

# A Genetic Algorithm Approach to the Problem of Factorization of General Multidimensional Polynomials

Ioannis F. Gonos, Nikos E. Mastorakis, *Senior Member, IEEE*, and M. N. S. Swamy, *Life Fellow, IEEE*

**Abstract**—In this paper, a solution to the problem of the multidimensional ( $m$ -D) polynomial factorization is attempted by using genetic algorithms (GAs). The proposed method is based on an appropriate minimization of the norm of the difference between the original polynomial and its desirable factorized form. Using GAs, we can obtain better results than with other methods of minimization (numerical techniques, neural networks, etc.). The present methodology, which can also be used for every type of  $m$ -D factorization, is illustrated by means of a numerical example.

**Index Terms**—Genetic algorithm (GA), multidimensional ( $m$ -D) polynomial factorization, multivariate polynomials.

## I. INTRODUCTION

THE factorization of a general multidimensional ( $m$ -D) (multivariable) polynomial into polynomial factors of lower order is a difficult problem, since the fundamental theorem of algebra holds only for one-dimensional (1-D) (or one-variable) polynomials. The problem of factorization of a real-coefficient  $m$ -D polynomial into real-coefficient  $m$ -D polynomial factors of lower order has great technical interest, even though it is still unsolved in the general case. It has great technical interest because of its many applications in the study of  $m$ -D systems, distributed-parameter systems, and, of course, in  $m$ -D signal processing. For example, a linear, shift-invariant ( $m - D$ ) system is described by a transfer function, which is a ratio of two  $m$ -D polynomials

$$G(z_1, \dots, z_m) = \frac{B(z_1, \dots, z_m)}{A(z_1, \dots, z_m)} = \frac{\sum_{i_1=0}^{N_1} \dots \sum_{i_m=0}^{N_M} b(i_1, \dots, i_m) z_1^{i_1} \dots z_m^{i_m}}{\sum_{i_1=0}^{N_1} \dots \sum_{i_m=0}^{N_M} a(i_1, \dots, i_m) z_1^{i_1} \dots z_m^{i_m}}$$

where  $N_1, \dots, N_m$  (positive integers) are the degrees of the polynomials  $B, A$  with respect to  $z_1, \dots, z_m$  and  $a(i_1, \dots, i_m)$ ,

$b(i_1, \dots, i_m) \in \mathfrak{R}$ . If  $B(z_1, \dots, z_m)$  and  $A(z_1, \dots, z_m)$  can be factorized as

$$B(z_1, \dots, z_m) = B_1(z_1, \dots, z_m) \dots B_N(z_1, \dots, z_m) \\ A(z_1, \dots, z_m) = A_1(z_1, \dots, z_m) \dots A_N(z_1, \dots, z_m)$$

where  $B'_i$ s and  $A_i$ s ( $i = 1, \dots, m$ ) are obviously simpler than  $B$  and  $A$ , then our original system or filter can be realized by a cascade connection of simpler  $m$ -D systems with transfer functions

$$G_1(z_1 \dots z_m) = \frac{B_1(z_1, \dots, z_m)}{A_1(z_1 \dots z_m)} \dots \\ G_N = \frac{B_N(z_1 \dots z_m)}{A_N(z_1 \dots z_m)}$$

Moreover, since all the stability tests are in the form: “check if  $A(z_1, \dots, z_m) = 0$  in appropriate regions of  $z_1, \dots, z_m$ ”, if  $A(z_1, \dots, z_m)$  is written as a product of  $A_1(z_1, \dots, z_m) \dots A_N(z_1, \dots, z_m)$ , then, the initial stability test can be checked by checking  $N$  simpler (i.e. of lower order) stability tests.

The factorization results of  $m$ -D polynomials are also useful in the theory of distributed—parameter systems (DPS), which are described by partial differential equations, since the characteristic polynomials of DPS are actually  $m$ -D polynomials. Some of the properties of  $m - D$  systems such as controllability and observability, may be studied in a straightforward manner if  $B(z_1, \dots, z_m)$  and  $A(z_1, \dots, z_m)$  are  $m - D$  factorizable polynomials.

It should be noted that, up to now, the general factorization problem, i.e., the factorization of any factorizable polynomial, has not yet to be fully solved. For this reason, some more or less special types of  $m$ -D polynomial factorization have been studied by Tzafestas *et al.* [1]–[3], Chakrabarti *et al.* [4], [5], Musser [6], Wang [7], Ekstrom *et al.* [8]–[10], and Mastorakis [11]–[14].

In this paper, the efficient technique of genetic algorithms (GAs) will be used for the solution to the problem of  $m$ -D polynomial factorization.

## II. GAs IN $m$ -D POLYNOMIAL FACTORIZATION

Generally, it is very difficult and rare to obtain exactly a certain type of factorization (Mastorakis [11], [12]). For this reason, if one type of factorization does not hold though it is desirable, the (optimum) approximation of the original given polynomial  $A(z_1, \dots, z_m)$  by a factorizable (of the type

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I. Gonos is with the High Voltage Laboratory, School of Electrical and Computer Engineering, National Technical University of Athens, Athens GR 15780, Greece (e-mail:igonos@ieee.org).

