

# Applying Genetic Algorithm to Modeling Nonlinear Transfer Functions

Sergey L. Loyka

**Abstract-** A genetic algorithm technique for the approximation of nonlinear transfer functions is proposed in this paper. It is shown that the GA approximation method gives better accuracy than the classical Chebyshev approximation, which is sometimes considered to be the best one on the minimax criterion. Application of this technique to behavioral-level simulation is also discussed.

**Keywords-** genetic algorithm, nonlinear transfer function, approximation, behavioral-level simulation

## I. INTRODUCTION

Extensive growth in radio communication systems, especially in mobile communications, under conditions of limited spectrum available places strict limits on equipment characteristics. Such equipment nonperfections as amplitude-to-amplitude (AM-AM) and amplitude-to-phase (AM-PM) conversions can severely distort the overall system performance [1-5]. Computer-aided nonlinear simulation tools allow a design engineer to improve and optimize the system performance. However, nonlinear simulation of digital communication systems presents new challenges: old simulation techniques and old parameters applied to analog systems are ill-suited for digital ones [3]. Such new standard parameters as power spectrum regrowth, adjacent-channel power ratio (ACPR) and error-vector magnitude (EVM) are used for the characterization of digital system equipment performance. In order to simulate these parameters, single or several-tone (up to 10) simulation techniques must be replaced by multiple-tone (up to  $10^3$ - $10^6$ ) ones.

Behavioral-level simulation techniques are most widely used for this purpose [1-8]. They require a representation (or approximation) of measured transfer functions. Various kinds of series expansion are usually used for this purpose. Most popular ones are Bessel function series, sine series and Chebyshev polynomials [2]. Polynomial approximation gives also some advantages for the simulation over wide frequency range [7-9]. In this paper, we consider the genetic algorithm technique of the series approximation of nonlinear transfer functions recently proposed [10], discuss its application to nonlinear behavioral-level simulation and some further development (especially improvement in computational efficiency).

In general, series expansion of the transfer function can be written in the following form:

$$K(x) = \sum_{k=1}^N a_k f_k(x) \quad (1)$$

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where  $K(x)$  – is the transfer function,  $f_k(x)$  – are basis functions,  $a_k$  – are expansion coefficients. Several methods can be used for calculation of the expansion coefficients [2, 6, 9, 11]. Here we discuss a new method of coefficient calculation, which uses the Genetic Algorithm (GA), and show that this method can achieve better accuracy as compared to traditional ones.

## II. FUNDAMENTALS OF THE GENETIC ALGORITHM

Rapid progress in the field of computer technology and numerical methods allows one to use the natural selection principles for engineering problems. Applying genetic algorithm to electromagnetics allows one to solve complex problems unattainable for conventional methods [12, 13]. In general, GA methods are very effective in finding an approximate global maxima in a high-dimension function domain [12]. GA methods differ from conventional ones in that:

- They operate on a group (or population) of trial solutions at the same time,
- They use stochastic operators (selection, crossover and mutation) to explore the solution domain in search of an optimal solution.

Generally, a genetic algorithm method performs the following main operations [12]:

1. Encode the solution parameters as genes. In our case, series coefficients are used as genes.
2. Create a string of the genes to form a chromosome,
3. Initialize a starting population,
4. Assign fitness values to individuals in the population.
5. Perform reproduction through the fitness-weighted selection of individuals from the population,
6. Perform recombination and mutation to produce members of the next generation.
7. Steps 4-6 are performed until termination criterion is met (either the number of generation or the fitness value are used as the criterion).

Although a binary-coding is used more frequently, we use here a real-coding in which real-value parameters are used as genes because physical-problem codings work better if they resemble the parameters they model [13]. Binary tournament selection strategy is used for the reproduction due to faster operation and the absence of convergence problems [13]. In our case, fitness function is defined to be the maximum difference between the transfer function and its approximation:

$$Fitness(a_1 \dots a_N) = \max \left( \left| f(x_i) - \sum_{k=1}^N a_k f_k(x_i) \right| \right) \quad (2)$$

where  $i = \overline{1, I}$ . The difference is estimated at sample points  $x_i$ . This fitness function is more appropriate for nonlinear analysis problems than, for example, the root-mean square difference.

