Genetic Algorithms as Applied to the Numerical Computation of Electromagnetic Scattering by Weakly Nonlinear Dielectric Cylinders

Salvatore Caorsi, *Member, IEEE*, Andrea Massa, and Matteo Pastorino, *Senior Member, IEEE*

***Abstract*— This paper deals with the application of an optimization procedure based on a genetic algorithm (GA) to the prediction of the electromagnetic fields scattered by weakly nonlinear dielectric objects. Starting by an integral approach and describing the nonlinearities of the constitutive parameters by the Volterra-type integrals, the nonlinear scattering problem is numerically solved by an iterative procedure developed for the minimization of a suitable defined cost function. A GA is applied in order to deal with a large number of unknowns related to the harmonic components of the nonlinear internal electromagnetic field. In a preliminary stage, the behavior of typical parameters of the GA is analyzed; then numerical solutions are carried out and compared with those provided by other methods. Finally, some considerations are made concerning the rate of convergence of the iterative procedure.**

***Index Terms*— Cylindrical scatterers, genetic algorithms, nonlinear media.**

I. Introduction

In the past decade, there has been a notable interest in the study of the interactions between electromagnetic waves and nonlinear materials. The problem has been addressed both with reference to the propagation in infinite media and by considering the interactions between waves and bounded objects. Several analytical and numerical techniques have been applied to obtain field solutions and to study a number of physical phenomena associate with waves and nonlinear materials. From a theoretical point of view, some of the most relevant approaches to propagation and scattering in the nonlinear case are based on Volterra series [1]–[3], whereas additional heuristic hypothesis on the nonlinear medium (i.e., Kerr-like nonlinearities or, more generally, nonlinearities that can be expressed as power series of the field [4]–[6]) are usually assumed in the scientific literature in order to obtain "simple" solutions whose validity is often limited to specific assumed situations [7]–[11]. When addressed from a numerical point of view, the problems do not usually results in simple and straightforward computations as in the case of most of the numerical solutions to linear scattering and diffraction problems. The authors developed in [11] a numerical procedure to solve a set of integral equations obtained by approaching the nonlinear scattering starting from equivalent sources and harmonic expansions of the field. The above procedure resulted in a set of nonlinear algebraic equations to be solved. A solution was rather inefficiently reached in [12] by using a deterministic algorithm, the Wolfe's iterative method, which is a generalization of the secant method to multivariable functions. Fortunately, the recent development of efficient optimization techniques allows us to obtain solutions, even to rather complex problems considered relatively intractable in the past.

Among these techniques the electromagnetic community is beginning to devote notable attention to genetic algorithms (GA's) [13], [14], which exhibit several interesting features related to their capabilities in performing optimization processes in a very robust way [15]. Recently, GA's have been proposed to synthesize thinned planar or linear arrays that produce the lowest maximum relative sidelobe level [16] or to design the shape of RF cavities that satisfies user defined characteristics such as fundamental resonant mode frequency and higher order modes frequencies [17]. Moreover, a typical application of the GA's in the microwave engineering is the design of radar absorbers [18]. Interesting reviews on GA's for electromagnetic applications have been recently published [13], [14]. In the present paper, a GA has been applied to minimize a cost function also called in genetic terminology, *fitness* function arising in the solution of the nonlinear scattering problem. Recently, the authors obtained rather significant results by using a statistical cooling procedure (SA) [19]. However, we focus on GA's in the light of their possibly easier parallelization. This is related to the fact that at each iteration, the SA considers only one search direction in the multidimensional solution space, whereas, in procedures based on GA's, different trial solutions are simultaneously evaluated, corresponding to search processes performed along different directions.

In short, the GA starts by choosing M trial solutions, which constitutes the initial *population* (usually we indicate as *population* the set of trial solutions that are used at each iteration to span the solution space). Each trial solution (or

Manuscript received January 22, 1998; revised January 24, 1999.

S. Caorsi is with the Department of Electronics, University of Pavia, Pavia, I-27100 Italy.

A. Massa and M. Pastorino are with the Department of Biophysical and Electronic Engineering, University of Genoa, Genova, I-16145 Italy.

Publisher Item Identifier S 0018-926X(99)07061-1.

individual) is coded in a binary sequence called *chromosome* (since the numerical algorithm is based on the analogy between the natural selection and the solution searching process in an optimization problem, it keeps some terms used in genetics). Then, the algorithm generates a new population of trial arrays by using three mechanisms: *selection*, *crossover*, and *mutation*. It is evident that GA's are "with-memory" methods. In particular, unlike the SA technique, which considers in the evolution of the trial solution toward the optimal solution only the history of one individual, the GA techniques take into account the structures of all the previous populations coded in the individuals of the current population. The selection mechanism selects the trial solutions of the current population that will generate the new population. To this end, the fitness function of each trial solution is estimated and candidate solutions are chosen to mate. The selected individuals are subjected to crossover and/or mutation with a given probability. The crossover works on two trial solutions and generates one or two new solutions: the binary sequences of the two arrays are swapped from a chosen bit. With the mutation procedure, a new individual is generated by changing (with a given probability) the binary sequence of the selected individual. The new population is completed by reproducing the individual of the old population for which the cost functions assume the smallest values. Once the new population has been generated, the fitness function of each individual is evaluated and the GA restarts with a new generation or terminates if the threshold for the stopping criterion is reached or when the iteration loops are terminated.

