A New Implementation of the Hybrid Taguchi GA: Application to the design of a Miniaturized Log-Periodic Thin-Wire Antenna

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Abstract – This paper proposes a modification of the hybrid Taguchi-genetic algorithm (HTGA) for solving global numerical optimization problems with continuous variables. The HTGA is a method that combines a conventional genetic algorithm (CGA), which has a powerful global exploration capability, with the Taguchi method, which can exploit the optimum offspring. The Taguchi method is utilized in the HTGA to help in selecting the best genes in the crossover operations. The new implementation proposed in this paper (nHTGA) involves producing, at each generation, a single offspring by Taguchi method, one of its parents being the best individual found so far, instead of repeatedly applying Taguchi to generate several individuals with both parents selected at random as HTGA does. Moreover, the efficiency of the algorithm is enhanced by only crossing via Taguchi individuals with a high enough number of different genes. The performance of the proposed HTGA is assessed by solving several benchmark problems of global optimization with large number of dimensions and very large numbers of local minima. The computational experiments show that the new algorithm causes a reduction, sometimes drastic, in the number of function calls, i.e. in computational time, for all the benchmark problems proposed. As an example of application of this novel algorithm to a real-world problem, the optimization of an ultra-broadband zigzag log-periodic antenna is carried out and discussed.

Keywords: Genetic algorithm, numerical optimization, Taguchi method, log-periodic antenas, zig-zag antenas.

I. INTRODUCTION

Genetic algorithms (GAs) [1] have come a long way toward solving optimization problems [2] where conventional optimization methods fail, such as system identification [3], design [4–7], scheduling [8], routing [9], control [10, 11], and others [12]. The GAs have been demonstrated to be robust stochastic search and optimization techniques. These algorithms are a type of evolutionary algorithms based on Darwin's theory of evolution. In GA, a population of N_{pop} individuals (trial solutions) evolve in parallel by means of selection of the fittest individuals, crossover and mutation of genes. Because of its implicit parallelism [2], and a reasonable tradeoff between global and local search abilities, the GAs are considered to be robust global optimization algorithms. However, one obstacle when applying GAs to optimize complex problems where the evaluation of functions is computationally intensive is the high computational cost due to their slow convergence rate.

Many efforts have been dedicated to accelerate the convergence of GAs, such as studying optimal crossover and mutation rates or selecting appropriate genetic operators [13]. More recently, new algorithms combining GAs with local searchers have been proposed to improve the performance of GAs on global optimization problems [14–17]. In particular, Tsai et. al. presented a hybrid algorithm, called HTGA, which combines the conventional GA (CGA) [2] with the Taguchi method by inserting a Taguchi-method-based crossover between crossover and mutation operators [17]. The Taguchi method selects two random individuals from offspring already resulting from crossover and recombines them, creating a single individual via an orthogonal array experiment. The systematic reasoning ability of the Taguchi method helps to select the best genes to achieve the crossover, and consequently enhance the genetic algorithm. The process is repeated until the expected population size is met. The hybrid method was demonstrated to be more robust, statistically sound, and quickly convergent than the ones proposed previously in [14–16].

In this paper, a new implementation of the HTGA is proposed. The new hybrid method, named nHTGA, is based on the hypothesis that two low-quality parents have little chance of beating, by crossover and mutation, the best individual found so far. Therefore, the offspring of two of the worst individuals in the population resulting from an orthogonal array experiment will be, in most cases, a low-quality individual, resulting in a waste of function calls, i.e. a waste of computational time. To avoid this, we propose some modifications of the HTGA code. The main one is that, at each generation of the

GA process, only one of the new offspring is produced via Taguchi method, the best individual found so far being one of its parents. With this, we expect to save computational resources as we avoid useless matrix experiments between individuals whose offspring don't have much chance of improving the performance of the best individual in the population. Moreover, the number of experiments needed to find the optimal solution in the whole nHTGA process is further reduced by requiring a certain degree of diversity of the two chromosomes to be mated via Taguchi method.

This paper is organized as follows. Section II briefly describes the Taguchi method, the fundamentals of the nHTGA and compares the performance of the new algorithm with that of HTGA and that of other algorithms frequently used in engineering applications. As an example of application, in Section III the nHTGA is used to optimize the performance of a log-periodic thin-wire antenna.

II. THE NHTGA

A. *The Taguchi Method*

The Taguchi method is a robust design approach based on improving the quality of a product by minimizing the effect of the causes of variation without eliminating the causes [18]. Two major tools are used in the Taguchi method, orthogonal arrays (OAs) and the signal-to-noise ratio (SNR). In laboratory experimentation, OAs are used for determining which combinations of factor levels to use for each experimental run and for analyzing the data. OAs are matrixes of numbers arranged in rows and columns where a row represents the level of all factors in a given experiment, and a column represents the values assigned to a specific factor in the various experiments. The array is called orthogonal because columns can be evaluated independently of one another.

In this paper, we will work with two-level OA whose general nomenclature is $L_n(2^{n-1})$ where n is the number of experimental runs, n-1 the number of columns in the array (or number of factors involved in the experiments), and 2 the number of possible different values (or levels) that a factor can take. A simple algorithm for the construction of OAs can be found in [16]. An example of an OA is given in table 1, where the OA indicates 8 possible experiments determined by specific combinations of two levels (values 1 or 2) of 7 different variables (A-G). According to OA's theory, the 8 experiments are selected so that they provide a balanced comparison of the two possible levels of any factor.

