A Bayesian Estimation of Distribution Algorithm Approach to the Definition of Linear Antenna Arrays Excitations

Un enfoque basado en algoritmos con estimación de distribuciones para el diseño de arreglos lineales de antenas

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Abstract. This paper introduces and investigates the family of aperture distributions whose members have the best Side Lobe Ratio (SLR) for a given Inverse Dynamic Range Ratio (IDRR). An optimization approach based on Estimation of Distributions Algorithms is used to find the family instances. The paper shows that the family has limiting distributions with a number of interesting properties, e.g. it has a good tradeoff between beamwidth and SLR and has the best IDRR for a given beamwidth. The numerical results allow us to conclude the following: 1) the IDRR impacts the complexity of the problem, i.e. the larger the IDRR the easier the optimization. 2) linear entropic mutation improves the performance of the algorithms and reduces the population size requirements. 3) the independence model seems to be adequate for very large IDRR but fails dramatically for the other cases.

Keywords. G.1.6: Optimization, G.1.10: Applications, J.2: Physical Sciences and Engineering, antenna arrays, Dolph-Chebyshev distribution, Taylor distribution, dynamic range ratio, estimation of distribution algorithms, side lobe ratio and linear entropic mutation.

Resumen. Este artículo introduce e investiga la familia de distribuciones de apertura cuyos miembros poseen el menor lóbulo lateral (SLR) para un rango dinámico inverso (IDRR) dado. Un enfoque de optimización basado en algoritmos de estimación de distribuciones es utilizado para encontrar los miembros de la familia. El artículo muestra que la familia presenta distribuciones límites con propiedades interesantes: muestra un buen compromiso entre el ancho del lóbulo central y SLR además del mejor IDRR para un HPBW dado. Los resultados numéricos nos permiten concluir lo siguiente. 1) el IDRR influye en la complejidad del problema: para altos IDRR es más fácil el proceso de optimización. 2) la mutación entrópica lineal mejora el comportamiento de los algoritmos y reduce el tamaño de la población. 3) el modelo de independencia parece resultar adecuado para altos IDRRs pero falla dramáticamente para otros casos.

Palabras clave. G.1.6: Optimización, G.1.10: Aplicaciones, J.2: Ciencias Físicas e Ingeniería, arreglos de antenas, distribución de Dolph-Chebyshev, distribución de Taylor, relación de rango dinámico, estimación de los algoritmos de distribución, relación de los lóbulos laterales y la mutación de entropía lineal.

1 Introduction

Our current aim is a preliminary discussion about the challenges of antenna arrays synthesis from an optimization point of view. Antenna arrays have been of great importance and widely used in many communication fields in a large variety of designs. They have been extensively investigated since the second half of the last century [7, 23]. In the 90's, with the use of optimization algorithms new configurations for arrays were achieved, overcoming most of the limitations of previous methods and improving performance. In the last years a great number of papers published about arrays involved optimization algorithms [2, 6, 8-12]. Besides helping to solve custom complex problems they can be used to describe the relationships and achievable limits between the figures of merit that characterize the arrays. It is important to know these relationships and limits for designers in advance when using optimization algorithms.

In this paper we study some relationships between popular figures of merit limited to simple scenarios by an optimization approach. A new family of amplitude distributions which has the best Side Lobe Ratio (SLR) for a given Inverse Dynamic Range Ratio (IDRR) is presented, which shows interesting properties.

The outline of the paper is as follows. To begin with, Sect. 2 presents background material about the main antenna concepts, the role of the IDRR in antenna design, the optimization algorithm used in the research and the concept of linear entropic mutation. Section 3 outlines our optimization approach to the definition of a new family of amplitude distributions, whereas Sect. 4 presents results about several optimization issues that arise in this approach. Finally, the conclusions are given.

