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Multiple Soft Fault Diagnosis of Analog Filter Circuit Based on Genetic Algorithm

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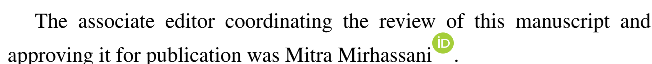
ABSTRACT Hard (open and short) faults and discrete parameter faults (DPF) are the mostly used fault models in simulation-before-test (SBT) method. Because that the parameter of analog element is continuous, the DPF can not elaborately characterize all possible continuous parameter faults (CPF) occurring in analog circuit, let alone the double soft fault. To address such problem, a genetic algorithm (GA) based simulation after test (SAT) fault diagnosis method is proposed in this paper. The fault diagnosis is transformed into an optimization problem. The genes represent the parameter values of potential faulty components. Our target is to minimize the difference between the actual faulty response and the GA simulated response. The chromosome that minimize the difference gives the solution. This method does not save all possible faults in advance whereas it can diagnosis single and double continuous faults. The effectiveness of the proposed method is examined by using filter circuit examples.

INDEX TERMS Fault diagnosis, genetic algorithm, optimization.

I. INTRODUCTION

With the increased complexity of the electronics industry, integration level of electronic products has been improved, and the technical requirements for the diagnosis of analog circuit faults are also rapidly increasing. Usually, short and open circuit are referred to as hard fault. This concept comes from the digital circuit fault. Hard fault is usually easy to diagnose and there are lots of methods [1], [2] still be proposed to handle such fault. A fault is called soft when the parameter deviates from its tolerance range, but does not produce a short circuit or an open circuit. By comparing to the hard (open and short) faults, the soft fault is harder to diagnose.

To simplify the problem, only few special fixed parameter shifting (such as $\pm\mathbf{25}\%$ or $\pm 50\%$ deviation from the nominal value) are considered in literatures [3]–[11]. An overdetermined equations fitting [9] based iterative method is proposed to estimate values of the considered set of the parameters. It is fit for the nonlinear circuits with no explicit analytical form. It can estimate some specific parameter shifting.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Because that the parameter value of analog element is continuous and can vary from 0 to infinity, the DPF can not elaborately characterize all possible continuous parameter faults (CPF) occurring in analog circuit. Hence, the DPF is not practical. Continuous range, such as [$\pm 20\% \sim \pm 50\%$], of parameter shifting is a more practicable fault model [12]–[15]. But is still can not cover all the possible parameter shifting, viz., $(0,\infty)$.

Methods are proposed in literatures [16]–[19] to handle the CPF within the range of $(0,\infty)$. The slope model (or ratios of voltage increments) used in literature [16] can model and diagnose such fault. If a parameter shifting happen to a component, no matter how much the faulty magnitude is, the ratio of voltage increments on different test nodes is constant. The components that have different ratios of voltage increments are distinguishable. The relationship between the fault number m and the test node number n is $n = m+1$. On the complex plane, the circle model is proposed in literatures [17], [18]. By using this model, CPF within the whole range of $(0, \infty)$ can be diagnosed too. If a parameter shifting happen to a component, no matter how much the faulty magnitude is, the voltage responses always locate on a specific circle on the complex plane. The components that have different

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circle are distinguishable. The relationship between the fault number m and the test node number n is $n = \lfloor \frac{m}{2} \rfloor + 1$, where '$\lfloor \ \rfloor$' denotes rounding the elements to the nearest integers towards minus infinity. Obviously, the circle model needs many fewer test nodes than the slope model. A genetic algorithm based simulation after test method is proposed in literature [19] to diagnose the CPF. The gene represents the parameter value. The fault diagnosis is transformed to an optimization problem, viz., finding an individual that can generate a response that has minimal Euclidean distance to the measured faulty response. Then the gene in this individual that out of the tolerance is the fault source.

In a word, except for the slope, circle model and the GA [19] method, there are few methods can handle the single CPF that cove the whole range (0,∞). The method that can diagnose the multiple parameter shifting within the range of (0,∞) is much less. Methods in literatures [5], [11], [13]can handle some double faults. But the faults are still fixed parameter values. The reason is that SBT method can not elaborately simulate all the possible combinations of the parameter shifting from multiple components. Tadeusiewicz et al. [20] solves least squares problem by minimizing the sum of squares of the differences between the measured voltages and the parametrized functions using the Levenberg Marquardt method. It is a SAT method. Theoretically, this method covers all the CPF within the whole range (0,∞).