The paper is organized as follows. In Section II, the formulation of the nonlinear scattering problem is outlined with some discussion concerning the heuristic hypotheses involved. Section III describes in more detail the application of the GA in order to provide enough information for the readers. Finally, Sections IV and V contain the numerical results of some computer simulations and some general conclusions, respectively.

II. Mathematical Formulation

The scattering problem in which an incident wave radiated from a known source $\bar{\mathbf{J}}^{\mathrm{im}}(\bar{\mathbf{r}},t)$ interacts with a bounded weakly nonlinear dielectric object can be addressed in the following rigorous way: at each point, the electromagnetic field vectors satisfy the Maxwell's equations and Sommerfeld's radiation conditions

$$\nabla\times\bar{\mathbf{E}}(\bar{\mathbf{r}},t)+\frac{\partial\bar{\mathbf{B}}(\bar{\mathbf{r}},t)}{\partial t}=\bar{\mathbf{0}} \tag{1}$$

$$\nabla\times\bar{\mathbf{H}}(\bar{\mathbf{r}},t)-\frac{\partial\bar{\mathbf{D}}(\bar{\mathbf{r}},t)}{\partial t}=\bar{\mathbf{J}}^{\mathrm{im}}(\bar{\mathbf{r}},t) \tag{2}$$

and, due to the weak nature of the nonlinearity, the relationships for the constitutive equations $\bar{\mathbf{D}}(\bar{\mathbf{E}})$ and $\bar{\mathbf{B}}(\bar{\mathbf{H}})$, expressed in terms of a truncated Volterra's functional series [1], [7], [20], [21] hold. In more detail, defining a Minkowski four-vector $\bar{\mathbf{X}}=\bar{\mathbf{X}}(\bar{\mathbf{r}},jct)$, with $j^2=-1$ and $\bar{\mathbf{X}}\cdot\bar{\mathbf{X}}=0$, and assuming nonlinearity only in the electric flux density, we can express the constitutive relation as follows:

$$\bar{\mathbf{D}}(\bar{\mathbf{X}})=\sum_{n=1}^{N}\bar{\mathbf{D}}^{(n)}(\bar{\mathbf{X}}) \tag{3}$$

where the truncation of the series is allowed by the weakness of the nonlinearity, and the nth term is

$$\bar{\mathbf{D}}^{(n)}(\bar{\mathbf{X}})=\int\!\!\int_{\cdots n\text{ times}\cdots}\int\{\hat{\varepsilon}^{(n)}(\bar{\mathbf{X}}_1,\cdots,\bar{\mathbf{X}}_n)\cdot\!\!\cdot\,\bar{\mathbf{E}}(\bar{\mathbf{X}}-\bar{\mathbf{X}}_1)\cdots\bar{\mathbf{E}}(\bar{\mathbf{X}}-\bar{\mathbf{X}}_n)\}d^4\bar{\mathbf{X}}_1\cdots d^4\bar{\mathbf{X}}_n \tag{4}$$

where the four-dimensional integrals are extended to the whole space and "$\cdot\!\cdot$" denotes the dyadic inner multiplication between the nth order dyadic $\hat{\varepsilon}^{(n)}$ (intrinsic parameters related to the medium) and the n field vectors $\bar{\mathbf{E}}$.

Under hypothesis of an electric field solution expressed in term of periodic waves and in the case of a not-spatially dispersive medium, we can rewrite (3) in the following form:

$$\bar{\mathbf{D}}(\bar{\mathbf{X}})=\sum_{n=1}^{N}\bar{\mathbf{D}}^{(n)}(\bar{\mathbf{X}})=\sum_{n=1}^{N}\sum_{a=-\infty}^{\infty}\bar{\mathbf{D}}_a^{(n)}(\bar{\mathbf{x}};a\omega)e^{ja\omega t} \tag{5}$$

being

$$\bar{\mathbf{D}}_a^{(n)}(\bar{x};a\omega)=\sum_{a}\gamma_{a;m_1\cdots m_n}\hat{\varepsilon}^{(n)}(\bar{\mathbf{x}};m_1\omega,\cdots,m_n\omega)\cdot\!\!\cdot\,\bar{\mathbf{E}}_{m_1}(\bar{\mathbf{x}})\cdots\bar{\mathbf{E}}_{m_n}(\bar{\mathbf{x}}) \tag{6}$$

where ω is the fundamental harmonic frequency of the illumination and the terms in (6) are regrouped as prescribed by the orthogonality properties of the exponentials (being $\gamma_{a;m_1\cdots m_n}=1$ if $a=m_1+\cdots+m_n$, $\gamma_{a;m_1\cdots m_n}=0$ otherwise).