N. Mastorakis is with the Military Institutions of University Education, Department of Computer Science, Hellenic Naval Academy, Terma Hatzikyriakou, 18539 Piraeus, Greece (e-mail: mastor@ieee.org; igonos@softlab.ntua.gr).

M. N. S. Swamy is with the Centre for Signal Processing and Communications, Department of Electrical and Computer Engineering, Concordia University, Montreal, QC H3G 1M8, Canada (e-mail: swamy@ece.concordia.ca).

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considered) one is attempted. So, an unknown factorizable polynomial  $\tilde{A}(z_1, \dots, z_m)$ , the coefficients of which fulfil some conditions, is considered

$$\tilde{A}(z_1, \dots, z_m) = \sum_{i_1=0}^{N_1} \cdots \sum_{i_m=0}^{N_m} \tilde{a}(i_1, \dots, i_m) z_1^{i_1} \cdots z_m^{i_m} \quad (1)$$

and the norm  $\|A - \tilde{A}\|_2$  is minimized, where

$$\begin{aligned} \|A - \tilde{A}\|_2^2 &= \|A(z_1, \dots, z_m) - \tilde{A}(z_1, \dots, z_m)\|_2^2 \\ &= \sum_{i_1=0}^{N_1} \cdots \sum_{i_m=0}^{N_m} (a(i_1, \dots, i_m) - \tilde{a}(i_1, \dots, i_m))^2. \end{aligned}$$

If we are not interested in a certain type of factorization, we can select the type of factorization for which the approximation is better, i.e.,  $\|A - \tilde{A}\|_2$  is minimum. Work in approximate  $m$ -D polynomial factorization can be found in Mastorakis [13], [14].

In this paper, we suppose that the  $m$ -D polynomial  $A = A(z_1, \dots, z_m)$  is written as follows:

$$\begin{aligned} A &= A(z_1, \dots, z_m) \\ &= z_1^{N_1} + \sum_{i_1=0}^{N_1-1} \cdots \sum_{i_m=0}^{N_m} a(i_1, \dots, i_m) z_1^{i_1} \cdots z_m^{i_m} \quad (2). \end{aligned}$$

(In other words, the only restriction placed upon  $A(z_1, \dots, z_m)$  is that there exists at least one independent variable, say  $z_1$ , such that the only existing monomial including the maximum power of  $z_1$  is  $z_1^{N_1}$ ).  $z_1$  is selected as the variable for which the only existing monomial including the maximum power  $N_1$  of  $z_1$  is  $z_1^{N_1}$ , that is,  $a(N_1, 0, \dots, 0) \neq 0$  ( $= 1$ , without loss of generality) and  $a(N_1, i_2, \dots, i_m) = 0$  when  $(i_2 + \dots + i_m) > 0$ . If this does not hold, another variable  $z_j$  of  $\{z_2, \dots, z_m\}$  can be selected as  $z_1$ , and the variables  $z_1$  and  $z_j$  interchanged. If none of the variables  $z_1, z_2, \dots, z_m$  satisfies this requirement, the attempted approximation—as one can see carrying out numerical experiments—has a great error and this type of approximate factorization is not recommended. In that case, other types of factorization may be more successful.

Two theorems [12] provide the necessary and sufficient conditions for the exact factorization of  $A$

$$\begin{aligned} A &= A(z_1, \dots, z_m) \\ &= \prod_{i=1}^{N_1} \left( z_1 + \sum_{i_2=0}^{n_2} \cdots \sum_{i_m=0}^{n_m} a_{i, i_2 \dots i_m} z_2^{i_2} \cdots z_m^{i_m} + c_i \right) \quad (3) \end{aligned}$$

and simultaneously provide the values of the unknown coefficients  $a_{i, i_2 \dots i_m}, c_1$ .

Suppose now the  $m$ -D polynomial, given in (2), cannot be factorized into a product of general  $m$ -D factors as in (3), i.e., the necessary and sufficient conditions formulated in [12], are not satisfied.

$$\begin{array}{ccc} 01100|100\dots11 & \rightarrow & 01100101\dots10 \\ 00011|101\dots10 & & 00011100\dots11 \\ \text{parents} & & \text{children} \end{array}$$

Fig. 1. Crossover.

In an attempt to “factorize”  $A(z_1, \dots, z_m)$  approximately, an unknown factorizable polynomial  $\tilde{A}(z_1, \dots, z_m)$  of the following type is considered:

$$\begin{aligned} \tilde{A}(z_1, \dots, z_m) &= \sum_{i_1=0}^{N_1} \cdots \sum_{i_m=0}^{N_m} \tilde{a}(i_1, \dots, i_m) z_1^{i_1} \cdots z_m^{i_m} \\ &= \prod_{i=1}^{N_1} \left( z_1 + \sum_{\substack{i_2=0 \\ (i_1, \dots, i_m) \neq (0, \dots, 0)}}^{n_2} \cdots \sum_{i_m=0}^{n_m} \right. \\ &\quad \left. \times \tilde{a}_i, i_2 \dots i_m z_2^{i_2} \cdots z_m^{i_m} + c_i \right) \quad (4) \end{aligned}$$