2 Background

A linear array of $2N$ antennas is shown in Fig. 1. Each antenna (element) is spaced by a distance d and fed with a current amplitude a_n. A common normalized amplitude current excitation of the array elements is shown in Fig. 2 and this is called the aperture or amplitude distribution. Considering the elements as isotropic, i.e. they radiate the same amount of power in all directions, and a symmetric distribution, the far-field pattern of this array can be obtained by (1) and the normalized power pattern by (2). A common power pattern is plotted in Fig. 3.

$$F(\theta) = 2\sum_{n=1}^{N} a_n \cos\left[(n-0.5)kd\cos(\theta)\right] \tag{1}$$

$$P(\theta) = 10\log_{10}\left[\frac{|F(\theta)|}{\max|F(\theta)|}\right]^2 \tag{2}$$

where k is the free-space wave number and $\theta \in [0, \frac{\pi}{2}]$ the direction of the radiation.

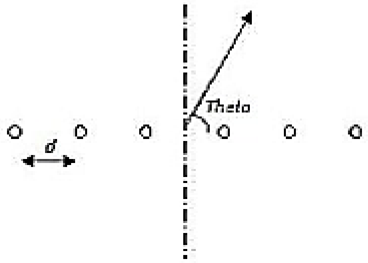

Fig. 1. Linear array of 6 antennas

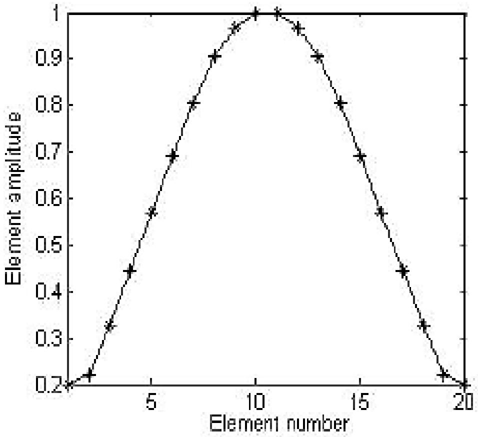

Fig. 2. An example of normalized amplitude distribution. Distribution of Dolph-Chebyshev

The SLR and the Half Power Beam Width (HPBW) are used for characterizing the power pattern (Fig. 3). SLR is the ratio of the main beam maximum amplitude to that of the highest side lobe (3), see Fig. 3. High SLR patterns are useful for rejecting transmitting sources which are in other directions rather than in the main lobe.

$$SLR = \max\{-P(\theta_i)\} \tag{3}$$

where *i* is the position of the side lobes maximum.

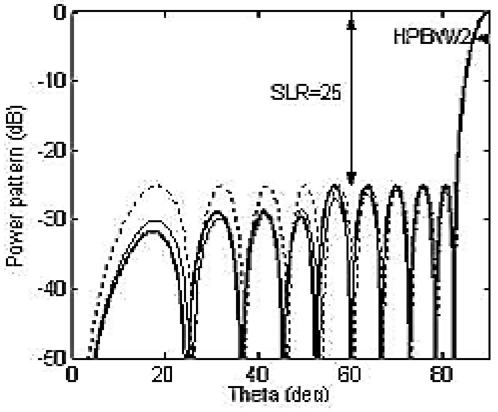

Fig. 3. Three power patterns (only plotted half pattern due to symmetry). Dolph (dashed line), Taylor $n = 6$ (solid line), our distribution (thick solid line)

The HPBW is the width of the main lobe at half the maximum power. Low HPBW (narrow beam) patterns are useful for distinguishing between two sources which are very close to each other. Narrow beam-low side lobes patterns, also known as pencil beam patterns, are of common use in radars, and high directivity low noise arrays in general.

The Inverse Dynamic Range Ratio (IDRR) characterizes the amplitude distribution and is defined as the ratio of the lowest to the highest element amplitude. The IDRR is strongly related with the size and cost of the array feeding networks and the mutual coupling between elements.

The mutual coupling measures the interchange of energy between two antennas which are close to each other. Even if both are transmitting, some of the energy transmitted from each will be received and rescattered by the other, acting as a second transmitter. So if one of the antennas is significantly more excited than the other, it overcomes the one which is poor excited and modifies its properties (e.g. impedance, power pattern). Note that by improving IDRR, the mutual coupling might improve too.

