

# Method for nonlinear transfer function approximation

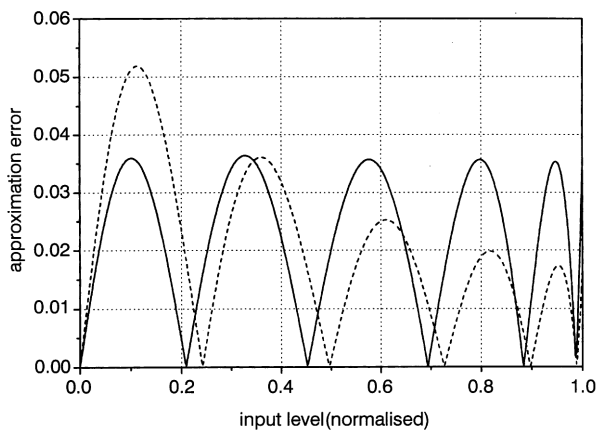
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The application of the genetic algorithm to the approximation of nonlinear transfer functions is considered. It is shown that the GA approximation method gives better accuracy than the classical Chebyshev approximation, which is sometimes considered to be the best available method for the minimax criterion. Other advantages of the proposed method include the ability to carry out a global search for the optimal solution and easy implementation of various approximation criteria.

**Introduction:** Behavioural-level simulation techniques are currently very popular in the field of modelling and the simulation of mobile communication systems [1, 2]. They require a representation (or approximation) of measured or simulated transfer functions of nonlinear stages (amplifiers, mixers, etc.). Analytical expressions as well as series expansions are usually used for this purpose. The latter frequently provide better approximation accuracy. The most popular series are Bessel function series, sine series and Chebyshev polynomial series [2]. The polynomial approximation also gives some advantages for the simulation over a wide frequency range [3]. In general, series expansions of the transfer function can be written in the following form:

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

where  $K(x)$  is the transfer function,  $f_k(x)$  represents the basis functions, and  $a_k$  represents the expansion coefficients. Several methods can be used to calculate the expansion coefficients [2–4]. The evaluation of the coefficients is simpler for orthogonal basis functions. However, non-orthogonal basis functions can also be used (using, for example, the least-squares curve fitting technique) [2]. In this Letter we propose a new method for coefficient calculation, which uses the genetic algorithm (GA), and show that this method can achieve better accuracy than traditional methods.



**Fig. 1** Approximation error for hyperbolic tangent against normalised input level

--- conventional Chebyshev polynomial series  
 — GA coefficient evaluation  
 $N = 9$  for both methods

**Applying genetic algorithm to expansion of nonlinear transfer functions:** The genetic algorithm appears to be a very effective tool for many kinds of problems [5–7]. GA methods differ from conventional methods in that they operate on a group (or population) of trial solutions at the same time, and they use stochastic operators (selection, crossover and mutation) to explore the solution domain in searching for an optimal solution. Generally, a genetic algorithm method performs the following main operations [5–7]:

- (i) Encode the solution parameters as genes, and create a string of the genes to form a chromosome. In our case, series coefficients are used as genes.
- (ii) Generate a starting population.
- (iii) Assign fitness values to individuals in the population.

- (iv) Perform reproduction through the fitness-weighted selection of individuals from the population.
- (v) Perform recombination and mutation to produce members of the next generation.
- (vi) Steps (iv)–(v) are performed until the termination criterion is met (either the number of generation or the fitness value are used as the criterion).