In a word, the slope [16] and circle [17] models are the SBT that can diagnose single CPF within the whole range (0,∞). The slope needs many test nodes. The circle model still has no explicit analytical form for multiple faults. The GA based [19] and parametrized functions based [20] methods can diagnose such fault too. They belong to the SAT category.

We using the genetic algorithm to simulate the parameter fault in this paper. The fault diagnosis is transformed into an optimization problem. It belongs to the SAT. We do not need any simulation before test. All single or double CPFs can be diagnosed. This paper is organized as follows. Section II illustrates how to transform the fault diagnosis to an optimization problem. The optimization problem is solved by a modified genetic algorithm (GA) in Section III. In this section, how to use the gene to express the fault and fault free components' values are illustrated first. Then, a new selection method is proposed to simultaneously ensure the diversity and convergence of the GA. In Section IV, simulated and actual examples are used to explain the proposed method, which are compared with the previous work to verify the effectiveness. Section V concludes this paper.

II. PROBLEM FORMULATION AND PREVIOUS WORK

In literature [19], we transform the fault diagnosis to an optimization problem. It is used in this paper too.

A. PROBLEM FORMULATION

The basic ideal is as follow. On a test point t, the transfer function of a linear filter circuit can be expressed as follows.

$$h^{(t)}(s,\boldsymbol{p}) = \frac{\dot{U}_o}{\dot{U}_i} = \left.\frac{a_n(\boldsymbol{p})s^n + a_{n-1}(\boldsymbol{p})s^{n-1} + \cdots + a_1(\boldsymbol{p})s^1 + a_o(\boldsymbol{p})}{b_m(\boldsymbol{p})s^m + b_{m-1}(\boldsymbol{p})s^{m-1} + \cdots + b_1(\boldsymbol{p})s^1 + b_o(\boldsymbol{p})}\right|_{s=j\omega} \quad (1)$$

where $\boldsymbol{p} = [p_1, p_2, \cdots p_K]$ is the potentially faulty parameter vector (K is the number of circuit components), ω is the test frequency. If the test frequency is fixed, the $h^{(t)}$ is only determined by vector $\boldsymbol{p}$. It is a complex phasor can be expressed as $h^{(t)} = h_r^{(t)} + jh_j^{(t)}$, where $h_r^{(t)}$ and $h_j^{(t)}$ respectively represents the real and imaginary parts of $h^{(t)}$. If there are T test points, all the $h^{(t)}$s are saved in the following vector.

$$\begin{aligned}\boldsymbol{h}(\boldsymbol{p}) &= \left[h^{(1)}(p), h^{(2)}(\boldsymbol{p}), \cdots, h^{(T)}(\boldsymbol{p})\right] \\ &= [h_r^{(1)}(\boldsymbol{p}), h_j^{(1)}(\boldsymbol{p}), h_r^{(2)}(\boldsymbol{p}), h_j^{(2)}(\boldsymbol{p}), \\ &\quad \cdots, h_r^{(T)}(\boldsymbol{p}), h_j^{(T)}(p)]\end{aligned} \quad (2)$$

The measured responses on the T test points are $\boldsymbol{M} = \left[\dot{U}^{(1)}, \dot{U}^{(2)}, \cdots, \dot{U}^{(T)}\right] = [U_r^{(1)}, U_j^{(1)}, U_r^{(2)}, U_j^{(2)}, \cdots, U_r^{(T)}, U_j^{(T)}]$. The real and imaginary parts of $\boldsymbol{h}(\boldsymbol{p})$ and $\boldsymbol{M}$ are separately equal. Hence we have $2T$ equations.

$$\left.\begin{array}{l} h_r^{(t)}(\boldsymbol{p}) = U_r^{(t)} \\ h_j^{(t)}(\boldsymbol{p}) = U_j^{(t)} \end{array} \quad t = 1, 2, \cdots T \right\} \quad (3)$$

Because that the analog component value can vary from 0 to ∞, fault signature must cover all possible responses of the parameter shifting from 0 to ∞. To diagnose single fault p_k, we need at least two linearly independent equations to eliminate one variable p_k. The remaining equation (signature equation) is independent of the fault parameter p_k. It is determined by the location of p_k in the circuit under test (CUT) and the parameters of other fault free components [17]. Hence, no matter how much the faulty parameter is, the signature equation can cover all possible responses.

