Genetic Algorithm Based Diode Model Parameters Extraction

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Abstract. In this paper, a genetic-based algorithm is proposed and implemented to extract diode circuit model parameters. Saturation current, ideality factor, and series resistance are extracted without a need for initial conditions. The proposed technique is found to be robust and capable to reach a solution that is characterized to be global and accurate. Compared with existing conventional techniques, the proposed one shows superior performance in terms of accuracy and being generic and applicable to extract parameters of other devices. The proposed technique performance has been tested using theoretical data, and used to extract real device parameters from its measured I-V characteristics.

Keywords: Diode, Extraction, Parameters, Genetic algorithms.

I. Introduction

Recently, circuit design tools have become indispensable in circuit design. Accurate circuit simulation is dependent on both the validity of the device model and the accuracy of the values used as model parameters. Therefore, accurate extraction of optimum set of device model parameter values is essential for modeling and the simulation of electronic devices as well as for monitoring of process parameters and device structure development [1].

Diode is one of the basic devices in electronics. Many other electronic devices are basically variations of it. For example, light emitting diodes, laser diodes, solar cells, Schottky diodes, photo diodes, etc., are all a variation of the simple conventional p-n junction diode. Therefore, developing techniques to extract the circuit model parameters for the basic p-n junction will serve all other device variations.

Most of optimization techniques reported in the literature to extract the diode parameters are based on local search techniques, such as the Levenberg-Marquardt (LM) method, which is used by HSPICE for parameter extraction [1], least squares method, integration method, minimizing area method [2-4].

Conventional optimization techniques are often subject to becoming trapped in local minimum, leading to sub-optimal parameter values. The distinction between local and global search for optimization techniques is that the local techniques produce results that are highly dependent on the starting point or initial guess, while global methods are largely independent of the initial conditions. This tight coupling enables the local methods to take advantage of the solution-space characteristics, resulting in relatively fast convergence to local solutions. However, the tight solution-space coupling also places constrains on the solution domain, such as differentiability and continuity. These constrains can be hard or even impossible to deal with in practice. The global techniques, on the other hand, are largely independent of the place of the initial conditions and place few constraints on the solution domain. This absence of constraints means that the global methods are much more robust and much better at dealing with solution space having discontinuities, constraints parameters, and with many potential local solutions. The downside to the global method is that it does not take advantage of local solution-space characteristics, during the search process, resulting in generally slower convergence than the local techniques. However, in most cases of parameter values extraction, convergence rate is often not nearly important as getting the best and global solution. Of the global techniques, genetic algorithms (GAs) are particularly well suited and are considerably more efficient, and provide much faster convergence. GAs can readily handle discontinuous and non-differentiable functions and well suited for constrained problem. Some work has been done in using GAs to extract the material parameters of compound structures [5], or to extract model parameters of some electronic devices. However, none of them deals with diode model parameters.

In this paper, GA is proposed to extract the diode circuit model parameters values. We wrote our own code in a generic way to be flexible and applicable to extract the parameters values for any other two terminal devices. The performance has been tested and the effect of string length and its uniformity is studied.

The paper is organized into five sections. After the introduction, the second section presents an overview of GAs. The third section focuses on the implementation of GAs to extract diode parameters. In the fourth section, the results of testing the validity of the technique and to extract the diode parameters from measured I-V characteristics are presented. Finally, conclusion and future work are presented in the fifth section.

II. Overview of Genetic Algorithms

The concept of genetic algorithms, first formalized by Holland in 1975, and extended to functional optimization by De Jong, involves the use of optimization search

strategies patterned after Darwinian notion of natural selection and evolution [6]. During a GA optimization, a set of trial solutions, or individuals, is chosen, and then evolved towards an optimal solution, under the selective pressure of the cost (fitness or objective) function.