The other parameter concerning the Taguchi method is the SNR, which has been traditionally used in engineering to measure the quality of a product corresponding to a specific choice of the values taken by the variables involved in a design. The SNR, for a set of quality characteristics of a given product, is related to the mean squared deviation from the target value of those quality characteristics. Several definitions of the SNR can be found depending on the type of characteristic and on the type of problem. Taguchi has generalized the concept of SNR and applied it to the assessment of the influence of the possible values of the different factors involved in a set of experiments. SNR is usually defined so that it is large for favorable situations. For example, in the GA application described in this paper, the SNR of a given experiment (chromosome or individual) will be defined in terms of the fitness function corresponding to that experiment in such a way so that better individuals correspond to greater values of SNR.

Table 1. Orthogonal array $L_8(2^7)$.

	Factors						
	A	B	C	D	E	F	G
experiment	column number						
number	1	2	3	4	5	6	7
1	1	1	1	1	1	1	1
2	1	1	1	2	2	2	2
3	1	2	2	1	1	2	2
4	1	2	2	2	2	1	1
5	2	1	2	1	2	1	2
6	2	1	2	2	1	2	1
7	2	2	1	1	2	2	1
8	2	2	1	2	1	1	2

The SNR helps on converting several repetitions of the value taken by a variable into a single number that accounts for the quality of the final product if that repeated value of the given variable is used. To this end, given a set of N experiments described by a specific OA, the effect of each variable involved is defined as,

$$E_{i,j} = \sum_{k}^{n} \delta(level(i,k) - j) SNR(k) \qquad i = 1, ..., N_v; j = 1, 2 \tag{1}$$

where N_v is the number of variables; i represents the ith-variable; k is the number of experiment; $level(i,k)$ is the level (1 or 2) taken by the ith-variable in the kth-experiment and j is either 1 or 2 (two effects are defined for each variable). The sum includes only the SNR of experiments where the level of factor i is equal to j as indicated by the delta of Kronecker symbol δ. For example, in the two-level OA of table 1, $E_{i,1}$ and $E_{i,2}$ can be defined for a given column i (i=1,..,7); $E_{i,1}$ corresponds to the sum of the SNR of all experiments where the value of factor i is equal to 1, and $E_{i,2}$ corresponds to experiments where the value of the ith-factor is equal to 2. An example of application is given in the next subsection, and, for further details, the reader is refereed to [18].

B. Generation of optimal offsprings by Taguchi method

The Taguchi method can be used to generate an optimal offspring from the mating of two parents with N_v genes. The process starts by selecting an appropriate orthogonal array $L_n(2^{n-1})$ with with $n-1 \geq N_v$ and by defining a fitness function that measures the quality of a given chromosome. The fitness function $F(k), k = 1, ..., n$ is evaluated for each of the n experiments in the OA and a signal-to-noise ratio, SNR(k), is defined in terms of $F(k)$. Subsequently the effect, $E_{i,j}$, of the various factors in the SNR is calculated for each factor (gene or column in the array) $(i = 1, .., N_v)$ and each level $(j = 1, 2)$ of that factor using equation (1).

To clarify the process, let us consider the problem of finding a chromosome, k_{best}, formed by the 7 genes, $C(i, k_{best}), i = 1, ..., 7$, that maximize the test function,

$$f(k) = \sum_{i=1}^{7} \sin\left(C(i,k)\right) \qquad (2)$$

where k refers to an specific chromosome whose genes take the values $C(i,k), i = 1, ..., 7$, respectively. The values permitted for each $C(i,k)$ are discrete fractions of π, ranging from 0 to π. In this context, we would perform the mating of the two 7-gene chromosomes (7 factors) given in Table 2 via Taguchi with the aid of the $L_8(2^7)$ OA given in Table 1. Table 3 shows the eight different chromosomes corresponding to the eight different experiments. The process starts with the definition of the fitness function that evaluates the goodness of a chromosome as $F(k) = \frac{f(k)}{7}$ and the calculation of the $SNR(k)$, defined in this case as $SNR(k) = F(k)^2$, for each experiment, $k = 1, ..., 8$, in the OA. The values of $F(k)$ and $SNR(k)$ are shown in the 9th and 10th columns in Table 3. Then the effects, $E_{i,1}$ and $E_{i,2}$, of the various genes are calculated for $i = 1, .., 7$ using equation (1), resulting in the values given in Table 3. As the optimal level for each factor is decided by the larger value of either $E_{i,1}$ or $E_{i,2}$, the process resulted in the optimal levels "2, 1, 1, 2, 2, 2, 1" for each of the seven factors respectively and therefore in the optimal chromosome given in Table 3.

Table 2. The two 7-gene chromosomes.