To diagnose double fault, at least three linearly independent equations are needed to simultaneously eliminate two variables. Similarly, to diagnose m-fault, the number of linearly independent equations must be no less than m+1. Double fault is handled in this paper. We need at least three linearly independent equations. Hence, two test points are necessary. Besides, to diagnose m-fault, we need $n = \lfloor \frac{m}{2} \rfloor + 1$ test points.

The $\boldsymbol{h}(\boldsymbol{p})$ with Q different test frequencies forms a vector as follows.

$$\boldsymbol{H}(\boldsymbol{p}) = [h_1(p), h_2(p), \cdots, h_Q(p)] \quad (4)$$

where $\boldsymbol{H}(\boldsymbol{p})$ is a complex vector with $Q \times T$ elements in it, $\boldsymbol{H}(\boldsymbol{p}) \in \mathbb{C}^{(Q\times T)\times 1}$. If the input $\dot{U}_i$ is taken as reference phasor, $\dot{U}_i = 1\angle 0^o$, we have

$$\boldsymbol{H}(\boldsymbol{p}) = \dot{\boldsymbol{U}}_{\boldsymbol{o}}(\boldsymbol{p}) \quad (5)$$

We should note that the increase of frequency number can not improve the testability of the CUT. But it can improve the fault diagnosis accuracy which is deteriorated by the tolerance influence of non-faulty components. How to choose the test frequency is out of the range of this paper. We transfer fault diagnosis into an optimization problem as follows.

$$\begin{aligned} &minimize\ E = \left\| \dot{\boldsymbol{U}}_{\boldsymbol{o}}(\boldsymbol{p}) - \boldsymbol{M} \right\| \\ &subject\ to\ \boldsymbol{p} > 0 \end{aligned} \tag{6}$$

Our object is to find a $\boldsymbol{p}^*$ that make the vector $\dot{\boldsymbol{U}}_{\boldsymbol{o}}(\boldsymbol{p})$ has minimal Euclidean to $\boldsymbol{M}$ under the specific test frequencies. Elements in vector $\boldsymbol{p}^*$ that out of the tolerance range are fault sources. The basic flow is as follows.

Step1: The actual response vector $\boldsymbol{M}$ of the faulty circuit is measured.

Step2: By using the GA and formula (1) to find a $\boldsymbol{p}^*$ that minimize the E in formula (6). In $\boldsymbol{p}^*$, the component values that out of tolerance range are the faulty parameters.

B. CODING AND PROBLEM EXPRESSION

The chromosome is a real string with the same form as vector $\boldsymbol{p}$. According to Fedi *et al.*[21], the K components fall into l ambiguity groups, where $l \leq K$. From each group, any component can be chosen as representative fault source. Therefore, there are totally l representative fault sources. Hence, the coding method or chromosome is as follows.

$$\boldsymbol{p} = [p_1, \ldots, p_i, \ldots, p_l, \ldots, p_k, \ldots, p_K] \tag{7}$$

where, $p_k, l+1 \leq k \leq K$, is the fault free component varying within its tolerance range $[N_k \times 0.95, N_k \times 1.05]$, and N_k is the nominal value of the kth component. The p_i, $1 \leq i \leq l$, represents the fault source and it varies within the range of $(0, \infty)$.

In [19], the population is divided into l sets according to their gene values. If the ith gene of an individual is out of the tolerance range, this individual is grouped into the ith group. Then the crossover and mutation are executed in each group to ensure the representative fault components vary within $(0, \infty)$ whereas the other components vary within the tolerance range. The selection is within the whole population. This method is effective for single fault diagnosis. For multiple faults, this method tends to be trapped in local optima. To simultaneously handle the single and double fault diagnosis, a new regularization and alternative selection schemes are proposed in this paper. The regularization ensures the feasibility of the solutions and the alternative selection ensures the diversity to avoid the local optima.