With the above assumptions, substituting (5) in (2) and applying the curl operator to both side of (1), we obtain a harmonic representation of the field by solving the following set of nonhomogeneous vector wave equations:

$$\nabla\times\nabla\times\bar{\mathbf{E}}_a(\bar{\mathbf{x}})-(a\omega)^2\mu\sum_{n=2}^{N}\left\{\gamma_{a;m_1\cdots m_n}\sum_{m_1}\cdots\sum_{m_n}\times\left[\hat{\varepsilon}^{(n)}(\bar{\mathbf{x}};m_1\omega,\cdots,m_n\omega)\cdot\!\!\cdot\,\bar{\mathbf{E}}_{m_1}(\bar{\mathbf{x}})\cdots\bar{\mathbf{E}}_{m_n}(\bar{\mathbf{x}})\right]\right\}=-j(a\omega)\mu\bar{\mathbf{J}}_a^{\mathrm{im}}(\bar{\mathbf{x}}). \tag{7}$$

In particular, if we consider nonlinear scatterers having cylindrical geometries, embedded in the free-space (characterized by μ_0 and ε_0) and illuminated by an incident electric field of TM type, (7) reduces to the following scalar one:

$$\nabla_t^2E_{z;a}(x,y)+(a\omega)^2\mu_0\varepsilon_{zz}^{(1)}(x,y)E_{z;a}(x,y)=-(a\omega)^2\mu_0T_{z;a}(x,y)+j(\gamma_{a;1}a\omega)\mu_0J_{z;a}^{\mathrm{im}}(x,y). \tag{8}$$

In (8), $E_{z;a}$ indicates the ath complex Fourier component of the field (along the polarization axis) at the frequency $a\omega$ and $T_{z;a}$ are coupling terms dependent on the field components at

the same frequency and at other frequencies given by

$$T_{z;a}(x,y)=\sum_{n=2}^{N}\left\{\gamma_{a;m_1\cdots m_n}\sum_{m_1}\cdots\sum_{m_n}\{\varepsilon^{(n)}_{z\cdots z}(x,y)\times E_{z;m_1}(x,y)\cdots E_{z;m_n}(x,y)\}\right\}. \quad (9)$$

The above coupling terms $T_{z;a}$ can be easily computed once the type of the nonlinearity is chosen (subjected to the restrictions imposed by the previous considerations). The problem can be reduced to an equivalent one in which the scattering object is replaced by an equivalent current density distribution defined in the region of the nonlinear medium and radiating in a homogeneous medium with the same dielectric characteristics of the external medium. Under decoupling conditions, the electric field results as the sum of the incident electric field, i.e., the electric field produced by the electromagnetic source in the absence of the scattering object plus a scattered electric field as follows:

$$E_{z;a}=E^{\mathrm{scatt}}_{z;a}\left(J^{\mathrm{eq}}_{z;a}\right)+E^{\mathrm{inc}}_{z;a}\left(J^{\mathrm{im}}_{z;a}\right). \quad (10)$$

It follows that the pth harmonic component of the scattered electric field now fulfils the following [22]:

$$\nabla_t^2 E^{\mathrm{scatt}}_{z;a}(x,y)+(a\omega)^2\mu_0\varepsilon_0 E^{\mathrm{scatt}}_{z;a}(x,y)=-j(a\omega)\mu_0 J^{\mathrm{eq}}_{z;a}(x,y) \quad (11)$$

where $J^{\mathrm{eq}}_{z;a}(x,y)=j(a\omega)\{\varepsilon^{(1)}_{z;z}(x,y)-\varepsilon_0\}E_{z;a}(x,y)+j(a\omega)T_{z;a}(x,y)$.

Therefore, we obtain a formal solution to (8); that is, the expression for the ath generic harmonic component of the periodic solution (to simplify the notation, the subscript z, denoting the Cartesian component of the electric field vector along the direction of propagation, is omitted in this relation as well as in the following ones) [26]

$$E_a(x,y)=E^{\mathrm{inc}}_a(x,y)-j\frac{(ak_z)^2}{4}\int_S\left[\frac{\varepsilon^{(1)}_{z;z}(x',y')}{\varepsilon_0}-1\right]\times E_a(x',y')H_0^{(2)}(ak_z\rho)\,dx'\,dy'-j\frac{(ak_z)^2}{4}\int_S T_a(x',y')H_0^{(2)}(ak_z\rho)\,dx'\,dy' \quad (12)$$

where $H_0^{(2)}(ak_z\rho)$ is the Hankel function of the second kind and zeroth order, S is the cross section of the nonlinear scatterer, ρ is given by $\rho=\sqrt{(x-x')^2+(y-y')^2}$ and $k_z=\omega\sqrt{\mu_0\varepsilon_0}$.

After discretization, performed by using the Richmond formulation [22], the solution of the arising nonlinear algebraic system is then obtained by minimizing a *fitness* function defined as follows:

$$\aleph(\bar{\Psi})=\frac{1}{S}\sum_a\sum_{q=1}^{P}\left|E_a(x_q,y_q)-\left\{E^{\mathrm{inc}}_a(x_q,y_q)-j\frac{(ak_z)^2}{4}\sum_{p=1}^{P}\left[\left(\frac{\varepsilon^{(1)}_{z;z}(x_p,y_p)}{\varepsilon_0}-1\right)E_a(x_p,y_p)+T_a(x_p,y_p)\right]H_0^{(2)}(ak_z\rho_{pq})\Delta S_{pq}\right\}\right|^2 \quad (13)$$

where (x_p,y_p) is the center of the pth discretization subdomain, $\underline{\Psi}$ is an array of complex unknowns

$$\bar{\Psi}=[E_a(x_p,y_p),a=1,\cdots,I;p=1,\cdots,P] \quad (14)$$

of $L=I\times P$ elements, being I the maximum order of the harmonic terms (a series truncation is used) and P the number of discretization subdomains.