Chromosome 1:	$\pi/9$	$\pi/2$	$\pi/2$	$\pi/3$	$\pi/9$	$4\pi/5$	$\pi/2$
Chromosome 2:	$\pi/2$	$\pi/3$	$\pi/5$	$\pi/2$	$\pi/2$	$\pi/2$	$2\pi/3$

C. The HTGA method

The HTGA is based on the insertion of the Taguchi method between the crossover and mutation operations in a CGA. The stages in the HTGA algorithm are [19]:

1) Appropriate parameters needed for the implementation of the algorithm are decided such as the probability of crossover, p_{cross}, and probability of mutation, p_{mut}.
2) A suitable two-level OA for matrix experiments is selected.
3) A population of N_{pop} individuals is randomly created.
4) The N_{pop} individuals performance is evaluated according to the specific objective or fitness function at hand.
5) A roulette wheel selection is applied.
6) On average, p_{cross} chromosomes undergo one-point crossover as in the CGA.
7) Two chromosomes from the current population are randomly selected and mated via the Taguchi experiments, producing an optimal offspring as explained in the previous subsection. This step is repeated $\frac{1}{2} \times p_{cross} \times N_{pop}$ times.
8) Mutation with a probability of p_{mut} is applied.
9) The N_{pop} better chromosomes are selected to be the parents of the next generation.
10) Steps 5 to 9 are repeated until the stopping criterion is met.

This hybrid algorithm, which combines the powerful global exploration capabilities of GA with that of the Taguchi method for producing optimum offspring, was proven in [19] to be fast converging, robust, and statistically sound when applied to optimize several high-dimension benchmark problems.

D. The nHTGA method

In this paper we propose a new hybridization of the Taguchi and GA methods (i.e. the nHTGA) which is sketched in Figs. 1 and 2. The objective is to improve the efficiency of the Taguchi method by decreasing the total number of fitness-function evaluations (function calls) needed to find the optimal solution of the problem at hand. To this aim, as we commented in the Introduction, instead of applying Taguchi method $\frac{1}{2} \times p_{cross} \times N_{pop}$ times to mate two randomly selected individuals each time (step 7 in the previous subsection), we just produce an 'optimal' offspring per generation using the Taguchi-based crossover operator. That offspring is the descendant of the best chromosome found so far and one chromosome randomly selected with the only condition of being different enough from its mate according to a criterion explained below. This means that the number of function calls per generation is reduced from $\frac{1}{2} \times p_{cross} \times N_{pop} \times n$ in the HTGA to n in the nHTGA, being n the number of experiments in the appropriate Taguchi OA. The idea behind the modifications is that two bad-quality individuals will not likely be candidates to produce a chromosome with a better performance than that of the best chromosome in the current population.

Aiming to reduce even more the number of function calls, we set a rule to select the second individual to be mated via Taguchi in such a way that we avoid redundant

Table 3. Generating a better chromosome from two chromosomes by using the Taguchi method.

	Factors								
	A	B	C	D	E	F	G		
Experiment	Column number								
Number(k)	1	2	3	4	5	6	7	F(k)	SNR(k)
1	$\frac{\pi}{9}$	$\frac{\pi}{2}$	$\frac{\pi}{2}$	$\frac{\pi}{3}$	$\frac{\pi}{9}$	$4\frac{\pi}{5}$	$\frac{\pi}{2}$	0.7340	0.5387
2	$\frac{\pi}{9}$	$\frac{\pi}{2}$	$\frac{\pi}{2}$	$\frac{\pi}{2}$	$\frac{\pi}{2}$	$\frac{\pi}{2}$	$2\frac{\pi}{3}$	0.8869	0.7865
3	$\frac{\pi}{9}$	$\frac{\pi}{3}$	$\frac{\pi}{5}$	$\frac{\pi}{3}$	$\frac{\pi}{9}$	$\frac{\pi}{2}$	$2\frac{\pi}{3}$	0.6957	0.4840
4	$\frac{\pi}{9}$	$\frac{\pi}{3}$	$\frac{\pi}{5}$	$\frac{\pi}{2}$	$\frac{\pi}{2}$	$4\frac{\pi}{5}$	$\frac{\pi}{2}$	0.7691	0.5915
5	$\frac{\pi}{2}$	$\frac{\pi}{2}$	$\frac{\pi}{5}$	$\frac{\pi}{3}$	$\frac{\pi}{2}$	$4\frac{\pi}{5}$	$2\frac{\pi}{3}$	0.8439	0.7122
6	$\frac{\pi}{2}$	$\frac{\pi}{2}$	$\frac{\pi}{5}$	$\frac{\pi}{2}$	$\frac{\pi}{9}$	$\frac{\pi}{2}$	$\frac{\pi}{2}$	0.8471	0.7176
7	$\frac{\pi}{2}$	$\frac{\pi}{3}$	$\frac{\pi}{2}$	$\frac{\pi}{3}$	$\frac{\pi}{2}$	$\frac{\pi}{2}$	$\frac{\pi}{2}$	0.9617	0.9249
8	$\frac{\pi}{2}$	$\frac{\pi}{3}$	$\frac{\pi}{2}$	$\frac{\pi}{2}$	$\frac{\pi}{9}$	$4\frac{\pi}{5}$	$2\frac{\pi}{3}$	0.8088	0.6542
E_{i1}	2.4007	$\underline{2.7551}$	$\underline{2.9044}$	2.6599	2.3945	2.4967	$\underline{2.7727}$		
E_{i2}	$\underline{3.0090}$	2.6546	2.5053	$\underline{2.7498}$	$\underline{3.0152}$	$\underline{2.9130}$	2.6370		
Optimal level	2	1	1	2	2	2	1		
Optimal chromosome	$\frac{\pi}{2}$	$\frac{\pi}{2}$	$\frac{\pi}{2}$	$\frac{\pi}{2}$	$\frac{\pi}{2}$	$\frac{\pi}{2}$	$\frac{\pi}{2}$	1	1