and the norm  $f = \|A - \tilde{A}\|_2$  is minimized, where

$$\begin{aligned} f^2 &= \|A - \tilde{A}\|_2^2 \\ &= \|A(z_1, \dots, z_m) - \tilde{A}(z_1, \dots, z_m)\|_2^2 \\ &= \left\| A(z_1, \dots, z_m) - \prod_{i=1}^{N_1} \left( z_1 + \sum_{\substack{i_2=0 \\ (i_1, \dots, i_m) \neq (0, \dots, 0)}}^{n_2} \cdots \sum_{i_m=0}^{n_m} \right. \right. \\ &\quad \left. \left. \times \tilde{a}_{i_1, i_2 \dots i_m} z_2^{i_2} \cdots z_m^{i_m} + c_i \right) \right\|_2^2 \\ &= \sum_{i_1=0}^{N_1} \cdots \sum_{i_m=0}^{N_m} (a(i_1, \dots, i_m) - \tilde{a}(i_1, \dots, i_m))^2 \end{aligned}$$

the symbol  $\sim$  being used for the corresponding quantities of the unknown factorizable polynomial  $\tilde{A}(z_1, \dots, z_m)$ .

In [13] the minimization has been attempted by using the Levenberg-Marquardt routine [15]. In this paper, we use a new optimization technique using an appropriate GA.

A brief overview of the methodology of GAs is as follows. Suppose we have to maximize (minimize) a function  $f(x)$ , which is not necessarily continuous or differentiable. GAs are search algorithms that were initially inspired by the process of natural genetics (reproduction of an original population, performance of crossover and mutation, selection of the best). The main idea for an optimization problem is to start our search not with one initial point, but with a population of initial points. The  $2n$  numbers (points) of this initial set (called population, quite analogous to biological systems) are converted to the binary system. In the sequel, they are considered as chromosomes (actually sequences of 0 and 1). The next step is to form pairs of these points, which will be considered as parents for a “reproduction” (Fig. 1). “Parents” go through “reproduction” where they interchange parts of their “genetic material”. (This is achieved by the so-called *crossover*, Fig. 1). However, there is always a very small probability for a mutation to exist. (Mutation is the phenomenon where quite randomly—though with a very small probability—a 0 becomes a 1 or a 1 becomes a 0). We assume that every pair of “parents” gives rise to  $k$  children.

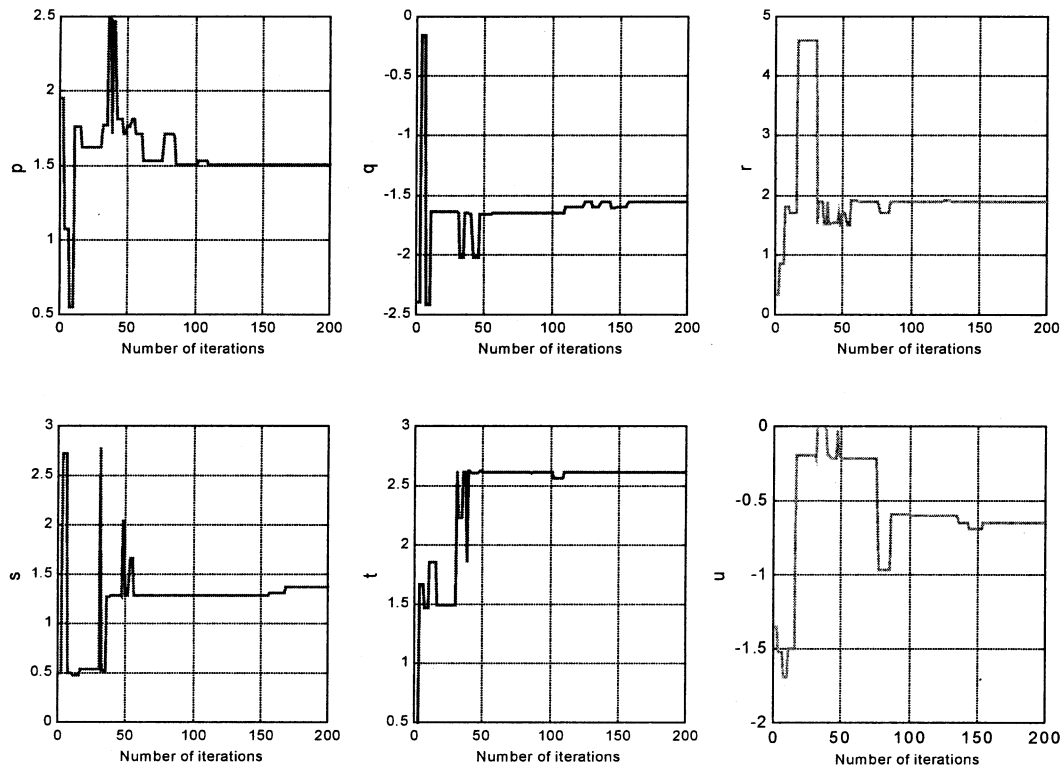


Fig. 2. The evolution of  $p, q, r, s, t, u$ , and their final values of convergence.