To illustrate how IDRR affects the size of the feeding network, suppose we have two identical array elements but with significant different currents feeding then. If we only have one transmitter, the transmission line needs to be split in two. As an example, in the case of microstrips, a commonly used transmission line, the ratio of the width of the split lines increases with the ratio of the currents. So, for high current ratios (i.e. low IDRR) either we obtain a wide split line, which affects the size of the design, or a thin one, which needs higher precision in the construction yielding a costly design. Furthermore, the width of the line is also related with its impedance and the line needs to be resized before feeding the elements, and the resized operation might also be related to its current width. So, we have design constraints which point to low IDRRs array distributions.

2.1 IDRR vs. SLR

IDRR was little addressed in literature before the 90's, but it has been somehow reborn the last two decades with the era of evolutionary algorithms. Shiwen studied the behavior of IDRR in the synthesis of power patterns in linear arrays [25, 26]. He concluded that is possible to improve the IDRR of conventional arrays. Ares and colleagues optimized IDRR and improved the shape of the amplitude distribution [1, 21, 22]. In [24], an approach for setting limiting bounds for IDRR given a set of nulls constraints is presented, although no other parameter like SLR or HPBW was taken on account. Recently two methods for array synthesis that take in account for IDRR were presented in [6, 5].

In summary, an IDRR improvement is possible without a significant degradation of the other characteristics of the array. However, to the best of our knowledge, it has not been any attempt to find distributions that optimize any of the relationships involving IDRR with other important characteristics like SLR or HPBW. Knowing these relations and the achievable limits before hand is helpful for designers for the construction of the cost function when using optimization methods. For example, it avoids searching for impossible solutions.

2.2 Bayesian Estimation of Distribution Algorithms

Given a random vector, X, that takes its values in the so called solution space, X, we seek the optima of a given function, F (X). A Bayesian Estimation of Distribution Algorithm (EDA) [13, 14, 20], is an evolutionary algorithm that can solve this problem using the following basic cycle. The algorithm uniformly samples the solution space to create an initial population. The population is then updated for a number of generations. First, a set of promising solutions (the selected set) is chosen using truncation, tournament or Boltzmann selection. A Bayesian network that captures the correlations of the selected set is constructed and new solutions are simulated from it. Finally, the new solutions are combined with the old ones and a new population – with better properties – is constructed.

The algorithm iterates until given termination criteria are met. Learning the Bayesian network is the critical step. Some algorithms use a greedy procedure that, starting from an empty (complete) graph, at each step adds (deletes) the edge that improves a certain metric, which is defined over the set of all acyclic graphs (see BOA [19] and EBNA [3]). Other algorithms, like the MMHC-EDA [17] are based on statistical tests instead. After more than ten years of research there exists a tremendous amount of literature about EDAs. The interested reader can easily find many detailed presentations on the topic. The references of this paper might be good starting points.

2.3 A Short Overview of Linear Entropic Mutation

Linear Entropic Mutation acts as an operator that regularizes the entropy of a joint probability mass and computes a convex sum of the current and the maximum entropy with the regularization parameter a. In this way the distribution is shrunk toward the maximum entropy distribution. It turns out that this process can be interpreted as a mutation process as far as it increases the level of uncertainty or randomness in the system [16, 17]. For multivariate discrete systems the following definition introduces the LEM.

Let $p(x_1; x_2; \dots; x_n$, $p_a(x_1; x_2; \dots; x_n)$ denote two discrete joint probability masses and $H(X)$, $H_a(X)$ their respective entropy values.