Although binary coding is used more frequently, we use here real coding in which real-value parameters are used as genes, because physical-problem codings work better if they resemble the parameters they model [6]. A binary tournament selection strategy is used for the reproduction due to faster operation and the absence of convergence problems [6]. In our case, the fitness function is defined to be the maximum difference between the transfer function and its approximation:

$$\text{fitness}(a_1 \dots a_N) = \max_{i = \overline{1, I}} \left( \left| f(x_i) - \sum_{k=1}^N a_k f_k(x_i) \right| \right) \quad (2)$$

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. Single-point crossover is used, in which a random point in the parents' chromosomes is selected and the portions of the chromosomes beyond the selected point are exchanged. The probability of crossover  $p_{\text{cross}} = 0.7$  is chosen, since it has been reported to be the optimal value [6]. During the mutation operation, a gene in the chromosome is changed with the probability  $p_{\text{mut}} = 0.001\text{--}0.1$ . 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 chromosomes per generation [6]. For a real coding, the gene mutation is a small random perturbation of its initial value:

$$\hat{g} = g + 0.1g_{\text{max}}G(0, 1) \quad (3)$$

where  $\hat{g}$  and  $g$  represent the gene values after and before the mutation, respectively,  $g_{\text{max}}$  the maximum value of the gene, and  $G(0, 1)$  a random Gaussian-distribution number with mean value = 0 and standard deviation = 1. An elitist strategy is also employed (the best individual from the previous generation is inserted into the next generation if the fitness value of the best individual in the next generation is lower than in the previous generation). The choice of the initial population may substantially influence the GA performance. Therefore, some *a priori* knowledge should also be used.

Thus, by using the genetic algorithm we can evaluate the expansion coefficient  $a_k$  in a new way. Furthermore we consider the Chebyshev polynomials as basis functions and apply a GA to evaluate the expansion coefficients. However, the use of a GA is not limited to this particular kind of basis function: any other basis functions can also be used (including non-orthogonal).

**Chebyshev polynomial expansion:** Polynomials are often used as basis functions. The use of Chebyshev polynomials for the nonlinear transfer function approximation has many advantages due to the exceptional properties of these polynomials [4]. 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  $t_j$  represents the zeros of the Chebyshev polynomials, and  $T_k$  a  $k$ th order Chebyshev polynomial. An integral formulation can also be used for this purpose.

It is commonly believed that Chebyshev polynomials give the best polynomial approximation to a given function for the minimax criterion [4]. This is true when the approximation error is a polynomial. Here we show that the GA method enables a better polynomial approximation to be obtained than the Chebyshev polynomial for the minimax criterion. For this purpose, we used the instantaneous transfer characteristic of a single-stage microwave amplifier, which has been calculated from the measured first-harmonic transfer characteristic using the integral equation approach [8]. We also calculated the expansion coefficients  $a_k$  using the conventional approach (eqn. 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, we used the fact that higher-order coefficients are smaller than lower-order coefficients. Thus, the following maximum coefficient values were used:

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

Some particular results are as follows. For  $N = 4$ , the maximum error for the conventional approach is  $\epsilon_{conv} = 0.034$  and for the GA method is  $\epsilon_{GA} = 0.029$ . For  $N = 6$ ,  $\epsilon_{conv} = 0.036$  and  $\epsilon_{GA} = 0.024$ . For  $N = 14$ ,  $\epsilon_{conv} = 0.012$  and  $\epsilon_{GA} = 0.0093$ . Thus, the main result is that the GA method gives the maximum difference between the transfer function and its approximation which is on average 1.2–1.5 times smaller than for 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 the 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. This means that the approximation is not optimal for the minimax criterion [4] 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 optimal.

Further optimisation of the GA method is possible in several ways:

- (i) 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
- (ii) 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
- (iii) more advanced forms of the genetic algorithm can also be used.

*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 Letter. It is a robust approach that has many advantages, including optimisation

possibilities, global searching for the optimal solution, improvement in the approximation accuracy, easy implementation of various approximation criteria, etc. We should also note that in general the GA method operates well for almost every kind of transfer function, without any strict requirements (continuous or bounded derivatives etc.). Improvement in the approximation accuracy by 1.2–1.5 times when compared to the conventional Chebyshev polynomial approach, which is generally considered to be the best polynomial approximation, is possible by using the GA method. Hence, it seems that this method can potentially give the best possible polynomial approximation.

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