By the process of reproduction, the population of the “parents” is enhanced by the “children” and we have an increase in the original population because new members have been added (parents always belong to the population considered). The new population has now  $2n + kn$  members. Then, the process of *natural selection* is applied. According the concept of natural selection, from the  $2n + kn$  members, only  $2n$  survive. These  $2n$  members are selected as the members with a higher value of  $f$ , if we attempt to achieve maximization of  $f$  (or with a lower value of  $f$ , if we attempt to achieve minimization of  $f$ ). By repeated iterations of reproduction (under crossover and mutation) and natural selection, we can find the maximum (or minimum) of  $f$  as the point to which the best values of our population converge. The termination criterion is fulfilled if the mean value of  $f$  in the  $2n$ -members population is no longer improved (maximized or minimized). More detailed overviews of GAs can be found in [16]–[19].

In our problem of  $m$ -D polynomial factorization, we wish to minimize  $f$  where  $f = \left\| A - \tilde{A} \right\|_2$  over  $\tilde{a}(i_1, \dots, i_m)$ . To this end, every  $\tilde{a}(i_1, \dots, i_m)$  is converted to the binary system and is considered as part of a big chromosome, 100110010|001000111|...|111001010, where every part corresponds to a particular  $\tilde{a}(i_1, \dots, i_m)$ . If we assume that every  $\tilde{a}(i_1, \dots, i_m)$  is converted to a  $t$ -bits binary number, for the “chromosome” of  $\tilde{a}(i_1, \dots, i_m)$  we need  $Mt$  bits, where  $M$  is the number of  $\tilde{a}(i_1, \dots, i_m)$ . Our search starts with a randomly generated population of such  $2n$  chromosomes. In a quite random manner, this population is split into pairs of parents that will be crossed, i.e., they will interchange their genetic material (with  $c$  crossovers) always under a very small probability  $P$  for mutation (for example  $P = 0.01$ ).

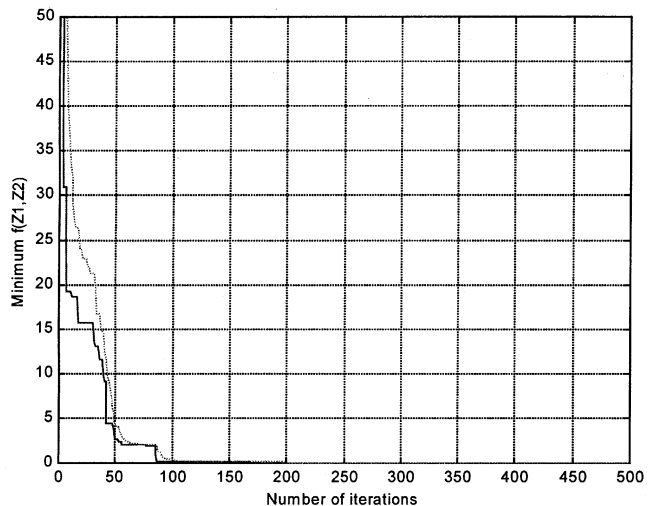


Fig. 3. Convergence of the optimum value of  $f$  in every generation (—), as well as of the mean value of  $f$  in every generation (---).

By this reproduction, a new population of  $2n + kn$  members will be formed, since each pair of parents give birth to  $k$  children. The new population is filtered and only the  $2n$  better members (here “better” means the  $2n$  lower values of  $f$ ,  $f = \left\| A - \tilde{A} \right\|_2$ ) are retained in the population, and the others deleted. This is the so-called “natural selection”. By repeated iterations of reproduction (under crossover and mutation) and natural selection, we can find the minimum of  $f = \left\| A - \tilde{A} \right\|_2$  as the point to which the best values of our population converge. The termination criterion is: “the mean value of  $f$  in the population is no longer improved”. The algorithm is summarized as follows.