experiments. Note that if, for example, we perform a matrix experiment using the OA in Table 1 with two individuals in which factors D to G are the same for both, experiments 1 and 2 will be the same, as also will be experiments 3 and 4, 5 and 6, and 7 and 8. Thus in this application of the Taguchi method, we waste four function evaluations since several experiments are repeated. In Appendix A, we describe an empirical study aimed at deciding how many experiments are redundant as a function of the number of genes with repeated values of the two mating individuals. We give an example for the case of an OA $L_{32}(2^{31})$ and $N_v = 30$. We conclude that no matrix experiments should be made if the difference between individuals is less than 15%, since nearly half of the experiments will have been already performed, resulting in a waste of computational resources. As a rule of thumb, in the present work we increase this threshold up to 25%.

E. Benchmark testing

Next we assess the performance of the nHTGA algorithm by solving several global numerical optimization problems, which fulfill the conditions to form a suitable touchstone to check the performance of evolutionary algorithms [19]. In particular, we consider the minimization of the 30-dimensional functions ($N = 30$) described in table 4 by applying the nHTGA and subsequently compare our results with the ones reported in [19].

We apply the nHTGA using a smaller population ($N_{pop} = 20$) than the one reported in [19], where HTGA was employed to solve the same problems with $N_{pop} = 200$. Therefore, in order to make a fair comparison, we increase the crossover and mutation rates to $p_{cross} = 1$ and $p_{mut} = 0.2$ so that we have the same number of fitness-function evaluations per generation due to the action of the genetic operators than in HTGA. On the other hand, as it was previously commented, we use a Taguchi-based crossover operator was used only once in each evolutionary cycle, on individuals with at least one quarter of the genes being different. Both the nHTGA and the HTGA use real encoding where each chromosome is represented by a vector of N floating-point numbers, i.e, $x_1, ..., x_N$. The criterion for stopping the execution of the nHTGA algorithm is that the value of the fitness function of the best individual in the population should be less than or equal to the mean function value reported in [20] using HTGA. Aiming for statistically robust results, each test function minimization problem is performed 50 times.

The mean number of fitness-function evaluations, the mean function value of the optimized solution calculated

Table 4. Benchmark of test functions.

Test Function	Feasible Solution Space
$f_1 = \sum_{i=1}^{N} \left(-x_i \sin\left(\sqrt{\lvert x_i \rvert}\right)\right)$	$[-500, 500]^N$
$f_2 = \sum_{i=1}^{N} \left(x_i^2 - 10\cos(2\pi x_i) + 10\right)$	$[-5.12, 5.12]^N$
$f_3 = -20\exp\left(-0.2\sqrt{\frac{1}{N}\sum_{i=1}^{N} x_i^2}\right) - \exp\left(\frac{1}{N}\sum_{i=1}^{N}\cos(2\pi x_i)\right) + 20 + \exp(1)$	$[-32, 32]^N$
$f_4 = \frac{1}{4000}\sum_{i=1}^{N} x_i^2 - \prod_{i=1}^{N}\cos\left(\frac{x_i}{\sqrt{i}}\right) + 1$	$[-600, 600]^N$
$f_5 = \frac{1}{10}\left\{\sin^2(3\pi x_1) + \sum_{i=1}^{N} -1(x_i - 1)^2\left[1 + \sin^{(3\pi x_{i+1})}\right] + (x_N - 1)^2\left[1 + \sin^{(3\pi x_N)}\right]\right\} + \sum_{i=1}^{N} u(x_i, 5, 100, 4)$	$[-50, 50]^N$
$f_6 = \sum_{i=1}^{N} x_i^2$	$[-100, 100]^N$
$f_7 = \sum_{i=1}^{N} \lvert x_i \rvert + \prod_{i=1}^{N} \lvert x_i \rvert$	$[-10, 10]^N$

over the 50 runs, and the standard deviation of the function values were all calculated for each test function and are presented in Table 5. Note as the table reflects, the new nHTGA gives closer to optimal solutions than the HTGA and moreover uses a lower mean number of fitness-function evaluations, greatly improving the efficiency of the algorithm. In this table we also show these data when a CGA is used (numerical results extracted from [16]).

III. LOG PERIODIC ANTENNA DESIGN

The Taguchi method has been applied to some electromagnetic optimization problems [21, 22] with success. In this work we employ the nHTGA hybrid GA and Taguchi method algorithm to optimize the design of a thin-wire antenna that must fulfill the following requirements throughout the operating band, which ranges from 450MHz to 1.35GHz:

1) Standing voltage wave ratio (SVWR) less than 2 (referenced to 75Ω)
2) Gain range (GR) less than 3dB.
3) Gain (G) greater than 5dB.
4) Front-to-back ratio (FTB) greater than 15dB.
5) Beamwidth (BW) in azimuth greater than $120°$.
6) Vertical polarization.

Moreover, as the antenna is going to be mounted on a pole, its environmental impact needs to be reduced and therefore, its greatest dimension is required to be less than or equal to half of thewavelength at the lowest frequency, i.e. $\lambda_{low}/2 = 0.33m$.