GA is a stochastic optimization algorithm that has the following basic properties [7]:
- It works with a binary encoding of the parameter set, not the parameters themselves.
- It searches from a population of points, not from a single point.
- It uses only the cost function values in optimization, therefore no derivatives or other auxiliary knowledge are needed.
- It uses probabilistic transition rules by stochastic operands, and not deterministic rules.

The scope of GA is global, as they use a population of binary strings (called chromosomes) to explore the search space. Each chromosome encodes a point in the parameter space, i.e. a possible solution of the problem solved. These binary strings are evaluated through a "fitness" (sometimes called objective or cost function) which contains all the information about the problem. Evaluation means that the performance of each possible solution is determined and the fitness value of the corresponding chromosome is calculated accordingly. The better the solution encoded by the chromosome, the higher the fitness. The GA then tries to improve the fitness of the population by combining information contained in high fitness chromosomes.

The search evolves through the subsequent generations of binary chromosomes. Each generation produces the next one by means of probabilistic operators. These operators ensure that the best members of the population will survive, and their information content is preserved and combined to generate even better offspring. In the simplest GA, a new generation is created by three basic operators. First, chromosomes are selected for reproduction with a probability proportional to their fitness. This simple mechanism assures that the most successful ones will produce the next generation. Then the selected chromosomes are mated randomly and each couple produces two children by crossover and mutation reproduction operators. Crossover means exchange of substrings between two parent chromosomes combining valuable information of the parents. The simplest crossover operator is the one-point crossover where first crossing site is selected with uniform probability over the chromosome length, then the corresponding strings are exchanged.

Mutation maintains diversity in the string population by flipping an arbitrary bit in the chromosomes with a given probability that is generally low. This operator results in a random walk in the parameter space and introduces new information into the evolution process which might have been lost with premature convergence of the algorithm. The link between the algorithm and a particular problem is the parameter encoding and the evaluation function [8].

The algorithm can be terminated after a prespecified number of generations and then the quality of the best members of the population are tested against the problem definition. If no acceptable solutions are found, the GA may be restarted or fresh search is initiated.

Implementation of GA can be summarized in the following steps:

1. **Encoding solution variables:** The population size and the chromosome string length are selected. Large population size is preferable to avoid premature convergence. Typically, 30-100 population size is used. String length depends on the accuracy requirements. A chromosome string (solution) is composed of several genes (variables). String can be divided between variables uniformly or non-uniformly. Any encoding technique can be used but binary encoding is convenient and the one mostly used.
2. **Generating initial population:** A random number generation technique is used to produce the first generation with the specified population size and chromosome length.
3. **Defining problem cost function:** The suitability (fitness) of each solution from any generation is determined by the cost (object) function. For each problem this function should be defined. It is used as a deterministic tool to evaluate each chromosome (solution). The optimization problem may be a minimization or a maximization type.
4. **Evaluating cost function:** This determines the fitness score attached to each chromosome (solution). The higher this score, the greater is the chance of the chromosome (solution) being selected for reproduction.
5. **Applying selection for reproduction:** Methods of selecting chromosomes for reproduction are numerous and include roulette wheel sampling, stochastic universal sampling, tournament selection, rank selection, etc. [9].
6. **Applying selection for crossover:** Before applying crossover operator, a selection has to be applied to determine the parent chromosomes. Usually, this selection is implemented through using the roulette wheel selection method with a typical probability 0.6-0.95. High crossover probability ensures rapid searching.
7. **Applying crossover operator:** Each pair of parents is used to generate two children bearing some of their parents' useful characteristics. They are expected to be more fit than their parents. A number of variations of crossover are in use such as single-point, multi-point or uniform crossover. In single crossover where a binary encoding is used, a locus (bit location) is randomly chosen. Bits after that locus are exchanged between two chromosomes to create two offspring (new solutions).
8. **Applying selection for mutation:** Bits which undergo mutation have to be selected randomly using a very small probability attached to each bit location. Typically, the probability of mutation is in the range of 0.01-0.1.
9. **Applying mutation operator:** Bits selected for mutation are flipped (0 to 1 or 1 to 0) to ensure that new areas of the solution are explored.