III. Application of the Genetic Algorithm

The developed iterative procedure based on a GA consists of the following steps. At the initialization step (Step 0) Φ (indicated as "dimension of the population") trial solutions (the "individuals") $\{\bar{\Psi}^{(0)}_h,(h=1,\cdots\Phi)\}$ are randomly generated.

The lth element of the hth trial solution—$(E_l)^{(0)}_h$—is chosen by means of a random uniform distribution of values in the range $\{\min_p(-2|\mathrm{Re}(E^{\mathrm{inc}}(x_p,y_p))|),\max_p(2|\mathrm{Re}(E^{\mathrm{inc}}(x_p,y_p))|)\}$ for its real part and $\{\min_p(-2|\mathrm{Im}(E^{\mathrm{inc}}(x_p,y_p))|),\ \max_p(2|\mathrm{Im}(E^{\mathrm{inc}}(x_p,y_p))|)\}$ for its imaginary part, where $E^{\mathrm{inc}}(x_p,y_p)$ is the value of the incident electric field at the center of the pth subdomain of the discretized cross section, $\mathrm{Re}(\cdot)$ and $\mathrm{Im}(\cdot)$ indicates the real and imaginary part, respectively.

At the "coding step" (Step 1), each trial solution is encoded in a binary sequence (*chromosome*). After quantization, the component $(E_l)^{(0)}_h$ results in a string, denoted by $(\xi_l)^{(0)}_h$, of $\log_2 Q$ bits where Q is the number of quantization levels used to code each component of the trial solution. Each individual in the trial population $\underline{\Psi}^{(0)}_h$ results coded in a string of $B=L\log_2(Q)$ bits as follows:

$$\bar{\Psi}^{(0)}_h=\left\{(E_1)^{(0)}_h,\cdots,(E_l)^{(0)}_h,\cdots,(E_L)^{(0)}_h\right\}\Leftrightarrow\Omega^{(0)}_h=\left\{(\xi_1)^{(0)}_h,\cdots,(\xi_l)^{(0)}_h,\cdots,(\xi_L)^{(0)}_h\right\}. \quad (15)$$

At this point, the algorithm continues with a generation of a new population. Then (Step 2), we compute the value of the fitness function for each individual of the population $\aleph^{(k)}_h=\aleph(\bar{\Psi}^{(k)}_h)$, $h=1,\cdots,\Phi$, (where k indicates the iteration of the procedure) and the probability of selection of each individual $\Theta^{(k)}_h$ in the following way:

$$\Theta^{(k)}_h=\frac{\aleph^{(k)}_h}{\sum_{h=1}^{\Phi}\aleph^{(k)}_h}. \quad (16)$$

We also set the optimal fitness value at each iteration $\aleph^{(k)}_{\mathrm{opt}}=\min_h\{\aleph^{(k)}_h\}$ and the corresponding trial configuration $\bar{\Psi}^{(k)}_{\mathrm{opt}}$ ("optimal configuration").

Step 3 is related to the selection of the individuals of the current population that will be used for generating the new population. Φ pairs of chromosomes are chosen. Let us indicate the cth pair with the notation $(\Omega^{(k)}_s;\Omega^{(k)}_r)_c$, $c=1,\cdots,\Phi$. A chromosome is randomly chosen and it constitutes one element of the pair only if its selection probability is less than a random value in the range $[0,1]$. In this way, more highly fit individuals (i.e., those individuals with lower fitness values) have a higher number of offsprings in the next population.

At step 4, the crossover mechanism acts on the cth pair of chromosomes with a probability $\wp_c$, in order to generate a new individual $\Omega_c^{(k+1)}$

$$\Omega_c^{(k+1)} = \left\{\left\langle\Omega_s^{(k)}\right\rangle_1, \cdots, \left\langle\Omega_s^{(k)}\right\rangle_t, \left\langle\Omega_r^{(k)}\right\rangle_{t+1}, \cdots, \left\langle\Omega_r^{(k)}\right\rangle_B\right\} \tag{17}$$

where the symbol $\langle\cdot\rangle_n$ indicates the binary value of the nth bit in the chromosome and the subscript "t" is the crossover position randomly chosen.

At step 5, after the crossover, the individuals of the current population are subjected to the mutation operator with a probability $\wp_m$. Mutation alters only one bit randomly chosen among the B bits of the chromosome by changing a "1" to a "0" or vice versa. The new individual presents the following chromosome:

$$\Omega_u^{(k+1)} = \left\{\left\langle\Omega_u^{(k+1)}\right\rangle_1, \cdots, \subset \left\langle\Omega_u^{(k+1)}\right\rangle_v, \cdots, \left\langle\Omega_u^{(k+1)}\right\rangle_B\right\} \tag{18}$$

where v is the changed bit and $\subset$ indicates the binary "not" operator.

Finally (Step 6), the *elitism* operator is used to ensure that the chromosome of the individual $\bar{\Psi}_{\text{opt}}^{(k)}$, generated up to now, be reproduced in the $(k+1)$th population. Although this mechanism is not necessary, it was found to help to prevent random loss of good chromosome strings.

The iterative process is repeated (we return to step 2) until the optimal fitness value $\aleph_{\text{opt}}^{(k)}$ is smaller than a fixed threshold for the stopping criterion η or if the maximum number of iterations K exceeded.