TABLE I  
CONVERGENCE OF THE COEFFICIENTS  $p, q, r, s, t, u$  AND THE OPTIMUM VALUE OF  $f$  IN EVERY GENERATION

| Step | p          | q           | r          | s          | t          | u           | Optimum $f$ |
|------|------------|-------------|------------|------------|------------|-------------|-------------|
| 25   | 1.62304688 | -1.64355469 | 4.59667969 | 0.53613281 | 1.48535156 | -0.19042969 | 15.67708910 |
| 50   | 1.76074219 | -1.65820313 | 1.70214844 | 1.28320313 | 2.61035156 | -0.21386719 | 2.59311650  |
| 75   | 1.52636719 | -1.64648438 | 1.87792969 | 1.28320313 | 2.61035156 | -0.21386719 | 2.03506183  |
| 100  | 1.50292969 | -1.64648438 | 1.88964844 | 1.28320313 | 2.61035156 | -0.59472656 | 0.17265512  |
| 125  | 1.50292969 | -1.55273438 | 1.91308594 | 1.28320313 | 2.61035156 | -0.60058594 | 0.13109452  |
| 150  | 1.50292969 | -1.59960938 | 1.88964844 | 1.28320313 | 2.61035156 | -0.69433594 | 0.09673949  |
| 175  | 1.50292969 | -1.55273438 | 1.88964844 | 1.37695313 | 2.61035156 | -0.64746094 | 0.05720788  |
| 200  | 1.50292969 | -1.55273438 | 1.88964844 | 1.37695313 | 2.61035156 | -0.64746094 | 0.05720788  |
| 225  | 1.50292969 | -1.55273438 | 1.88964844 | 1.37695313 | 2.61035156 | -0.64746094 | 0.05720788  |
| 250  | 1.50292969 | -1.55273438 | 1.88964844 | 1.37695313 | 2.61035156 | -0.64746094 | 0.05720788  |
| 275  | 1.50292969 | -1.55273438 | 1.88964844 | 1.37695313 | 2.61035156 | -0.64746094 | 0.05720788  |
| 300  | 1.50292969 | -1.55273438 | 1.88964844 | 1.35351563 | 2.61035156 | -0.69433594 | 0.04796740  |
| 325  | 1.50292969 | -1.55273438 | 1.88964844 | 1.35351563 | 2.56347656 | -0.69433594 | 0.03003242  |
| 350  | 1.50292969 | -1.55273438 | 1.88964844 | 1.35351563 | 2.56347656 | -0.69433594 | 0.03003242  |
| 375  | 1.50292969 | -1.55273438 | 1.88964844 | 1.35351563 | 2.56347656 | -0.69433594 | 0.03003242  |
| 400  | 1.50292969 | -1.55273438 | 1.88964844 | 1.35351563 | 2.56347656 | -0.69433594 | 0.03003242  |
| 425  | 1.50292969 | -1.55273438 | 1.88964844 | 1.35351563 | 2.56347656 | -0.69433594 | 0.03003242  |
| 450  | 1.50292969 | -1.55273438 | 1.88964844 | 1.35351563 | 2.56347656 | -0.69433594 | 0.03003242  |
| 475  | 1.50292969 | -1.55273438 | 1.88964844 | 1.35351563 | 2.56347656 | -0.69433594 | 0.03003242  |
| 500  | 1.50292969 | -1.55273438 | 1.88964844 | 1.35351563 | 2.56347656 | -0.69433594 | 0.03003242  |

STEP A: Find (randomly) the initial population of  $2n$  members.

STEP B: Split the population (randomly) into  $n$  pairs.

STEP C: Make  $c$  crossovers and from each pair of parents take  $k$  children. Every bit of every child has  $P$  probability for a mutation.

STEP D: Find the new population  $2n+2k$  (parents+children).

STEP E: From the new population select the  $2n$  members with a lower value of  $f$  compared to the previous value of  $f$ .

STEP F: If the absolute value of  $f$  is  $< \epsilon$ , then STOP, otherwise go to STEP B.

The present GA is the basic GA and one can use more sophisticated schemata. In many cases, GAs find the global minimum of the minimization problem in question, in spite of its slow rate of convergence. In spite of the slow speed, the method is quite useful, since in most cases, especially in  $m$ -D filter design applications, the factorization does not have to be done in real time.

For the selection of the initial population, we have made also use of the following improved technique: We start off with  $2n$  random parents, carry out our GA once and then select the best two members of the population. This must be done  $n$  times. Thus, we can start from an ‘‘improved’’ initial population of (initial) parents.

### III. EXAMPLE

Consider the following two-dimensional (2-D) polynomial which can be, for example, the characteristic polynomial of a 2-D system:

$$A(z_1, z_2) = -1.2 + 1.1z_1 + z_1^2 + 1.5z_2 + 8z_2^2 + 2.8z_1z_2 + z_1z_2^2 + 1.7z_2^3 - 4z_2^4. \quad (5)$$

After the calculations, it is seen that the necessary and sufficient conditions for factorization into general factors given in [12] are not satisfied. So, the approximation of  $A(z_1, z_2)$  by a factorizable polynomial  $\tilde{A}(z_1, z_2)$  in the following form will be attempted:

$$\tilde{A}(z_1, z_2) = \prod_{i=1}^2 \left( z_1 + \sum_{i_2=1}^2 \tilde{a}_{i,i_2} z_2^{i_2} + \tilde{c}_i \right) \quad (6)$$

or in a simpler notation

$$\tilde{A}(z_1, z_2) = (z_1 + pz_2 + qz_2^2 + r)(z_1 + sz_2 + tz_2^2 + u). \quad (7)$$

Therefore, the minimum of  $\|A - \tilde{A}\|_2^2$  is considered, where

$$\begin{aligned} \|A - \tilde{A}\|_2^2 = & (-1.2 - ru)^2 + (1.1 - r - u)^2 \\ & + (1.5 - rs - pu)^2 + (2.8 - p - s)^2 \\ & + (8 - ps - rt - qu)^2 \\ & + (1 - q - t)^2 + (1.7 - qs - pt)^2 \\ & + (-4 - qt)^2. \end{aligned}$$

Using the Levenberg–Marquardt routine [15] the following solution is obtained:

$$\begin{aligned} p &= 1.57274 \\ q &= -1.55809 \\ r &= 1.71299 \\ s &= 1.48338 \\ t &= 2.75002 \\ u &= -0.190665 \end{aligned} \quad (8)$$

and

$$\|A - \tilde{A}\|_2^2 = 3.774775. \quad (9)$$

This is same as the result found in a previous publication [13].