To satisfy the above requirement we have considered symmetrical log-periodic antennas (LP) as suitable starting points in our designs, because LP antennas are vertically polarized, endfire radiators, and possess good FTB ratios [23].

A. LP antenna geometry

Log periodic antennas are radiators for which the geometry is chosen so that the electrical properties are repeated periodically with the logarithm of frequency. The first successful design of this type of antenna was proposed by DuHammel and Isbell in [24], setting a new starting point for a variety of sheet and wire LP designs [25], [26]. Among this family of antennas, the symmetrical log-periodic antennas [27] focus our interest since they provide a promising model to be optimized with the nHTGA tool in an effort to fulfil all the design specifications described above. In particular, log-periodic bent zigzag antennas (LPBZA) as the one studied in [28] were considered the starting point of our design because they do not need any phase-reversal transformers to achieve broadband performance and they are less sensitive than the bent-monopole antenna [23]. An example of a basic thin-wire LPBZA antenna is schematized in Fig. 3, where only one arm of the antenna is represented, as the antenna is symmetric with respect to the XY plane. The geometrical factor τ is the ratio of two adjacent similar dimensions of the antenna ($\tau = R_{n+2}/R_n < 1$); α_E and α_S are the angles between tip to tip on the vertical and horizontal planes of the zigzag antenna, respectively; ξ is the distance between the two antenna arms and N_t

Table 5. Comparison between HTGA and nHTGA under the same evolutionary environment.

Test function	Mean number of function evaluations			Mean function value (standard deviation)			Globally minimal function value
	nHTGA	HGTA	CGA	nHTGA	HGTA	CGA	
f_1	14677	163468	458653	-12569.4655 (0.0077)	-12569.46 (0)	-8444.7583 (65.7326)	-12569.5
f_2	5596	16267	335993	0 (0)	0 (0)	22.967 (0.7800)	0
f_3	7989	16632	336481	0 (0)	0 (0)	2.697 (5.668×10^{-3})	0
f_4	19282	20999	346971	0 (0)	0 (0)	1.258 (1.657×10^{-2})	0
f_5	14405	59003	348356	0.9×10^{-4} (1×10^{-5})	1×10^{-4} (0)	2.978 (7.210×10^{-2})	0
f_6	8917	20844	181445	0 (0)	0 (0)	4.9655 (11.3614)	0
f_7	6747	14285	170955	0 (0)	0 (0)	7.9315×10^{-1} (5.5943×10^{-1})	0

the number of tips in one arm (in the particular case shown in Fig. 3 $N_t = 7$). The antenna is excited with a voltage source at its center (see Fig. 3). In our designs, the radius of the wire, r, is constant, despite breaking the log-periodicity, in order to facilitate the future construction of the antenna.

Next, we modify the geometry of the LPBZA antennas in order to reduce their size so that the design specifications regarding the compact size of the antenna are fulfilled. With this aim, we have considered two alternative ways of keeping the antennas maximum dimension smaller that $\lambda_{low}/2$: 1) either we reduce to $\lambda_{low}/4$ (since the antenna is symmetrical over the XY plane) the height of the tooth that exceed the limit imposed (as in Fig. 4(b)); or, 2) following the ideas already presented in [29], we bend the antenna tooth in a quasi-fractal way until the antenna shrinks to the appropriate dimensions (see Fig. 4(c)). With the first option the number of peaks is kept invariant, while the second option maintains the total length of the wire.

Furthermore, to increase the electrical size of the antennas without increasing their physical size, we propose to use resistive loads located along the antenna geometries. The use of resistive loading is crucial to operate within the required frequency range and to broaden the bandwidth. This is due to the fact that, in LP antennas, most of the radiation takes place in the region where the dipole length ranges from $\lambda/2$ to $3\lambda/2$ [23]. Then, since the maximum height of our antenna must be less than $\lambda_{low}/2$, energy with a wavelength greater than approximately $\lambda_{low}/3$ will not be fully radiated if the antenna is made of perfect electric conducting wires. One way to solve this is to lengthen the wires electrically by means of loading the antenna segments with a resistive profile.

B. Antenna optimization

In this subsection, we describe how the nHTGA approach has been applied in conjunction with the method-of-moments-based NEC code to optimize the performance of an LPBZA. The design parameters are α_E, α_S, τ, ξ and the value of the resistance per unit length loading the antenna structure, which, to keep the problem tractable, is chosen to be constant for each tooth of the LPBZA and ranges from 0 Ω/m to 100 Ω/m. LPBZA, both with reduced tooth size and with bent teeth, are being considered. The radius of the wire is r=2mm, the number of tips $N_t = 25$ and, for practical reasons, designs with segments shorter than 2cm are not permitted. The variation range of the geometrical design parameters is shown in Table 6.

Table 6. Parameter design range.