IV. Numerical Results

In this section, we present the results of some numerical simulations performed in order to explore the possibility of an efficient application of a GA to the nonlinear electromagnetic scattering problem. We considered an infinite cylinder with a circular cross section of radius $r = 0.3\lambda_1, \lambda_1$ being the free-space wavelength related to the frequency of a uniform plane wave. The scatterer, discretized in $P = 225$ subdomains (according to the rule defined in [23]), was characterized by $\varepsilon_{z;z}^{(1)}(x,y) = 1.1\varepsilon_0$, $\varepsilon_{z;zzz}^{(3)}(x,y) = \varepsilon_0\beta$, $\beta = 0.1$ with the remaining nonlinear parameters set to zero. In the following, for this geometry we show the behavior of the GA for different values of its characteristic parameters.

First of all, the optimum value of the fitness function $\aleph(\bar{\Psi}_{\text{opt}}^{(k)})$ at different iterations is shown in Fig. 1 for various values of the number of levels of the uniform quantizier Q. In more detail, starting by the same initial population and at initial iteration $(k = 0)$, in the case of $Q = 8$ the value of $\aleph(\bar{\Psi}_{\text{opt}}^{(0)})$ is greater than 50, whereas for $Q = 1024$ $\aleph(\bar{\Psi}_{\text{opt}}^{(0)}) \approx 0.7$. On the other hand, for $Q = 4096, 8192, \cdots$ (12, 13, ... bits necessary to encode each component) the coding error is approximately equal to that in the case of $Q = 1024$.

Let us consider the problem of the population size for the GA. It is well known [24] that an optimal population size Φ

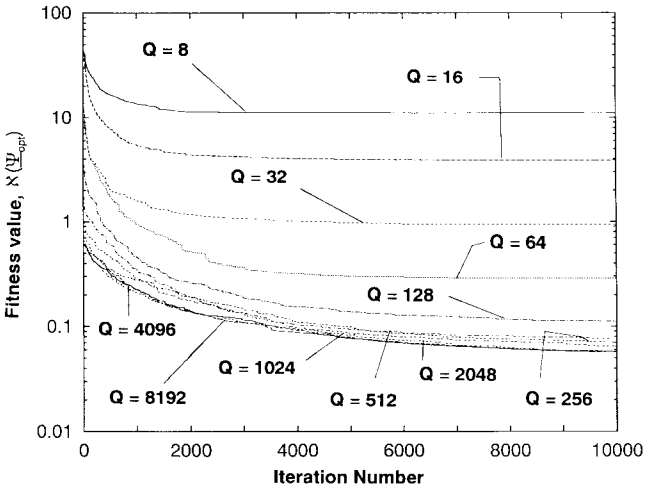


Fig. 1. Behavior of the fitness function versus the number of iterations for various values of the number of quantization levels Q.

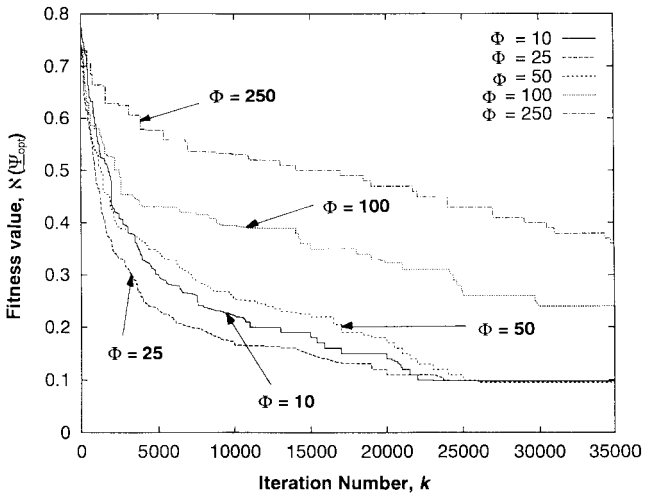


Fig. 2. Behavior of the fitness function versus the number of iterations for various values of the population size Φ.

for a GA is in the order of

$$\frac{L\log_2(Q)}{\gamma}2^{\gamma} \tag{19}$$

where γ is the size of the schema (defined as "a similarity template describing a subset of strings with similarities at certain string positions" [15]) of a chromosome. In our problem, and for $Q = 1024$, the application of (19) indicates that an appropriate value of Φ will be of the order of about hundred individuals. Therefore, we investigated the behavior of GA considering a population size between 10 and 250 trial arrays. Fig. 2 presents the plot of $\aleph(\bar{\Psi}_{\text{opt}}^{(k)})$ versus the number of GA iterations. In this figure, it is possible to note that with a lower population size, the optimum value of the fitness function more rapidly decreases, but after fewer iterations all the individuals of the current population are very similar. On the other hand, when the population size increases, (e.g., $\Phi = 100$ or 250) the convergence is very poor. A value of $\Phi = 25$ individuals seems to allow a good balance among rate of convergence