10. **Applying termination criteria:** the algorithm either stops or restarts again from step 4 (evaluating cost function of the new generation). It stops if the termination criterion is met. The termination criterion can be either completing a large number of generations (iterations), or obtaining a cost (fitness) value within a predefined tolerance.

III. Applying GAs to Extract Parameters

The diode circuit model is based on the I-V relationship which can be described by the general equation:

$$I = Is\ [e^{(V-IRs)/nVT} - 1] + [(V-IRs)/Rsh] \tag{1}$$

where I: is the diode current, Is: the saturation current, V: the applied bias voltage, Rs: the series resistance, n: the ideality factor, VT: the thermal voltage (0.026 Volt at room temperature), and Rsh: the shunt resistance.

The diode is modeled by an equivalent circuit which consists of an ideal diode with saturation current (Is) and ideality factor (n). The ideal diode is shunted by a resistance Rsh and both are connected to a series resistance (Rs). The four parameters (Is, n, Rs, Rsh) are circuit parameters, but they reflect the physical parameters and the operational mechanisms inside the p-n junction. Normally, good diodes have a very high shunt resistance (Rsh), therefore the second term in Eq. (1) will be very small. In forward bias region, the first term will dominate and the equation can be reduced to:

$$I = Is\ e^{(V-IRs)/nVT} \tag{2}$$

This equation has the three parameters Is, n and Rs. Most researchers have employed calculus-based techniques (deterministic techniques) to extract the three parameters from the measured I-V characteristics [10]. Looking at these techniques with their need for a suitable initial conditions and the possibility of being trapped to a local solution have motivated us to propose using GA to extract these parameters.

To implement GA to extract the three parameters, the coded algorithm was executed using Pentium 4 with 1.7 GHz speed, and it involves the following decisions:
1. A binary encoding is used with population size of 40 chromosomes per generation and 30 bits per chromosome. Each of the three parameters (Is, n and Rs) is represented uniformly (with 10 bits). In some cases, shorter or non-uniform chromosomes are used to test the quality of parameter extraction.
2. The cost function is chosen as follows:
   - The error in all points squared and summed per each chromosome.
   - The total error per generation is calculated by summing all chromosomes errors. The average error per each generation is calculated by dividing the total error by the number of chromosomes.

- The cost is calculated by dividing the error per chromosome with the average error, and this value represents the final cost for each chromosome.
- The cost function is minimized; i.e. the best chromosome in each population is the one with minimum cost.

3. Roulette wheel sampling is used as a selection technique for reproduction and crossover. Crossover and mutation probabilities are taken to be 0.95 and 0.01, respectively.
4. The number of generations is made very high (20,000) to allow enough space to get the global optimum solution. This will increase the execution time. The CPU time used by each generation is estimated to about 6.5 m seconds.
5. The best chromosome in each generation (which has the minimum cost function) is recorded and compared throughout all generations. The final solution (chromosome) is the best one obtained during the entire process. This will keep the best solutions from being lost in new generations.

IV. Results and Discussions

To verify the validity of the technique, a theoretical I-V data is generated by assuming values for Is, n and Rs. The GA is used to extract the values of these parameters. Table 1 shows three sets of parameters used to generate 40 points, and the corresponding extracted parameters with their costs. Each parameter is encoded using 10 bits; i.e. (10:10:10), resulting in 30 bits per chromosome. Figure 1 shows the I-V curve for each set using the assumed values and the extracted ones. The result for each set shows a close matching with small deviations between theoretical and extracted parameters. Cost value, which represents the best chromosome error divided by the average error in each generation, reflects the quality of parameters extraction.