If

$$H_a(X) = (1-a)H(X) + na \tag{4}$$

for a given real number, $0 < a \leq 1$, we say that $p_a(x_1; x_2; \dots; x_n)$ is a LEM-mutation of $p(x_1; x_2; \dots; x_n)$ with mutation intensity a. There are many distributions that fulfill (4), thus the computation of a meaningful $p_a(x_1; x_2; \dots; x_n)$ given $p(x_1; x_2; \dots; x_n)$ is challenging. Notice that these distributions must be similar, which in the context of EDAs algorithms has the important meaning that the mutation does not destroy the learned distributions. The mutation intensity a controls the strength of the mutation, i.e. how much the entropy of a random variable is changed. The computation of the LEM-mutation of one binary variable, X, is accomplished in two steps. Firstly, $H_a(X)$ is computed according to (4), and then the new probability distribution $p_a(X)$ is obtained from $H_a(X)$. As the entropy of binary variables is symmetric –each entropy value is mapped to exactly two probability values– a simple procedure to resolve the ambiguity was introduced in [16], where the case of multivariate independent variables is also solved. An algorithm for computing the LEM-mutation of a general multivariate random binary variable is presented in [18]. The most popular mutation operator of binary genetic algorithms is, without any doubt, the so-called bitflip mutation. Bit-flip means negating with probability $\mu = \frac{1}{n}$ (n - size of the problem) the value of every variable in all individuals of a population. However, it can be shown that this operator performs poorly when there are strong dependencies among the variables of a problem. In these cases LEM-mutation is particularly powerful as it was shown in [18].

3 A new Approach to the Synthesis of Aperture Distributions

We propose a family of distributions that optimizes the pair IDRR-SLR, i.e. its members have the best SLR possible for a given IDRR. This idea resembles Dolph-Chebyshev distributions which have the best HPBW for a given SLR. The paper presents some basic properties of the proposed family. To accomplish this, our strategy was to run many times the MMHC-EDA to find out the best approximation possible of the new family members.

The MMHC-EDA [17] is a powerful member of the class of Bayesian EDAs that learns the structure of the search distributions with a modification of the algorithm reported in [4].

We tested the following boolean representation of the real vector $\boldsymbol{a} = (a_1;\ a_2;\ \dots\ ;\ a_N)$. Denoting by $a_{\min}$ the minimum component of $\boldsymbol{a}$, the real interval $[a_{\min}; 1]$ is quantified with M bits, i.e. a quantum $q = (1 - a_{\min})2^{-M}$ is defined. Let $\boldsymbol{X} = (X_1; X_2; \dots; X_{\boldsymbol{N}})$ be a partition of a boolean vector and let the X_i represent non-negative integers. Each X_i codifies the excitation a_i with M bits, i.e. $a_i = a_{\min} + qX_i$. Thus, the length of the boolean vector is NM bits. With the proposed boolean codification all the simulated solutions are feasible and have IDRRs not smaller than $a_{\min}$.

Taking on account the tolerance limits achievable in practice, the element amplitudes are quantified with 10 bits, which is less than 0.1% error in the interval $[0; 1]$. The resulting length of the random vector is $10N$. To compute the curves of the family, the IDRR range under study is divided in l equal parts. For each IDRR value several optimization runs are performed. The amplitude distributions simulated by the MMHC-EDA are used to compute (3) which is the fitness function.

Three basic relationships, namely SLR vs. IDRR, HPBW vs. IDRR, and HPBW vs. SLR are investigated for our and three well known popular distributions: Dolph-Chebyshev (Dolph) and Taylor *n* [7, 23].

Our case study is a $2N = 20$ element array and thus the number of binary variables was set to 100. We study the IDRR range $[0.2; 0.75]$ with a resolution of 0.05 and compute $F(\theta)$ with an angle resolution of $0.5\pi 10^{-4}$. For each IDRR we run the optimizer several times and the vector found with the best SLR is output as the approximation of the best solution for that IDRR. The algorithm uses truncation selection. Each run takes about few seconds on a standard computer. The run is stopped when the fitness difference between any two individuals in the population does not exceed $\delta = 10^{-6}$. The population size was set equal to 900, which guarantees a high degree of robustness of the obtained results. It is worth noting that in a normal optimization run we do not require full convergence in the last population. However, for the purposes of this section, this kind of “intelligent brute force” search is adequate. We will remove this assumption in Sect. 4.

3.1 Basic Relations and Shape Characteristics

Figure 4 shows for 20 elements, the plot of SLR vs. IDRR for our distribution, Dolph-Chebyshev, Taylor one parameter and Taylor *n*. For Taylor one-parameter SLR decreases as IDRR increases. However, Dolph and Taylor n-parameter show this behavior up to a limiting IDRR where it no longer increases but decreases as SLR decreases. As it was expected (due to the definition) our family has the best SLR values for the given IDRRs. We have found that for low IDRRs our family approximates Dolph (Taylor *n* also approximates it as *n* increases).