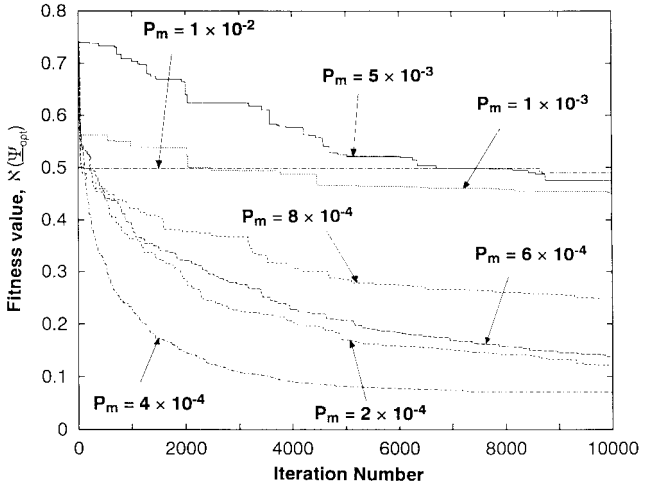


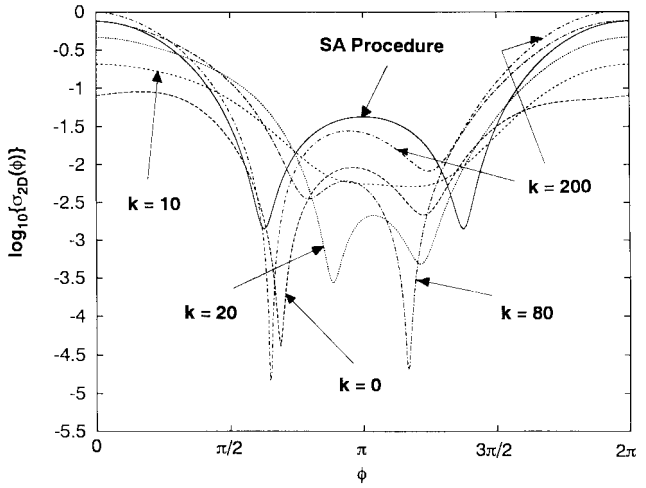
Fig. 3. Behavior of the fitness function versus the number of iterations for various values of the mutation probability $\wp_m (\wp_c = 0.7)$.

of GA, amount of required computer time, and number of iterations for which a not negligible diversity between the individuals of the same population is kept.

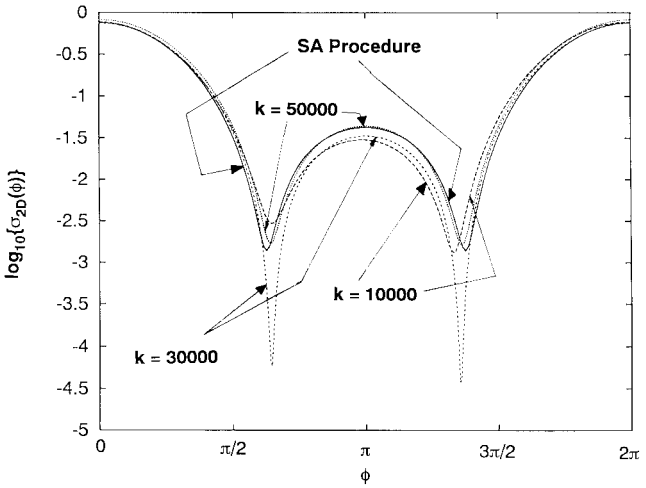
As suggested in literature [25], also in the present application we have obtained good results with a high crossover probability $(\wp_c = 0.7)$, but with a lower value of the mutation probability, as shown in Fig. 3. For example, in the case of a value equal to $\wp_m = 4 \times 10^{-4}$, we obtained a high rate of convergence with a good convergence value.

Now, to compare the results obtained by GA with those by other numerical techniques, Fig. 4 gives the computed values of the bistatic scattering width (BSW) $\sigma_{2D}(\phi)$ defined in [26] for the same scatterer previously considered. In this figure, ϕ denotes the angular coordinate related to the observation direction. These values are compared with those computed by using the statistical cooling approach (SA) [19]. In particular, Fig. 4(a) shows the values of $\sigma_{2D}(\phi)$ at the iterations $k = 0$, 10, 20, 80, 200. As can be seen, the accuracy of the GA solution is very poor and the related plots significantly differ from the SA solution in both the forward and backward directions. Instead, starting from iteration $k = 10\,000$, as the number of the iterations increases, the approximated $\sigma_{2D}(\phi)$ tends to become more and more similar to the solution computed by the statistical cooling approach. The not symmetric behavior that the BSW keeps at the first iterations [Fig. 4(a)], tends to disappear as k increases [as shown in Fig. 4(b)] and the solution agrees very well with that obtained by means of SA procedure.

In a corresponding way, the fitness value for $\bar{\Psi}_{\text{opt}}^{(k)}$ presents a different rate of convergence depending on the iteration number. For example, at the first iterations [Fig. 5(a)], $\aleph(\bar{\Psi}_{\text{opt}}^{(k)})$ decreases of about 300 in 90 iterations, whereas in the range around $k = 10\,000$ (Fig. 5(b)), the decrement is about 0.6 in 100 iterations. This fact can be due to a reduced number of different chromosomes. This hypothesis seems to be confirmed also by the results of Fig. 6, which shows the values of the fitness function of each individual of a population during the iteration process of the GA: at the iteration $k = 50\,000$ (indicated as convergence iteration), the fitness values of



(a)



(b)

Fig. 4. Bistatic scattering width. Nonlinear values obtained by using statistical cooling approach (convergence values) and GA at the iterations (a) $k = 0$, 10, 20, 80, 200 and (b) $k = 10\,000$, $30\,000$, $50\,000$. (Nonlinear circular cylinder: $a = 0.3\lambda_1$, $\varepsilon_{z;z}^{(1)}(x,y) = 1.1\varepsilon_0$, $\varepsilon_{z;zzz}^{(3)}(x,y) = 0.1\varepsilon_0$, $\Phi = 50$, $Q = 1024$, $\wp_m = 4 \times 10^{-4}$, $\wp_c = 0.7$).

the individuals of the same population are about the same. This is a clear indication that many individuals of the same population, are very similar. Moreover, it is evident that further improvements in the fitness function value, would require a lucky random mutation in a chromosome of an individual of the population.