The single-points crossover is used, in which a random point in parents' chromosomes is selected and the portions of the chromosomes after the selected point are exchanged. The probability of crossover  $p_{\text{cross}}=0.7$  is chosen, since it is reported to be the optimal value [13].

During the mutation operation, a gene in chromosome is changed with the probability  $p_{\text{mut}}=0.001-0.1$ . Higher probabilities give faster convergence in the initial phases. In general,  $p_{\text{mut}}$  corresponds to at most the mutation of one or two genes per chromosome and at least a few chromosome per generation [13]. For a real-coding, the gene mutation is a small random perturbation of its initial value:

$$\hat{g} = g + 0.5g_{\text{max}}G(0,1) \quad (3)$$

where  $\hat{g}$  and  $g$  – are gene values after and before the mutation correspondingly,  $g_{\text{max}}$  – the maximum value of the gene,  $G(0,1)$  – random Gaussian-distribution number with the mean value = 0 and the standard deviation = 1.

Elitist strategy is also employed (the best individual from the previous generation is inserted into the next one if the fitness value of the best individual in the next generation is lower than in the previous one).

The choice of the initial population may substantially influence the GA performance. Thus, some a priori knowledge should also be used.

Thus, using Genetic Algorithm we can evaluate the expansion coefficient  $a_k$  in a new way. Further we consider the Chebyshev polynomials as basis functions and apply GA to evaluate the expansion coefficients. However, the use of GA is not limited to this particular kind of basis functions – any other basis functions can also be used.

### III. APPLYING GENETIC ALGORITHM TO CHEBYSHEV POLYNOMIAL SERIES EXPANSION

Polynomials are often used as basis function for the nonlinear transfer function. The use of Chebyshev polynomials in this case gives many advantages due to exceptional properties of these polynomials [11]. Usually, the expansion coefficients are calculated using the orthogonality of the Chebyshev polynomials:

$$a_k = \frac{2}{J} \sum_{j=1}^J f(t_j)T_k(t_j) \quad (4)$$

where  $t_j$  – are zeros of the Chebyshev polynomials,  $T_k$  – is  $k$ -th order Chebyshev polynomial. Integral formulation can also be used for this purpose.

It is a common belief that Chebyshev polynomials give the best polynomial approximation to a given function on minimax criterion [11]. Here we show that GA method allows one to build a polynomial approximation better than Chebyshev one on the minimax criterion. For this purpose,

we have used an instantaneous transfer characteristic of a single-stage microwave amplifier, which has been calculated from the measured envelope transfer characteristic using the integral equation approach [14-16]. Further, we have calculated the expansion coefficients  $a_k$  using the conventional approach (eq.(4)) and the GA method described above. Since the performance of the genetic algorithm depends substantially on the initial population generated, we used some physical observations in order to improve the algorithm performance. In particular, the normalized transfer function was used, such that  $a_1=1$ . We have also used the fact that higher-order coefficient are smaller than lower-order ones. Thus, the following maximum coefficient values have been used:

$$a_{k,\text{max}} = 2^{-k} \quad (5)$$

Some particular results are as follows. For  $N=5$ , the maximum error for the conventional approach is  $\epsilon_{\text{conv}}=0.034$ , and for the GA method is  $\epsilon_{\text{GA}}=0.029$ . For  $N=7$ ,  $\epsilon_{\text{conv}}=0.036$  and  $\epsilon_{\text{GA}}=0.024$ . And for  $N=15$ ,  $\epsilon_{\text{conv}}=0.012$  and  $\epsilon_{\text{GA}}=0.0093$ . Thus, the main result is that the GA methods give the maximum error between the transfer function and its approximation in average 1.2-1.5 times lower than the conventional method.

Fig. 1 shows the approximation error for the conventional method and for the GA method applied to the approximation of a hyperbolic tangent function (this function is frequently used in nonlinear simulation of active circuitry). It can be seen from this figure that the approximation curve peaks for the classical Chebyshev series are not of equal amplitude. It means that this approximation is not optimal on the minimax criterion [11] and may be further improved. At the same time, all peaks of the GA method curve are almost equal, indicating that this approximation is very close to the optimal one.