Figure 5 shows the plot of HPBW vs. IDRR for the same distributions discussed above. The behavior of HPBW is similar to that of SLR in Fig. 4. However, in this case “best” amounts to “low”, and therefore, our family does not display the best HPBW for a given IDRR. This is an expected result that can be explained by the well known tradeoff between HPBW and SLR. The good news is that our distribution does have the best IDRR for a given HPBW. Figure 6 shows the plot of HPBW vs. SLR. HPBW increases with SLR. The Dolph distributions have the best HPBW for a given SLR. It can be observed that our distribution performs like Taylor *n*, and both are very close to Dolph. We can say that optimizing SLR under an IDRR constraint improves the relationship between HPBW and SLR. Another observation we can draw from the figure is that our distribution has the best IDRR for any of the given magnitudes SLR or HPBW.

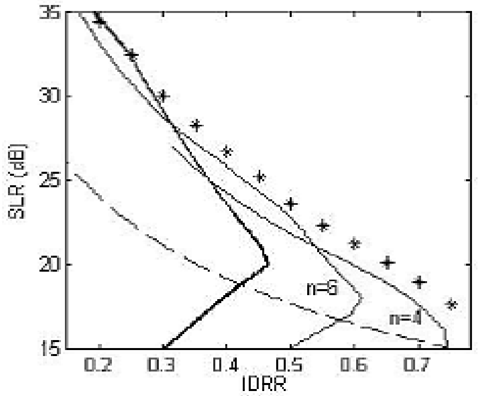

Fig. 4. SLR vs. IDRR for 20 elements. Dolph (thick solid line), Taylor $n = 4,\ 6$ (solid line), Taylor one-parameter (dashed line), our distribution (asterisk)

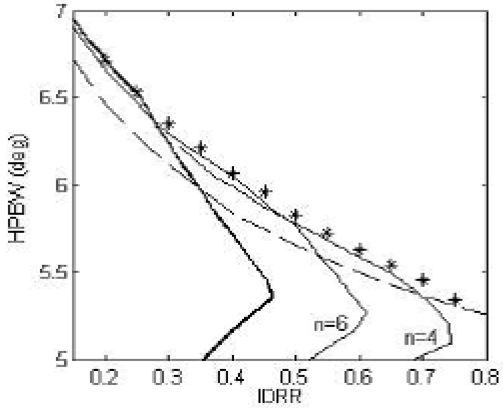

Fig. 5. HPBW vs. IDRR for 20 elements. Dolph (thick solid line), Taylor $n = 4,6$ (solid line), Taylor one-parameter (dashed line), our distribution (asterisk)

SLR = 25 dB. Our distribution presents the first sidelobes of equal amplitude as Dolph, while the far-out sidelobes decay similar to Taylor $n = 6$ but not monotonically. This is interesting due to the fact that the original idea of Taylor was to obtain a distribution that approximates the location of the inner pattern nulls to the ones of the Dolph [23]. Here the remarkable fact is that the optimizer was able to approach this behavior, based solely upon the optimization of SLR under the constraint of IDRR

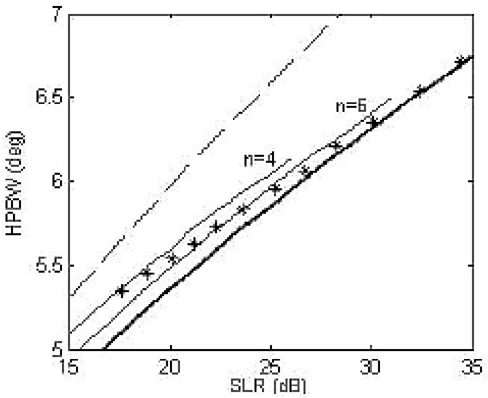

Fig. 6. HPBW vs. SLR for 20 elements. Dolph (thick solid line), Taylor $n = 4,6$ (solid line), Taylor one-parameter (dashed line), our distribution (asterisk)