Finally, Fig. 7 shows the values of the bistatic scattering width computed at the convergence iteration by using the GA procedure, the SA approach, and iterative methods based on the Born approximation (BA) [23], the distorted-wave Born approximation (DWBA) [27], and the Rytov approximation (RA) [28]. The plots concerning the GA and SA procedures are in good agreement and significantly differ from those obtained with approximate techniques. This fact is due to the magnitude of the nonlinearity: it is well known [19], [28] that at the increase of the nonlinearity the approximate techniques are unable to exactly predict the harmonic generation and the corresponding harmonic mixing effect.

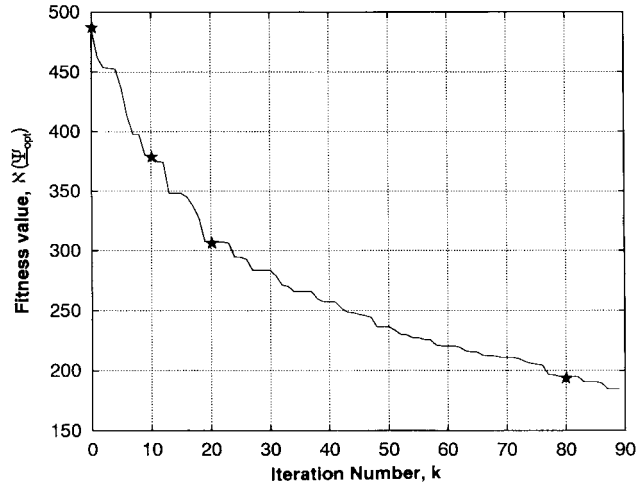


Fig. 5. Behavior of the fitness function versus the number of iterations: (a) $0 \leq k \leq 90$, (b) $9980 \leq k \leq 10\,080$.

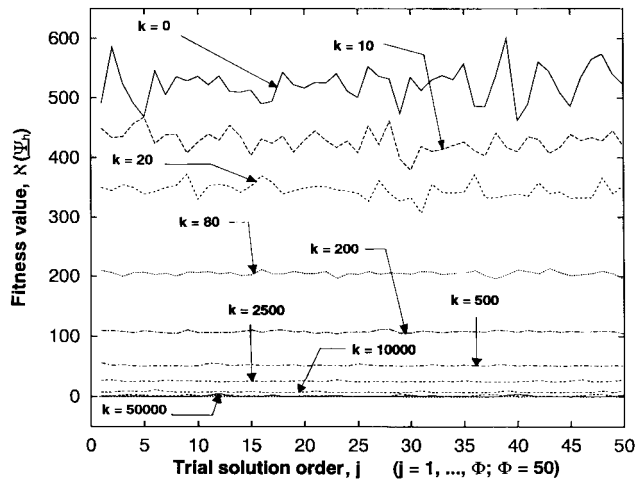


Fig. 6. Values of the fitness function for each individual of a population at different iterations.

Similar conclusions can be achieved from Fig. 8, which shows the error parameter $\Xi(x_p, y_p)$ defined as

$$\Xi(x_p, y_p) = \frac{|E_1(x_p, y_p) - E_1^*(x_p, y_p)|}{|E_1^*(x_p, y_p)|} \qquad (20)$$

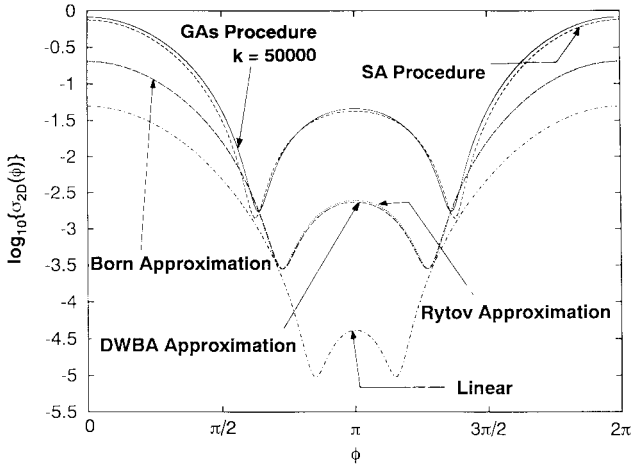


Fig. 7. Bistatic scattering width. Convergence values computed by using the GA, the statistical cooling procedure, and approximate iterative methods.