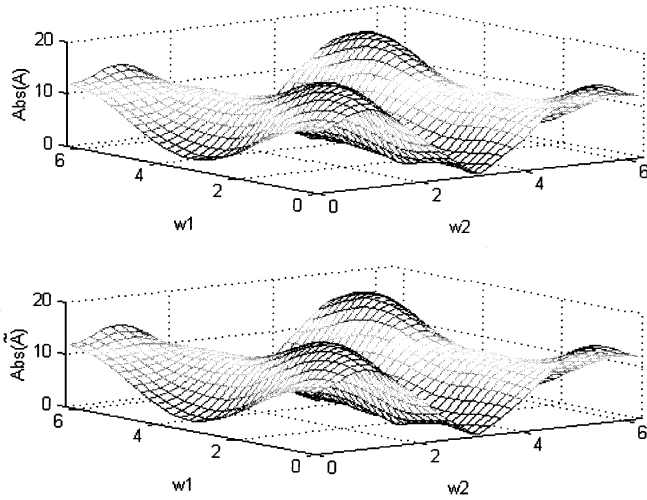


Fig. 4.  $Abs(A)$  and  $Abs(\tilde{A})$  versus  $w_1, w_2 : w_1 \in [0, 2\pi], w_2 \in [0, 2\pi]$ .

We now use the GA described in Section II with  $n = 5$ ,  $k = 4$ ,  $t = 12$ ,  $M = 6$ , and  $P = 0.01$ . Then, the following solution is obtained:

$$\begin{aligned} p &= 1.50293 \\ q &= -1.55273 \\ r &= 1.88965 \\ s &= 1.35352 \\ t &= 2.56348 \\ u &= -0.69434. \end{aligned} \quad (10)$$

The evolution of  $p, q, r, s, t, u$ , and their final convergence to the above values is shown in Fig. 2. Using these values for  $p, q, r, s, t$ , and  $u$  we obtain

$$f^2 = \left\| A - \tilde{A} \right\|_2^2 = 0.03003 \quad (11)$$

which is an improvement over the result of (9), i.e., [13]. In Table I, the evolution and the convergence of the coefficients  $p, q, r, s, t$ , and  $u$  as well as that of the optimum value of  $f$  in every generation are given. Convergence of the optimum value of  $f$  in every generation, as well as that of the mean value of  $f$  in every generation is shown in Fig. 3.

Hence

$$\begin{aligned} \tilde{A}(z_1, z_2) &= (z_1 + 1.50294z_2 - 1.55273z_2^2 + 1.88965) \\ &\quad \times (z_1 + 1.35352z_2 + 2.56348z_2^2 - 0.69434) \end{aligned}$$

or in an expanded form

$$\begin{aligned} \tilde{A}(z_1, z_2) &= z_1^2 + 7.95645z_2^2 + 1.01075z_1z_2 + 1.75108z_2^3 \\ &\quad - 3.98039z_1^4 + 2.85645z_1z_2 + 1.19531z_1 \\ &\quad + 1.51413z_2 - 1.31206. \end{aligned} \quad (12)$$

So, one can write  $A \cong \tilde{A}$ , i.e.

$$\begin{aligned} A(z_1, z_2) &= z_1^2 + 7.95645z_2^2 + 1.01075z_1z_2^2 + 1.75108z_2^3 \\ &\quad - 3.98039z_1^4 + 2.85645z_1z_2 + 1.19531z_1 \\ &\quad + 1.51413z_2 - 1.31206. \end{aligned}$$

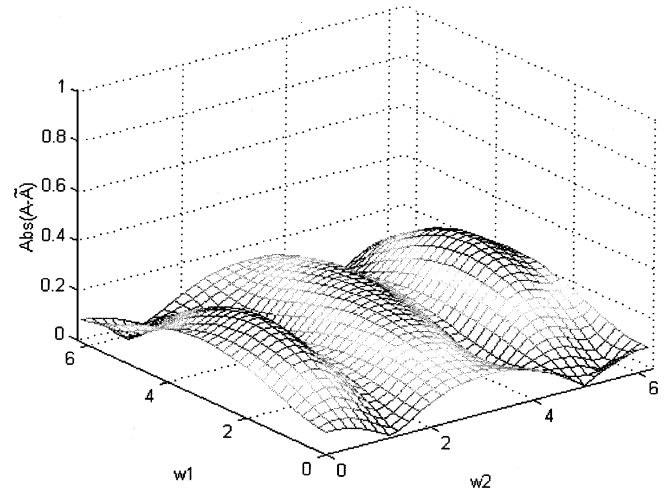


Fig. 5.  $Abs(A - \tilde{A})$  versus  $w_1, w_2 : w_1 \in [0, 2\pi], w_2 \in [0, 2\pi]$ .