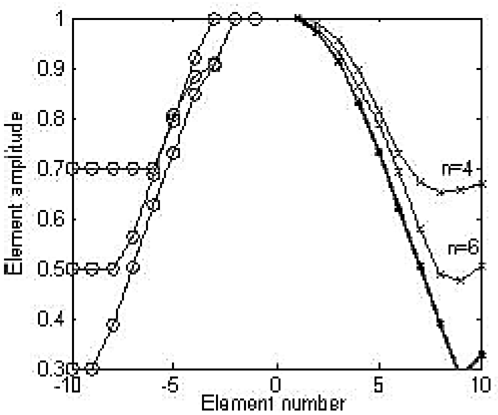

Fig. 7. Comparison of amplitude distributions. Dolph(cross and thick solid line), Taylor $n = 4,6$ (cross and solid line), our distribution (circle and solid line)

Figure 3 shows three power patterns of 20 element array for Dolph, Taylor $n = 6$, and our distribution for

In Fig. 7 several members of Dolph and Taylor $n = 4, 6$ distributions are plotted for different IDRRs. Taking advantage of the symmetry we show only half of the Dolph and Taylor *n* distributions (on the right) and relate each one with our distribution (on the left) for the corresponding SLR. As an example, for IDRR = 0.7 our distribution has SLR = 19 dB, so we plot Taylor *n* = 4 with that SLR. An interesting property of our family is that it has uniform excited elements at the ends and center of the distributions. The amount of such elements increases with the IDRR. This is an advantage over the other distributions as far as the feeding network is easier to implement.

At this point it is interesting to ask whether there are more than one solution (distributions) with the same SLR for a given IDRR. We collect solutions for the same IDRR by running the optimizer many times. The solutions are plotted in Fig. 8. The edge and center elements remain unchanged, and the main differences are observed in the elements between the center and the edges. The solutions show little differences between their SLR. This means that in a small neighborhood of the global SLR optimum there are several distributions with significant shape differences with the same IDRR.

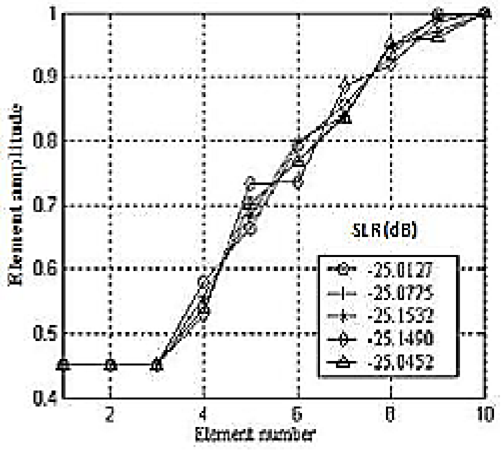

Fig. 8. Five amplitude distributions with the same IDRR

4 Some Optimization Issues

Hereafter we test the fitness function of the previous section using a simple EDA algorithm augmented with Linear Entropic Mutation (LEM) [16, 17, 18]. The algorithm, called here BnL-LEM, works with binary variables following the general lines explained in Sect. 2.2. Notice that now we are not interested in learning a Bayesian network that captures all the important correlations and therefore the maximal number of parents of a node is set to be either zero or two. In the former case the variables are considered independent and the algorithm is called Univariate Marginal Distribution Algorithm (UMDA) [15].

The aim of this section is to gain preliminary insights into the nature and complexity of the optimization problem we are dealing with in this paper. Concretely, we are seeking answers to the following questions:

1. How does IDRR affect the complexity of the optimization problem?
2. Is the independent model a good search distribution for this problem?
3. How does linear entropic mutation impact the optimization?

The results presented in Fig. 9 and Fig. 10 were obtained with the MMHC-EDA. The first hitting time (FHT) is the first generation where a particular vector (e.g. the optimum) is found. Figure 9 shows the FHT of a distribution with the best SLR found in the previous section for each IDRR. It turns out that the algorithm encounters earlier the members of our family for large IDRR values than for lower values. In the figure dots represent runs without elitism and crosses with 10% elitism. As can be seen elitism does not seem to change the observed behavior.