Parameter	Min. Value	Max. Value
α_E	25 (deg)	65 (deg)
α_S	25 (deg)	65 (deg)
τ	0.8	0.95
ξ	6 (mm)	20 (mm)
Ω	0 (Ω/m)	100 (Ω/m)

The nHTGA starts by generating an initial population of $N_{pop} = 20$ LPBZA antennas which are encoded using real values. Then, to measure the goodness of a given individual, we define a fitness function as a weighted aggregation of the different objectives described at the

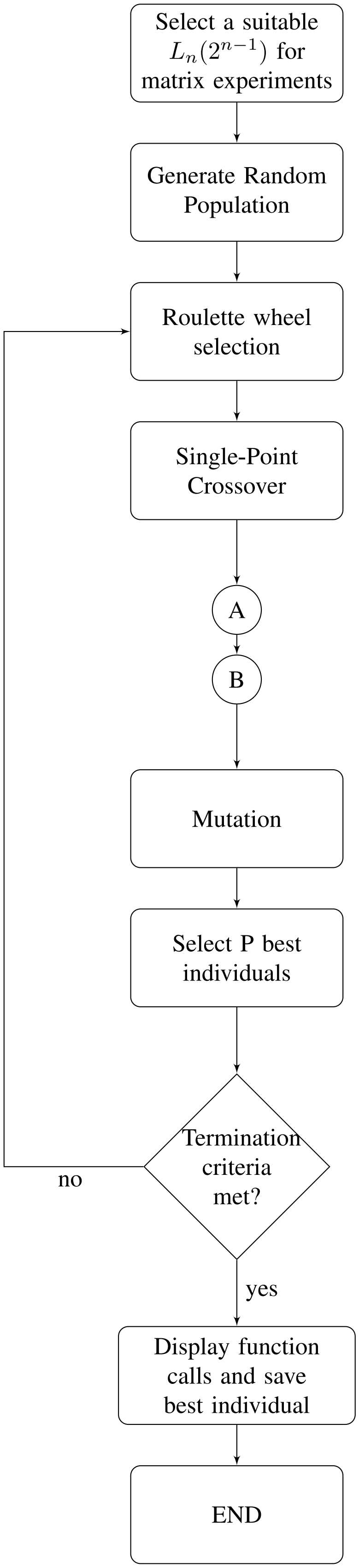


Fig. 1. Flowchart of the nHTGA for global numerical optimization problem.

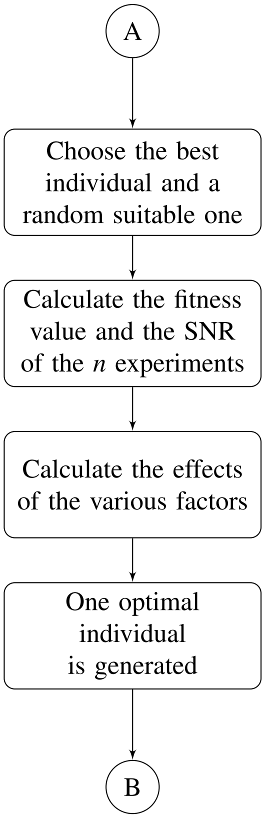


Fig. 2. New implementation of the Taguchi method over a GA.

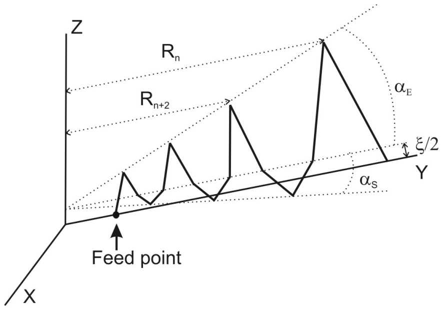


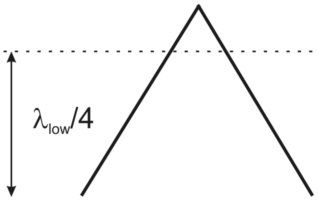
Fig. 3. Geometry of a single arm of the LPBZA.

beginning of this section as,

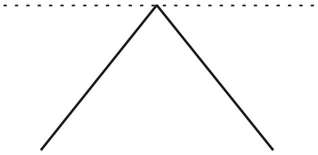
$$F = \frac{1}{N_\nu}\sum_{i=1}^{N_\nu} \varpi(\nu_i)\times \left[\frac{1}{4}\Theta\left(\frac{2}{SVWR(\nu_i)}\right) + \frac{1}{8}\Theta\left(\frac{3}{GR(\nu_i)}\right) + \frac{1}{8}\Theta\left(\frac{G(\nu_i)}{5}\right) + \frac{1}{4}\Theta\left(\frac{FTB(\nu_i)}{15}\right) + \frac{1}{4}\Theta\left(\frac{BW(\nu_i)}{120}\right)\right] \quad (3)$$

where

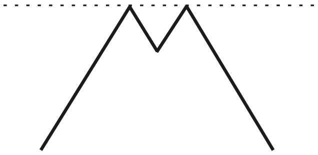
$$\Theta(x) = \begin{cases} 1 & \text{if } x \geq 1 \\ x & \text{otherwise} \end{cases} \quad (4)$$