Table 1. Testing the algorithm with theoretical data

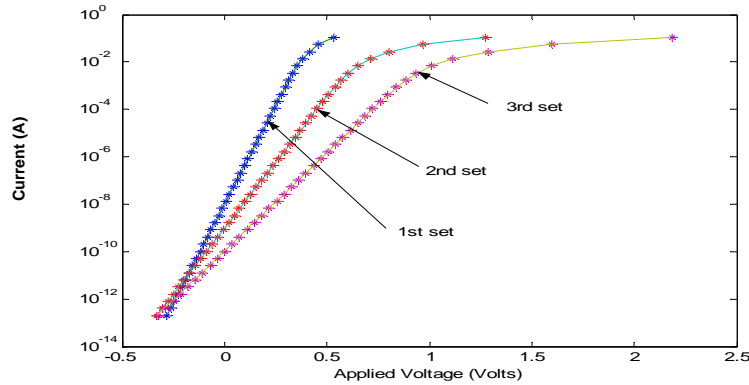| Set	Theoretical	Extracted	Cost %
1	Is =1e-8 A n =1 Rs =1 Ohm	9.9797e-9 A 1 0.9971 Ohm	3.5218e-5 %
2	Is =1e-9 A n = 1.5 Rs = 5 Ohm	9.8742e-10 A 1.5015 4.9853 Ohm	2.5172e-3 %
3	Is =1e-10 A n = 2 Rs =10 Ohm	1.0774e-10 A 2.0176 9.9120 Ohm	5.4605e-2 %

Fig. 1. I-V curve for each set using theoretical (**) and extracted data (–).

By comparing the extracted parameters with the corresponding theoretical ones, it is found that the highest contribution to the error comes from the deviation in the saturation current (Is). While the maximum deviation in other parameters is 0.88%, saturation current is found to be the most sensitive parameter with deviations of 0.2% (set: 1), 1.26% (set: 2), and 7% (set: 3). This increase in the error has impacted the cost and caused its increase.

The high sensitivity of Is could be explained by its wider range compared to the other parameters. The encoding step in GA involves defining a range of maximum and minimum real values for each parameter. For example, if Is varies between 10^{-7} A and 10^{-11} A, and using a fixed gene length (10 bits), this results in a resolution of $9.765*10^{-11}$ A. As the extracted value gets smaller and approaches the resolution value, the error will increase. To keep the error less than 1%, the best approach is to keep the resolution 100 times smaller than the minimum expected extracted values. This can be achieved easily by selecting the gene length (k) using the following formula:

$$[Is_{(max)} - Is_{(min)}] / 2^k < Is/100 \tag{3}$$

In order to investigate the effect of string length, the extraction of the three parameters is repeated for the second set using the same size of population but with chromosomes of 18 bits (i.e. 6:6:6). Table 2 shows the results for the two cases and Fig. (2) shows the corresponding I-V curves plots.

The impact of reducing the genes lengths is clear on errors and consequently on the cost value, and supports our conclusion about the need to choose the gene length carefully in order to obtain good parameter extraction results. As seen, although using 6 bits to encode the ideality factor (n), and series resistance (Rs) is still acceptable, it produces poor result for Is.

Bandar A. Almashary

Table 2. Effect of string length on the cost

Case	Parameter values	Cost %
Theoretical	Is = 1e-9 A n = 1.5 Rs = 5 Ohm	-
Extracted with (10:10:10) string	9.8742e-10 A 1.5015 4.9853 Ohm	0.00251 %
Extracted with (6:6:6) string	1.5971e-9 A 1.5238 5.0794 Ohm	1.12 %

The effect of non-uniform encoding of parameters per string is investigated using chromosomes with 24 bits, but with different substring (genes) distribution. It should be noted that the order of parameters in each string is the same (Is:n:Rs). Table 3 summarizes the results and Fig. (3) shows the corresponding I-V curves for all cases.

