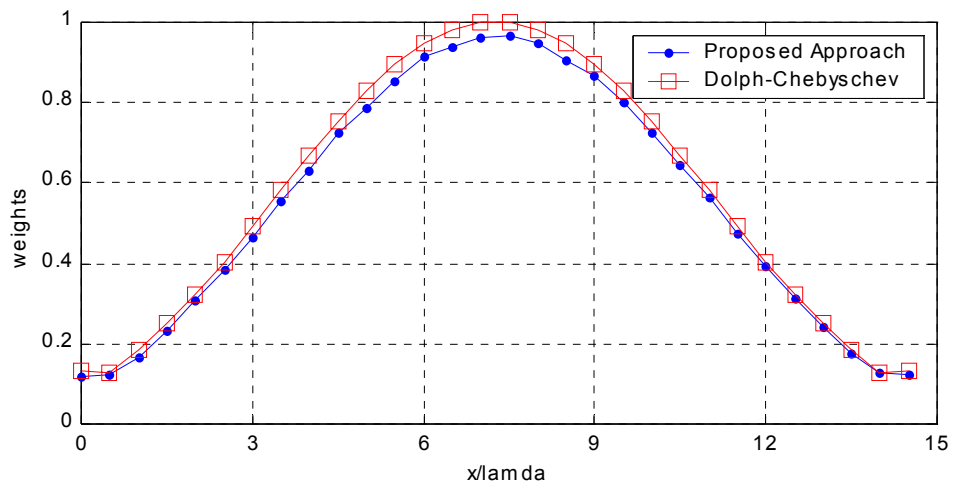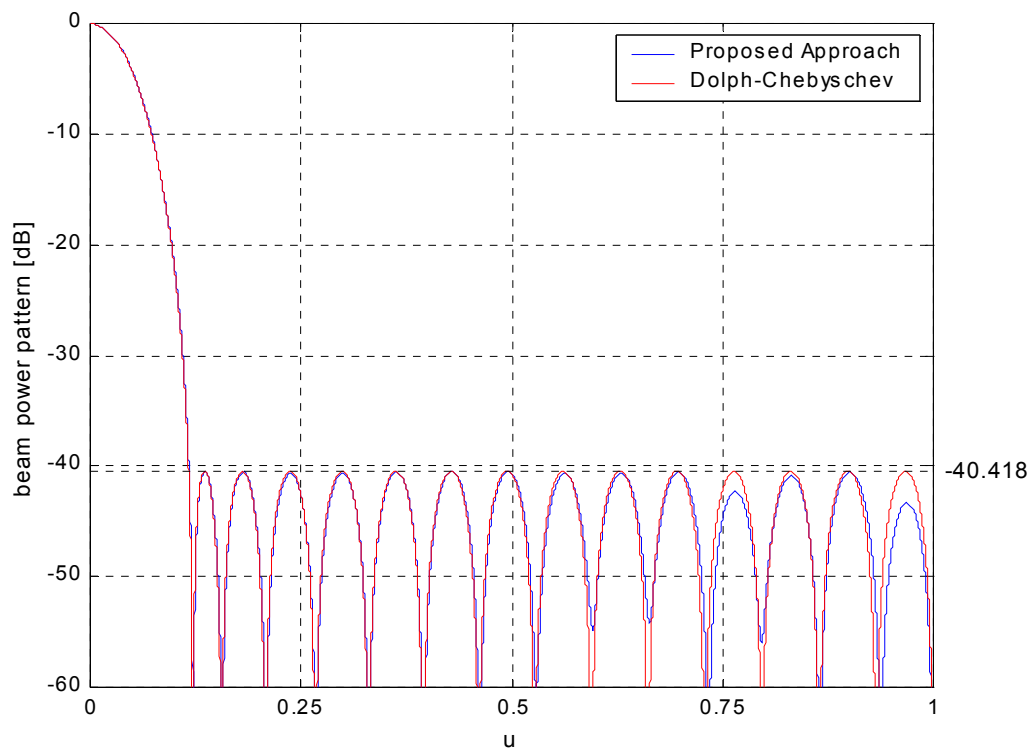**Fig. 8 - M. Donelli et *al.*,** "Linear Antenna Synthesis ..."

(*a*)

(*b*)

Fig. 9 - M. Donelli et *al.*, "Linear Antenna Synthesis ..."

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

Tab. I - M. Donelli et *al.*, "Linear Antenna Synthesis ..."

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

Tab. II - M. Donelli et *al.*, "Linear Antenna Synthesis ..."

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

Tab. III - M. Donelli et *al.*, "Linear Antenna Synthesis ..."