(a) Original

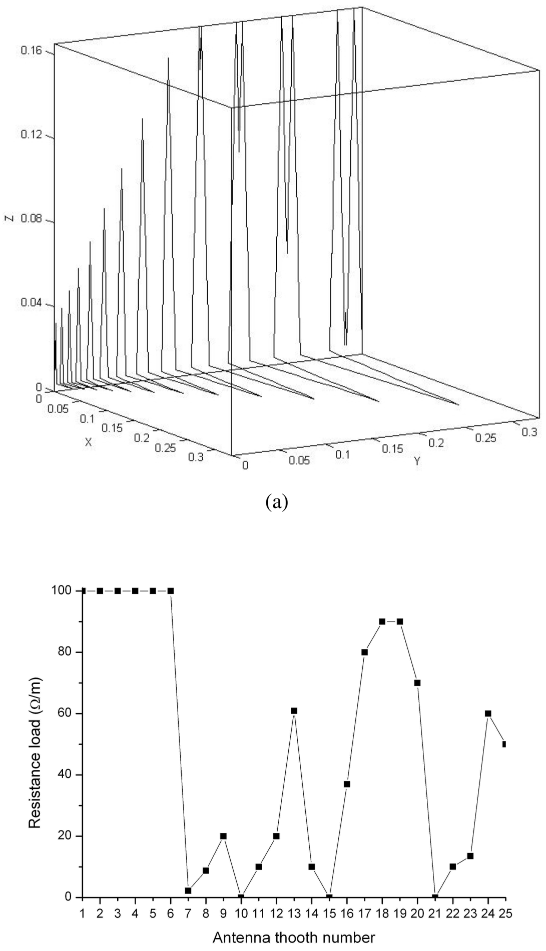


(b) Option 1



(c) Option 2

Fig. 4. Miniaturization techniques applied to an oversized tooth (a), by decreasing the tooth height (b), and by bending the tooth on a quasi-fractal way (c).



(a)

(b)

Fig. 5. Optimized LPBZA. (a) Geometry of the optimized antenna. (b) Resistive loading profile for each tooth in the optimized antenna.

and $\varpi(\nu) = C(1/\nu^3 + \nu^8)$ is a normalized weighting function that gives more importance to the accomplishment of the objective functions at the edges of the frequency band. N_ν is the number of frequency samples and ν the frequency in GHz. F is defined so that its maximum value, 1, is achieved by any antenna that fulfils all the design requirements. Thus, the application of the nHTGA operators makes the population evolve towards better antenna designs, i.e. towards individuals with higher F values.

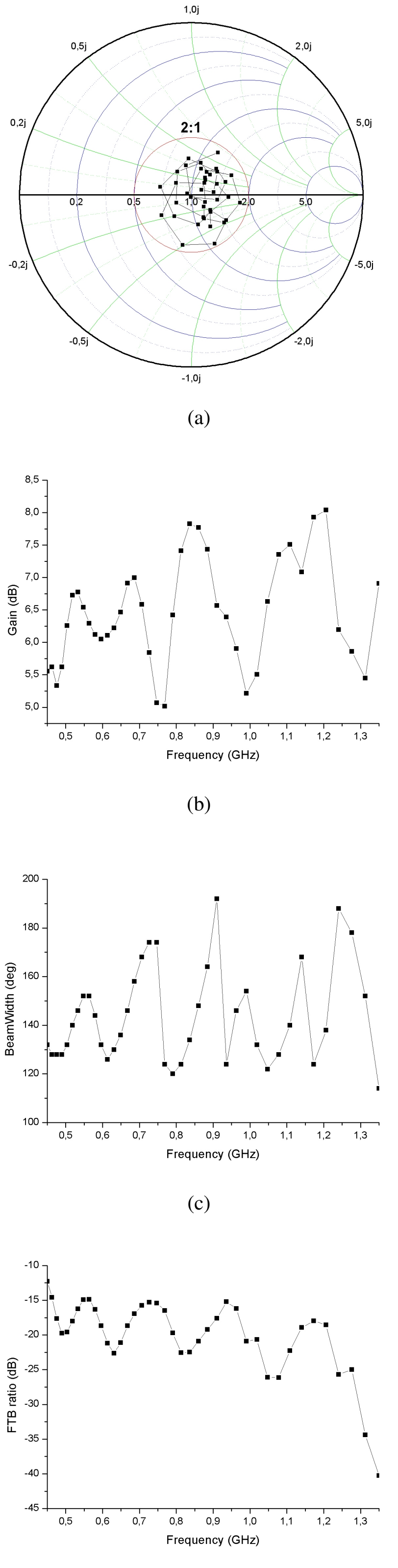
C. Numerical results

The nHTGA code has been applied three times to ensure that the code has not been trapped in a local maximum. The best antenna found had a value of the fitness function F equal to 0.9856. Its geometry, shown in Figure 5(a), corresponds to $\tau = 0.815$, $\alpha_E = 44.691°$, $\alpha_H = 41.000°$, $\xi = 6.746\ mm$. The 25 teeth in each arm have been miniaturized in a quasi-fractal way and the resistive profile for each teeth is shown in Fig. 5(b) (the tooth are numbered from larger to smaller sizes).

The performance of the resulting antenna has been analyzed using NEC and the results are given in Figs. 6 and 7. The input impedance, normalized to $Z_0 = 75\Omega$, is plotted on a Smith chart in Fig. 6(a). The impedance plot lies at the center of the Smith chart, with all the points inside the 2:1 circle, meaning the fulfilment of objective 1 ($SVWR \leq 2$). Moreover, the impedance is balanced and can be matched to a 75Ω commercial coaxial cable without using an impedance transformer. From Fig. 6(b), which represents the gain versus frequency, it can be seen that the gain ranges from 5dB to 8dB within the band, satisfying requirements 2 ($GR \leq 3dB$) and 3 ($G \geq 5dB$).