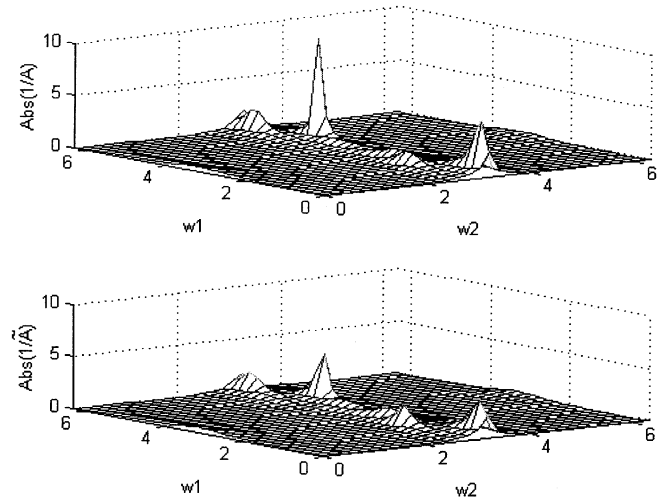


Fig. 6.  $Abs(1/A)$  and  $Abs(1/\tilde{A})$  versus  $w_1, w_2 : w_1 \in [0, 2\pi], w_2 \in [0, 2\pi]$ .

In Fig. 4, the amplitude of the transfer function  $A(z_1, z_2)$  given by (5) is sketched when  $z_1 = e^{jw_1}$ ,  $z_2 = e^{jw_2}$  and  $w_1 \in [0, 2\pi]$ ,  $w_2 \in [0, 2\pi]$ . In Fig. 4, the amplitude of the transfer function  $\tilde{A}(z_1, z_2)$  given by (12) is also sketched when  $z_1 = e^{jw_1}$ ,  $z_2 = e^{jw_2}$  and  $w_1 \in [0, 2\pi]$ ,  $w_2 \in [0, 2\pi]$ . In Fig. 5, the amplitude of the error  $A(z_1, z_2) - \tilde{A}(z_1, z_2)$  is sketched when  $z_1$  and  $z_2$  belong to the same domains.

In Figs. 6 and 7, the amplitude of the transfer functions,  $1/A(z_1, z_2)$ ,  $1/\tilde{A}(z_1, z_2)$  and  $1/A(z_1, z_2) - 1/\tilde{A}(z_1, z_2)$  are also sketched when  $z_1$  and  $z_2$  belong to the same domains. Changing the probability  $P$ , the number of the parents  $n$ , and the number of the children  $k$ , we may achieve better convergence speed. However, this analysis is not inside the scope of the paper, which is to demonstrate the application of GAs in the factorization of  $m$ -D polynomials.

#### IV. CONCLUSION

An  $m$ -D polynomial, which is not exactly factorizable into general  $m$ -D polynomials factors, is considered. This polynomial can be approximately factorized into general  $m$ -D factors in the sense of the least square approach. To minimize the

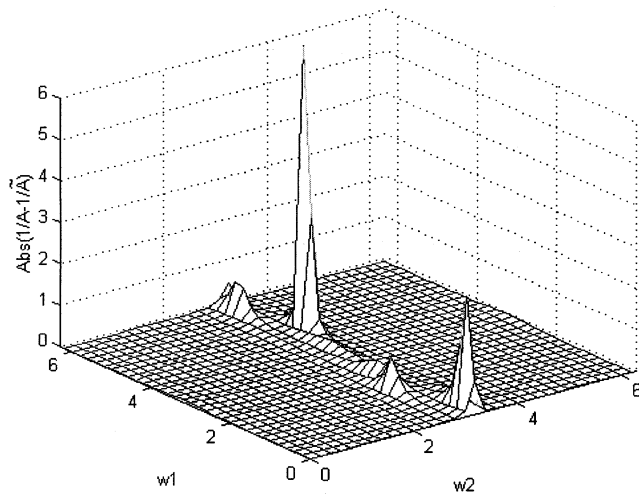


Fig. 7.  $Abs(1/\bar{A} - 1/\tilde{A})$  versus  $w_1, w_2 : w_1 \in [0, 2\pi], w_2 \in [0, 2\pi]$ .

least-square error, instead of numerical techniques or neural networks that in most cases find local minima, we use an appropriate GA. The methodology presented here can also be applied to many types of  $m$ -D factorization schemes, and could prove very useful in the design of  $m$ -D filters and  $m$ -D networks, since in most cases, an exact  $m$ -D factorization is impossible. The effectiveness and superiority of the present method over the previous ones has been illustrated through an example.

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**Ioannis F. Gonos** was born on May 8, 1970, in Artemisio, Arcadia, Greece. He received the diploma in electrical engineering and the Ph.D. degree from the National Technical University of Athens (NTUA), Athens, Greece, in 1993 and 2002, respectively.

He was a Teaching Assistant at the Greek Naval Academy and the Technological Education Institute of Athens from 1996 to 2001. He is currently a Researcher for the High-Voltage Laboratory of NTUA. His research interests concern grounding system, insulators, high voltages, modeling, and genetics algorithms.