This test demonstrates the importance of allocating enough bits for each gene to extract accurately its corresponding parameter. For the saturation current, the deviation increases significantly (from 1.25% to 12.5%) when its gene length is reduced from 10 to 8 bits, and produces a very poor result when its gene length is reduced to five. For ideality factor and series resistance, both show good extracted values with shorter genes due to the smaller range in the boundaries of their values.
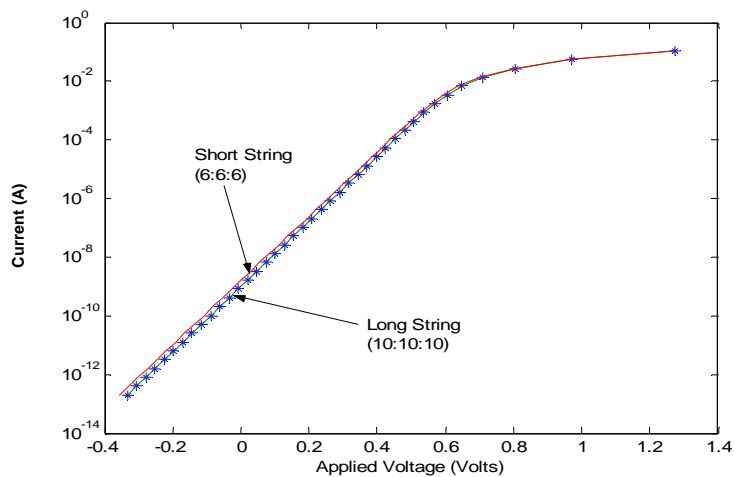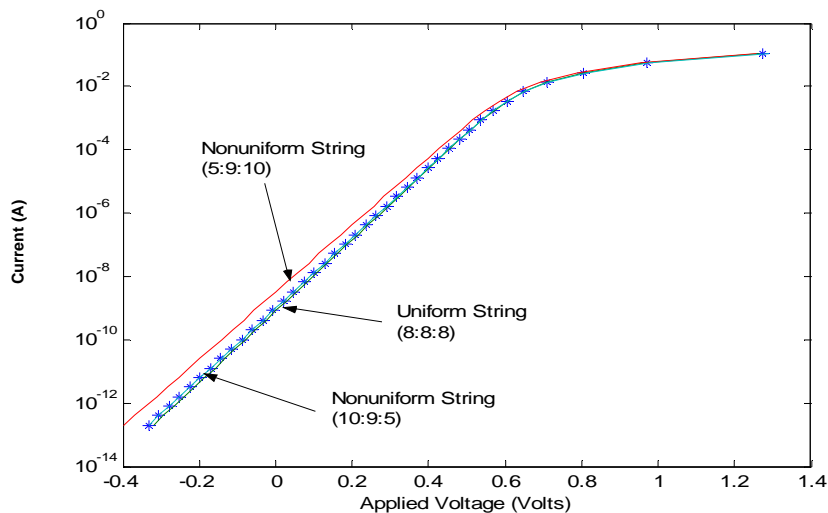

Fig. 2. The I-V curves for the theoretical (**) and extracted (--) cases listed in Table 2.

Table 3. Effect of nonuniform strings on cost

Case	Parameter values	Cost %
Theoretical	Is =1e-9 A n = 1.5 Rs = 5 Ohm	-
Extracted with (8:8:8) string	7.9424e-10 A 1.4824 4.9412 Ohm	0.29 %
Extracted with (5:9:10) string	3.2355e-9 A 1.5734 4.9658 Ohm	7.68 %
Extracted with (10:9:5) string	9.8742e-10 A 1.5029 5.1613	0.0908 %

Fig. 3. The I-V curves for theoretical (**) and extracted (--) case slisted in Table 3.

The proposed technique is used to extract the three parameters from a measured I-V characteristics of a silicon diode using 29 points measured in the forward region. A population size of 40 chromosomes and a uniform string of 30 bits were used; i.e. (10:10:10). The extracted parameters values are as follows: Is = 7.9194e-10 A, n = 1.6041, and Rs = 0.8602 Ohm, with solution cost equals to 0.0914%. The extracted parameters are used to plot the I-V curve as shown in Fig. 4, and the measured I-V curve is plotted on the same figure.