Figure 10 presents the SLR values obtained with a variant of the MMHC-EDA that deals more efficiently with small populations because it uses shrinkage estimation. This issue is beyond the scope of the paper, the interested reader is referred to [17] for further information. The population size was set equal to 100. For comparison purposes we have also included the results of Fig. 4 (circles). Once again we note that for low IDRR values the optimization problem is harder.

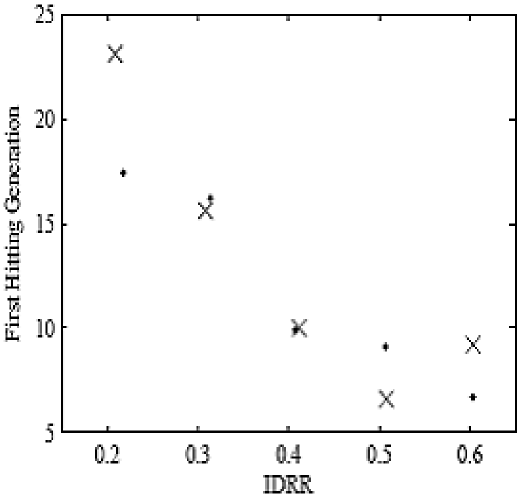

Fig. 9. First hitting time (generation) of distributions with SLR values that are close to the values of Fig. 4. Dots were computed without elitism and crosses with 10% elitism

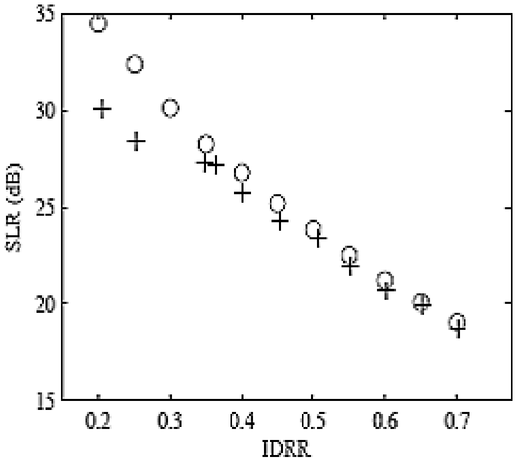

Fig. 10. SLR values vs. IDRR. (circles) – MMHCEDA with population size 900; (plus) - MMHC-EDA with shrinkage estimation what allows to work with a population of 100

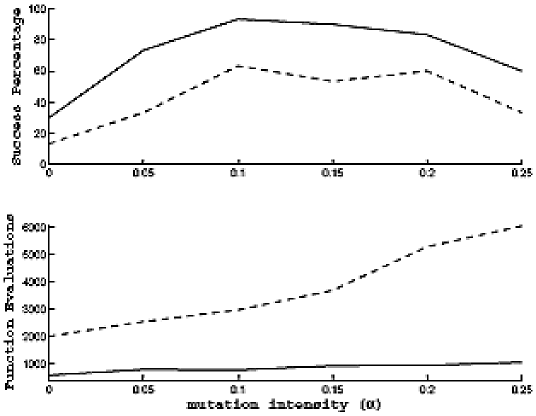

Fig. 11. Success percentage and number of function evaluations as a function of the mutation intensity, a, for IDRR = 0:67 (solid line) and IDRR = 0:4 (dashed line) using population sizes 50 and 100 respectively, using EDA-BnL with a maximum of two parents

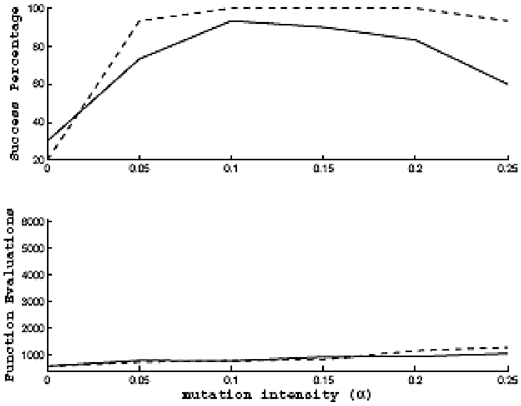

Fig. 12. Success percentage and number of function evaluations as a function of the mutation intensity, a, for IDRR = 0:67. Population size 50. Algorithms: (dashed line) - UMDA. (solid line) - EDA-BnL with a maximum of two parents