Figure 6(c) plots the antenna 3dB horizontal beamwidth vs. frequency, which is found to be greater than $120°$ throughout the frequency range except for three frequency samples that, in any case, correspond to beamwidth values quite close to $120°$. On the other hand, the front-to-back ratio, which is represented in Fig. 6(d) vs. frequency, is greater than 15dB, except for a couple of frequencies near the low-frequency part of the band, where values are around 12dB. Therefore, objectives 4 ($FTB \geq 15dB$) and 5 ($BW \geq 120°$) have been approximately accomplished.

Finally, Fig. 7 displays, for five different frequencies within the operating antenna bandwidth, the gain as a function of the horizontal angle ϕ. The behavior of the gain with frequency is similar in the five cases, therefore corroborating the broadband antenna performance, and the figure also confirms that the design objectives in terms



(a)

(b)

(c)

(d)

Fig. 6. Performance of the optimized LPBZA. (a) Input impedance on the Smith chart referenced to $Z_0 = 75\Omega$.(b) Gain in the endfire direction. (c) Beamwidth on the horizontal plane. (d) Front-to-back ratio.

of gain, beamwidth, and front-to-back ratio, have been accomplished for the five selected frequencies.

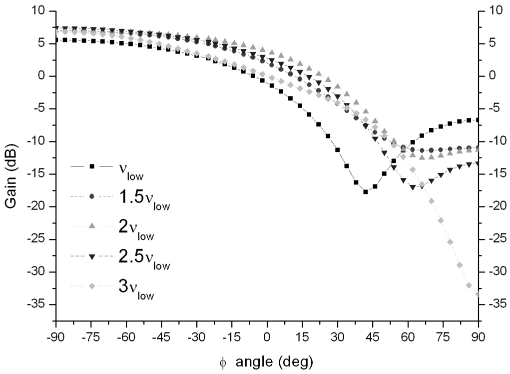


Fig. 7. Gain in the horizontal plane $(\theta = 90°)$ versus ϕ for the optimized LPBZA. $\nu_{low} = 450MHz$ is the lowest frequency of the considered band.

IV. CONCLUSION

A new implementation of the HTGA is proposed in this paper. Hybrid techniques combining the Taguchi method with traditional GAs incorporate Taguchi orthogonal arrays between the crossover and mutation operators to produce chromosomes with the best combination of design variables or genes. After the conventional GA gene-mating process, the new HTGA proposed here produces only one individual in each generation via the Taguchi-based crossover operator. The new individual is the Taguchi children of the best individual found so far and one selected at random. This process differs from previous versions of HTGA, where a percentage of the whole population at each generation is generated via Taguchi method. The computational solution of several test cases demonstrates that the proposed hybrid algorithm outperforms the HTGA and traditional GAs in terms of evolutionary efficiency. Finally an example of application of the nHTGA is given carrying out the optimization of a log-periodic thin-wire miniature antenna.

APPENDIX A
EFFICIENCY OF MATRIX EXPERIMENTS $L_{32}(2^{31})$

In this appendix, we explain how to perform a numerical experiment conceived to determine how many function evaluations are redundant in a matrix experiment when two individuals with several genes in common are crossed via Taguchi method. We propose to implement the following steps:

1) Two N_v-genes chromosomes are randomly generated.

2) N_{equal} genes of the two previous chromosomes are forced to be identical. The specific equal genes are selected at random.
3) The matrix of experiments that results from crossing the two chromosomes via Taguchi is built.
4) The number of different experiments is counted.

The numerical experiment is conducted one hundred times, each time varying $N_{equal} = 1 \ldots N_v$ (instead of considering all the $\frac{N_v!}{(N_v - N_{equal})! N_{equal}!}$ possibilities for N_{equal}). The number of different experiments found in average are plotted versus $\frac{N_{equal}}{N_v} \times 100$ and, from that graph, conclusions can be reached on how to select N_{equal} in order to avoid a certain percentage of redundant matrix experiments. As an example, Fig. 8 shows the results for the case of N=31 genes and the OA $L_{32}(2^{31})$. It plots the number of different matrix experiments (in average) versus the percentage of different genes in the pairs of 31-genes mating chromosomes considered. It can be seen that if at least 25% of the genes of the individuals going to be mated through Taguchi are different, just around the 2% of the matrix experiments are repeated. Therefore it seems reasonable to require the differences in genes to be greater than at least 25%. Numerical experiments with other OA lead to similar conclusions.

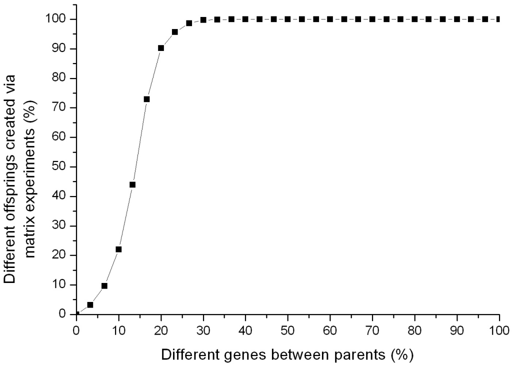


Fig. 8. Number of different experiments versus the percentage of different genes for the case of the OA $L_{32}(2^{31})$.

ACKNOWLEDGEMENT

This work was supported in part by the Spanish Projects TEC-2004-06217-C02-01, TEC-2004-04866-C04-03, PTR95-1025.OP.01, the training program and project of excellence TIC1541 of Junta de Andalucia.

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