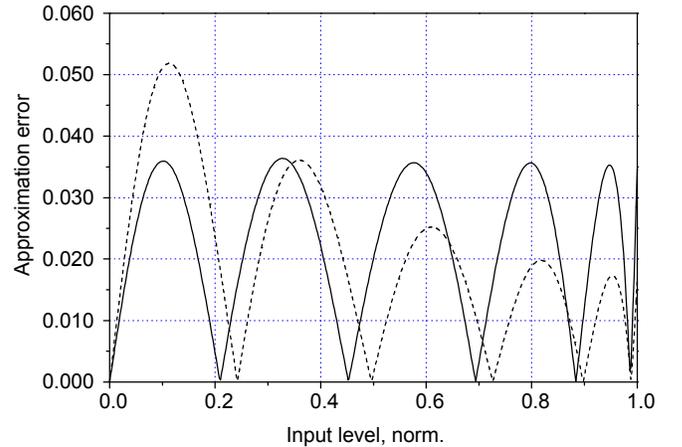


Figure 1. Approximation error for hyperbolic tangent versus normalized input level (dashed line – conventional Chebyshev polynomial series, solid line – the GA coefficient evaluation method,  $N=9$  for both methods).

#### IV. GENETIC ALGORITHM APPROXIMATION AND NONLINEAR BEHAVIORAL-LEVEL SIMULATION

As it was already mentioned above, behavioral-level simulations techniques require some representation or approximation of transfer functions. Due to nonlinear behavior of a circuit under simulation, approximation of its transfer characteristic is usually a very difficult task.

First, the envelope transfer characteristics (AM-AM and AM-PM) are usually measured (using network analyzer in power sweep mode or other appropriate equipment) or simulated at the circuit level. In the latter case, harmonic balance simulator is more appropriate tool because transient-mode simulation (using SPICE, for example) has rather small dynamic range [3], requires much computational resources (very time-consuming) and reveals large phase errors [17]. In any case, measured or simulated AM-AM or AM-PM characteristics includes measurement/simulation noise:

$$y(x) = y_{real}(x) + \epsilon(x) \quad (6)$$

where  $y(x)$  – is the measured (or simulated) characteristic  $y_{real}(x)$  – is the “real” characteristic (without any noise or inaccuracy), and  $\epsilon(x)$  – measurement (simulation) inaccuracy (noise). Consequently, an approximation of  $y(x)$  is a specific optimization problem: we need to approximate  $y_{real}(x)$  as accurate as possible and, at the same time, we need to suppress  $\epsilon(x)$  as much as possible. The first part of optimization requires high-order approximation (the more terms we use, the more accurate we approximate  $y_{real}(x)$ ). The second part requires low-order approximation (the lower order we use, the more we suppress  $\epsilon(x)$  because it usually contains higher-order components). Obviously, there is some optimum. Unfortunately, there is no any mathematical technique at the moment which would allow to calculate this optimum. Now we can see why the GA method is so important: it allows to calculate the best possible approximation (the best approximation of  $y_{real}(x)$ ) for a given approximation order (we keep it rather small to suppress  $\epsilon(x)$ ). Fig. 2 illustrates this situation. As we can see from this figure, the approximation error decreases and the noise contribution increases as the number of terms increases. The optimum number in this case is about 50.

Substantial difference between measured and simulated characteristics is that simulation noise is usually smaller than measurement one. Fig. 3 and 4 illustrate measured and simulated correspondingly AM-PM characteristic of a microwave amplifier (different amplifiers were used for Fig.3 and 4). As we can see, the measurement noise (ripples) is much higher. It has its impact on the modeling process: a procedure of noise filtering out can be neglected for HB-simulated characteristics, but it is a very important part of the modeling for measured characteristics. As a consequence, splines, which provide better approximation accuracy, can