The good matching between the two curves and the low cost value demonstrate the good quality of the extraction process and the accuracy of the extracted parameters. The deviation between the two curves at small forward current values (in the nA range) could

be attributed to the inaccuracy in the measurement of the current at this range, or due to the effect of neglecting the shunt resistance (Rsh) in our model.

Since the I-V curve of the diode is used to extract the three circuit model parameters, our approach can be extended to other two terminal devices. All what is needed is to have a mathematical model (or an equation) which relates its terminal current with the applied voltage to use it in calculating the cost. For devices with more than three parameters, an extra gene should be added to the chromosome (string) to account for each extra parameter.
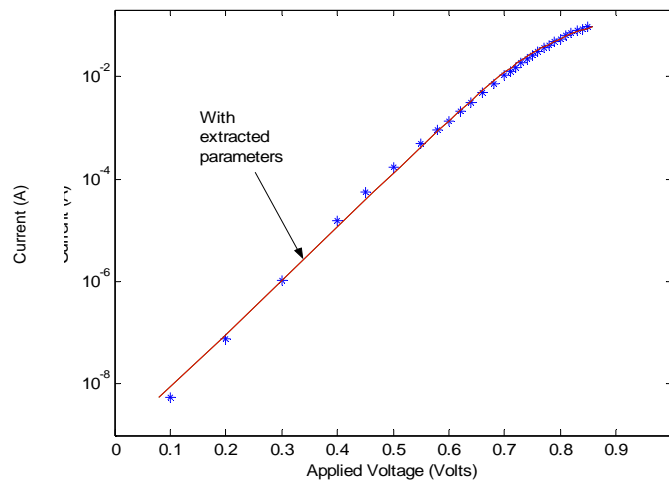

Fig. 4. I-V curve using measured data (**) and extracted parameters (--).

V. Conclusion and Future Work

In this paper, a new technique based on Genetic Algorithms (GAs) to extract the circuit model parameters values of the p-n junction diode is proposed and tested using theoretical and experimental data. The proposed technique is coded in a generic way to make it usable to extract the parameters of any two terminal devices from experimental data. Testing the technique showed very good performance with minimum error. The length of the string and the uniformity of the genes (substrings) per chromosome affect the performance, therefore careful attention should be made in this regard. Specifically, parameters with wider range, such as saturation current need longer genes lengths. A simple formula is proposed to help in estimating the gene length for each parameter to achieve better extraction. Future work will focus on generalizing this technique to extract all parameters including shunt resistance. Also, to apply the technique to extract solar cells parameters, or other two terminal devices. On the other hand, the genetic algorithm performance can be tested using extra operators, or different selection techniques.

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المملكة العربية السعودية

ملخص البحث. في تلك الورقة تم تطوير طريقة جديدة لحساب واستنباط قيم متغيرات النموذج الرياضي المستخدم
لوصف الصمام الثنائي (الدايود) في الدوائر الإلكترونية اعتمادا على الخوارزميات الجينية ، حيث تم حساب قيم
ثلاثة متغيرات أساسية وهي : تيار التشبع ، ومعامل المثالية ، والمقاومة المتوالية ، دون الحاجة إلى افتراض قيم
ابتدائية لتلك المتغيرات ، وقد أظهرت النتائج قدرة الطريقة المستخدمة على الوصول لنتائج عالية الدقة وبعيدة عن
احتمال الخطأ الذي يصاحب عادة استخدام الطرق التقليدية الأخرى. لقد أظهرت الطريقة المقترحة أفضلية في
الأداء من حيث الدقة وسهولة استخدامها لاستخلاص متغيرات نبائط أخرى ، ولقد تم اختبار الطريقة والتأكد من
أدائها باستخدام بيانات نظرية وبيانات مقاسة معمليا لعلاقة التيار بالجهد.