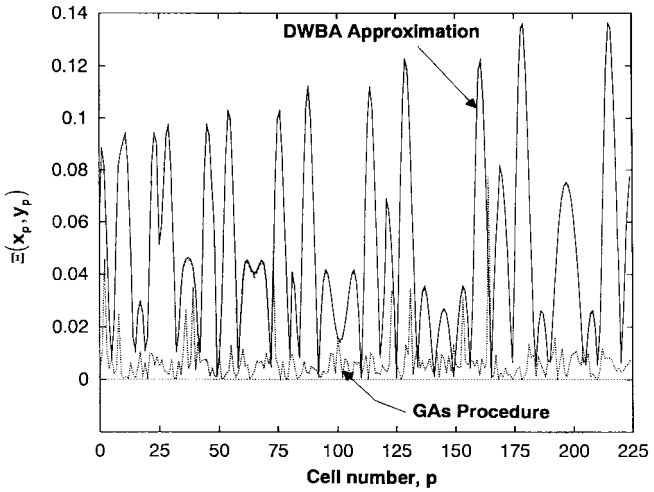


Fig. 8. Values of the parameter Ξ for the GA and the iterative methods based on distorted Born approximation, Rytov approximation, and Born approximation, at the convergence iteration.

where $E_1^*(x_p, y_p)$ is the first harmonic component of electric field computed at pth discretization subdomain by using the SA procedure (considered as the reference solution) and $E_1(x_p, y_p)$ indicates the same quantity as computed at the convergence iteration, either by GA or by any one of the aforementioned approximated approaches (BA, DWBA, RA). For the sake of clarity, in Fig. 8 we show only the plot of the DWBA solution because, at the convergence iteration, the other approximated solutions (BA, RA) do not significantly differ from this one.

V. Concluding Remarks and General Observations

In this paper, a numerical approach based on a GA to computing electromagnetic scattering by weakly nonlinear objects, has been developed. The mathematical formulation describes the nonlinear interactions between the electromagnetic field and scatterers in terms of nonlinear equivalent electromagnetic sources and by using truncated Volterra's

functional series. Weak nonlinearities are assumed such that harmonic generation may be present, but shock-wave formation is excluded. Then a harmonic representation of the electric field has been achieved, and the solution of the problem has been reduced to the solution of a set of coupled nonlinear integral equations. After discretization, an optimization process has been formulated, in which a nonlinear fitness function has been deduced. A GA has been applied and the capabilities of the approach have been assessed by means of numerical simulations. The obtained results show that the present approach may represent a computational tool able to deals with effects induced by nonlinearity. This point is of great interest as at high excitation power levels, at radio as well as at optical frequencies, these nonlinear effects are present and should be taken into account by proper computational methodologies.

In addition, a potential further development of the present approach may lie in an extension to the field of inverse scattering problems. In many cases, in fact, the nonlinearity might be considered as an additional degree of freedom for assessing the dielectric properties of an unknown scatterer (e.g., the generated higher harmonic waves might be used to glean more information about the scatterers).

ACKNOWLEDGMENT

The authors would like to thank Prof. D. Censor, Department of Electrical and Computer Engineering, Ben-Gurion University of the Negev, Beer Sheva, Israel, for his very constructive criticism and precious suggestions concerning both for the present paper and potential further developments. They would also like to thank Dr. D. L. Carroll, University of Illinois at Urbana-Champaign, Urbana, IL, and Prof. F. Glover, School of Business, University of Colorado, Boulder, for their very useful comments and suggestions about genetic algorithms.

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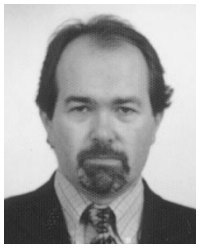
Salvatore Caorsi (M'98) received the Laurea degree in electronic engineering from the University of Genoa, Italy, in 1973.

He is a full professor of electromagnetic compatibility in the Department of Electronics, University of Pavia, Italy. He is also teaching a course in antennas at the University of Genoa, Italy His primary activities are focused on applications of electromagnetic fields to telecommunications, artificial vision and remote sensing, biology, medicine, and electromagnetic compatibility.

Prof. Caorsi is the past president and founding member of the Inter-University Research Center for Interactions Between Electromagnetic Fields and Biological Systems (ICEMB). He is a member of the AEI, EBEA, and ESHO.

Andrea Massa received the Laurea (electronic engineering) and Ph.D. (electronics and computer science) degrees from the University of Genoa, Genoa, Italy, in 1992 and 1996, respectively.

He is currently an Assistant Professor of Electromagnetic Fields in the Department of Biophysical and Electronic Engineering and member of the Inter-University Research Center for Interactions Between Electromagnetic Fields and Biological Systems (ICEMB). Since 1992 his research work has been principally on electromagnetic direct and inverse scattering, wave propagation in presence of nonlinear media and chiral media, applications of electromagnetic fields to telecommunications, medecine, and biology.



Matteo Pastorino (M'90–SM'96) received the Laurea (electronic engineering) and the Ph.D. (electronics and computer science) degrees from the University of Genoa, Italy, in 1987 and 1992, respectively.

He is an Associate Professor of electromagnetic fields in the Department of Biophysical and Electronic Engineering, University of Genoa, Italy, where he is responsible for the Applied Electromagnetics Group. He currently teaches courses in electromagnetic fields and remote sensing and electromagnetic diagnostics. His main research interests are in the field of electromagnetic direct and inverse scattering, microwave imaging, wave propagation in presence of nonlinear media, and analytical and numerical methods in electromagnetism.

Dr. Pastorino is a member of the IEEE Instrumentation and Measurement Technical Committee on Imaging Systems. He is also a member of the Associazione Elettrotecnica ed Elettronica Italiana (AEI) and of the European Bioelectromagnetic Association (EBEA).