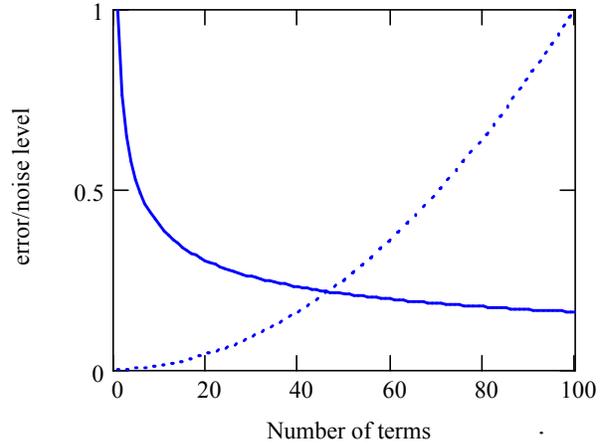


Figure 2. Error of approximation (solid line) and noise contribution (dot line) versus approximation order (number of terms in a series).

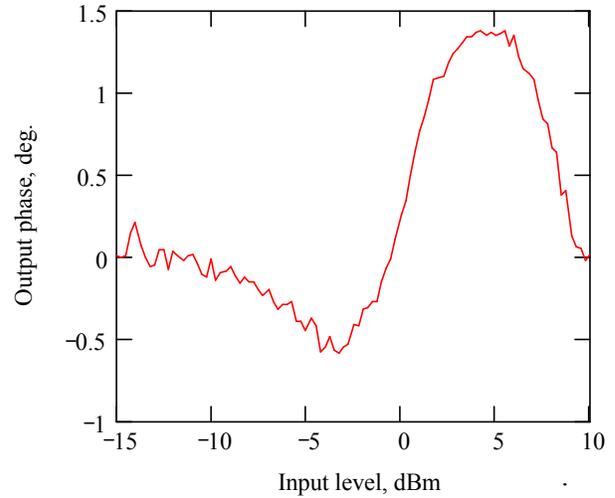


Figure 3. Measured AM-PM characteristic of a microwave amplifier

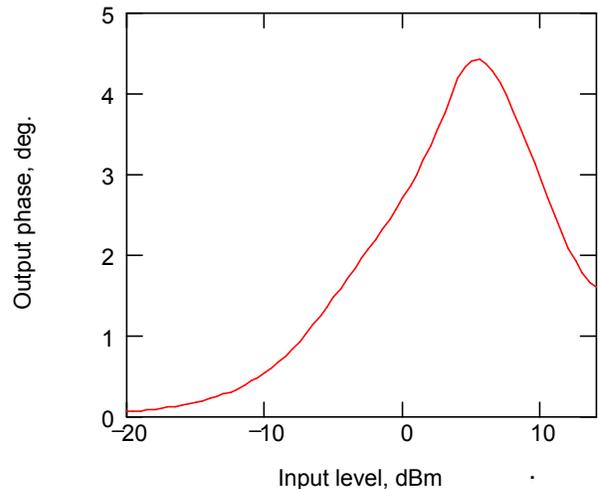


Figure 4. HB-simulated AM-PM characteristic of a microwave amplifier

be used for HB-simulated characteristics but not for measured ones. The GA method seems to be a very efficient tool for noise filtering out.

We should note that extreme care must be taken during measurement or simulation of AM-AM and AM-PM characteristics since small inaccuracies in these characteristics may result in very large inaccuracies of the simulation results (IMP levels, for example). The same is also true for the approximation of characteristics.

## V. CONCLUSION

The use of the genetic algorithm for the evaluation of expansion coefficients as applied to the nonlinear transfer function approximation has been considered in this paper. It is a robust approach that gives many advantages, including optimization possibility, improvement in the approximation accuracy, the possibility of using various approximation criterion etc. Improvement in the approximation accuracy by 1.2-1.5 times as compared to the conventional Chebyshev polynomials approach, which is considered to be the best polynomial approximation, are possible by using the GA method. It seems that the GA method gives the best polynomial approximation ever possible.

Further improvement of computational efficiency (convergence speed) of the proposed technique is possible in several ways:

- the coefficients calculated by the classical Chebyshev approximation method should be included in the initial population giving a good starting point for the directed random search performed by GA,
- the initial population genes are generated using the Gaussian distribution with the mean equal to the classical Chebyshev coefficients, and the standard deviation equal to 10 – 50% of the mean value,
- uniform crossover should be used together with the gradient descent method applied to each population member (faster convergence is achieved in this way).

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