For the results shown in Fig. 11, EDA-BnL was run with two IDRR values for a maximum of 50 generations. The curves in both graphics represent the success percentage and number of function evaluations, respectively, as a function of the mutation intensity (IDRR = 0:67

solid line and IDRR = 0:4 dashed line). A run is considered successful if the achieved best value is closer than 0.03 to the optimum value of Fig. 4.

The following observations are valid for Fig.11-13. LEM mutation increases the success rate for a fixed small population size. However, for large mutation intensities it decreases again. LEM also increases the number of function evaluations because higher entropy increases the number of generations until convergence. There is a mutation intensity window near a = 0:1, where the success rate reaches the maximum and the number of function evaluations is not too high.

Figure 11 tells us that the larger the IDRR the easier the optimization problem. Without mutation (a =0), the curve for the largest IDRR shows about 18% more success rate than the other, despite the fact that its population size, 50, is half the one utilized with the smallest IDRR. The needed amount of function evaluations is also much less for IDRR = 0.67.

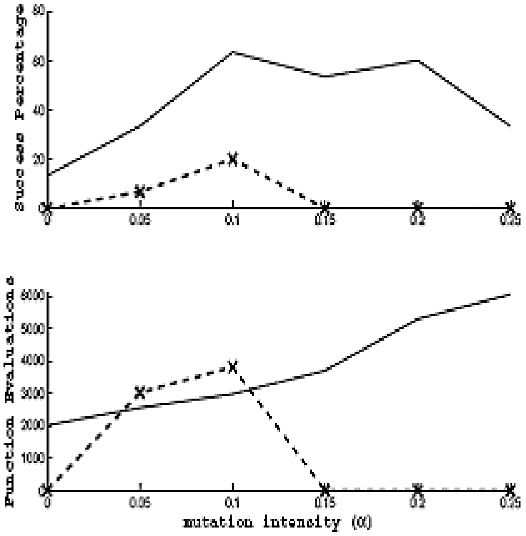

Fig. 13. Success percentage and number of function evaluations as a function of the mutation intensity, a, for IDRR = 0:4. Population size 100. Algorithms: (dashed line) - UMDA. (solid line) - EDA-BnL with a maximum of two parents

The experiments of Fig. 12-13 help to answer the second question posed in this section: a comparison between the independence model supported by the UMDA and the multivariate model of the EDA-BnL (bounded by two parents). Figure 12 shows the results for IDRR=0:67. Here the UMDA is the clear winner. However, as can be seen from Fig. 13 the assumption of independence is completely wrong for IDRR = 0.4.

5 Summary and Conclusions

This paper has introduced a new family of amplitude distributions for the excitation of linear arrays. The family members have the best SLR possible for a given IDRR. An EDA-based optimization approach was used to find out the family instances. The paper shows that the family is a limiting distribution, which is understood in a similar way as the Dolph-Chebyshev distribution shows the best HPBW for a given SLR. It is remarkable that the family also improves the relationship HBPW-SLR, and has the best IDRR for a given HPBW.

We consider the findings presented here only as preliminary results, because we have found that our family also displays a kind of limiting behavior with respect to other key figures of merit. Besides, we believe that the study of these distributions can help to gain some insights into the importance of the shape of the amplitude distributions and in the achievable limits of the solutions.

Another lesson we have drawn from this research is that EDA algorithms are powerful tools that can and must play a major role in the field of antenna analysis and design. Following this line of thinking we have included in the paper a section that explores a few important optimization issues.

The numerical results allow us to conclude the following: 1) the IDRR impacts the complexity of the problem, i.e. the larger the IDRR the easier the optimization; 2) linear entropic mutation improves the performance of the algorithms and reduces the population size requirements; 3) the independence model seems to be adequate for very large IDRR but fails dramatically for the other cases.

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