**Nikos E. Mastorakis** (M'97–SM'99) received the B.Sc. and M.Sc. degrees in electrical engineering, and the Ph.D. degree in electrical engineering and computer science from the National Technical University of Athens, Athens, Greece, and the B.Sc. (Ptychion) degree in pure mathematics from the National University of Athens, Athens, Greece.

He has served as a Special Scientist in computers and electronics in the Hellenic (Greek) Army General Staff (1993–1994) and taught courses in the Electrical Engineering Department of the National Technical University of Athens (1994–1998). He has also served as a Visiting Professor at the School of Engineering, University of Exeter, Exeter, U.K., in 1998. He is currently a Professor and the Head of the Department of Computer Science at the Military Institutions of University Education (MIUE)–Hellenic Naval Academy, Piraeus, Greece. He is an active Researcher in applied mathematics and computer science (systems theory, control, optimization theory, algorithms theory, signal processing, robotics, computational intelligence). He has been the Editor of 33 books and the author of five. He has over 200 published papers in international books, journals, and conferences. He has been a Reviewer for 18 international journals and a Member of the Editorial Board of eight International Journals including *Advances in Computation: Theory and Practice* (New York: Nova), Editor of the international book series *Electrical and Computer Engineering, Mathematics and Computers in Science and Engineering* (Athens, Greece: World Scientific), the Editor-in-Chief of the *International Journal of Computer Research* ((New York: Nova) and *International Journal of Communications and Networking*. He has organized many international conferences, invited sessions and lectures.

Dr. Mastorakis is a Member of the World Scientific and Engineering Society, Greece, the New York Academy of Sciences, the Armed Forces Communications and Electronic Association, and the American Association for the Advancement of Science. He is a Registered Professional Electrical and Mechanical Engineer, and has received several awards (Royal Society of England, Hellenic National Research Foundation, etc) for his academic studies and his scientific research.



**M. N. S. Swamy** (S'59–M'62–SM'74–F'80–LF'01) received the B.Sc. (Hons.) degree in mathematics from Mysore University, Mysore, India, in 1954, the Diploma in electrical communication engineering from the Indian Institute of Science, Bangalore, India, in 1957, and the M.Sc. and Ph. D. degrees in electrical engineering from the University of Saskatchewan, Saskatoon, SK, Canada, in 1960 and 1963, respectively.

He is presently a Research Professor and the Director of the Center for Signal Processing and Communications in the Department of Electrical and Computer Engineering at Concordia University, Montreal, QC, Canada, where he has served as the Chair of the Department of Electrical Engineering from 1970 to 1977, and Dean of Engineering and Computer Science from 1977 to 1993. Since July 2001, he holds the Concordia Chair (Tier I) in Signal Processing. He has also taught in the Electrical Engineering Department of the Technical University of Nova Scotia, Halifax, NS, Canada, and the University of Calgary, Calgary, AB, Canada, as well as in the Department of Mathematics at the University of Saskatchewan. He has published extensively in the areas of number theory, circuits, systems and signal processing, and holds four patents. He is the author of two book chapters and three books: *Graphs, Networks and Algorithms* (New York: Wiley, 1981) *Graphs: Theory and Algorithms* (New York: Wiley, 1992), and *Switched Capacitor Filters: Theory, Analysis and Design* (Prentice-Hall International: London, U.K., 1995). A Russian translation of the first book was published by Mir Publishers, Moscow, Russia, in 1984, while a Chinese version was published by the Education Press, Beijing, China, in 1987.

Dr. Swamy is a Fellow of the Institute of Electrical Engineers (U.K.), the Engineering Institute of Canada, the Institution of Engineers (India), and the Institution of Electronic and Telecommunication Engineers (India). Presently, he is the President-Elect for the Circuits and Systems (CAS) Society. He has served the IEEE in various capacities such as the Vice President of the CAS Society in 1976, Vice-President (Publications) CAS Society 2001–2001, Editor-in-Chief of the IEEE TRANSACTIONS ON CIRCUITS AND SYSTEMS—I: FUNDAMENTAL THEORY AND APPLICATION during 1999–2001, Associate Editor of the IEEE TRANSACTIONS ON CIRCUITS AND SYSTEMS—I: FUNDAMENTAL THEORY AND APPLICATION during 1985–87, Program Chair for the 1973 IEEE CAS Symposium, General Chair for the 1984 IEEE CAS Symposium, Vice-Chair for the 1999 IEEE CAS Symposium, and a member of the Board of Governors of the CAS Society. He is the recipient of many IEEE CAS Society awards including the Education Award in 2000, Golden Jubilee Medal in 2000, and the 1986 Guillemin–Cauer Best Paper Award. He is a member of Micronet, a National Network of Centers of Excellence in Canada, and also its coordinator for Concordia University. In August 2001, he was awarded the Doctor of Science in Engineering (Honoris Causa) by Ansted University “In recognition of his exemplary contributions to the research in electrical and Computer Engineering and to Engineering Education, as well as his dedication to the promotion of Signal Processing and Communications Applications.”