III. PROPOSED GA BASED METHOD

A vector $\boldsymbol{b} \in \{0, 1\}^l$ is used to identify the faulty parameters.

$$\begin{aligned} &\boldsymbol{b} = [b_1, b_2, \cdots b_l], \\ &b_i = \begin{cases} 0, & 0.95N_i \leq p_i \leq 1.05N_i \\ 1, & p_i > 1.05N_i\ or\ p_i < 0.95N_i \end{cases} \end{aligned} \tag{8}$$

Algorithm 1 Double Fault *GA*

Input: $\boldsymbol{M}$
Output: $\boldsymbol{p}^*$
1: P = Initiallization();
2: **For** $g = 1$ to $G_{\max}$
3: D = *Crossover* (P) ;
4: D = Mutation (D);
5: D = Regularization(D);
6: $C = P \cup Q$;
7: $\boldsymbol{S} = [S_1, S_2, \cdots S_h]$ = Sectionalization(C)
8: P = Environmental_selection($\boldsymbol{S}$);
9: **End**
10: $\boldsymbol{p}^*$ = Best_selection (P)
11: **Return** $\boldsymbol{p}^*$

If the p_i is within the tolerance range, $b_i = 0$. Otherwise, $b_i = 1$. Single and double-fault situations are considered in this paper. The amount of fault is no more than 2.

$$\sum_{i=1}^{l} b_i \leq 2 \tag{9}$$

Formulas (8) and (9) govern the coding rule and the range of each gene.

A. FRAME OF THE PROPOSED GA

The frequency vector $\boldsymbol{s}$, response $\boldsymbol{M}$ of CUT and transfer function $\boldsymbol{H}$ on selected test points are the input of the proposed GA. The population size is n and the initial population is P.

After the crossover and mutation, the combination of the new generated population D and the original population P is saved in a union set C. The next generation P with n individuals is selected from this set to substitute the original P. The above steps continue until the number of generation g reaches to its maximum value G_{max}. The output is the individual p that minimize E.

B. CROSSOVER, MUTATION AND REGULARIZATION OPERATION

The chromosome is real code that represent the component values. Hence, the simulated binary crossover (SBX) and polynomial mutation operators [22] are adopted.

The single point SBX is used in this paper. If the kth genes of parents $\boldsymbol{p}^{(1)} = \left[p_1^{(1)}, p_2^{(1)}, \ldots, p_k^{(1)}, \ldots, p_K^{(1)}\right]$ and $\boldsymbol{p}^{(2)} = \left[p_1^{(2)}, p_2^{(2)}, \ldots, p_k^{(2)}, \ldots, p_K^{(2)}\right]$ are chosen to crossover, then their 1st to (k-1)th genes do not change whereas the (k+1)th to K^{th} genes are switched. The kth genes are calculated as follows.

$$\left.\begin{aligned} &p_k^{(1)}(t+1) = 0.5\left[(1+\beta) \times p_k^{(1)}(t) + (1-\beta) \times p_k^{(2)}(t)\right] \\ &p_k^{(2)}(t+1) = 0.5\left[(1-\beta) \times p_k^{(1)}(t) + (1+\beta) \times p_k^{(2)}(t)\right] \\ &\beta = \begin{cases} (2u)^{\frac{1}{\eta_c+1}}, & if\ u = rand() \leq 0.5 \\ \left(\frac{1}{2(1-u)}\right)^{\frac{1}{\eta_c+1}}, & else \end{cases} \end{aligned}\right\} \tag{10}$$

where, $\eta_c = 20$, u is a uniformly distributed random number in the interval (0,1). Symbol t it the generation counter and $p_k^{(i)}(t)$ represents the value of the kth gene in the ith individual at the tth generation.

Therefore, the new generated two individuals are

$\boldsymbol{p}^{(1)} = \left[p_1^{(1)}, p_2^{(1)}, \ldots, p_k^{(1)}(t+1), p_{k+1}^{(2)}, \ldots, p_K^{(2)}(t)\right]$ and
$\boldsymbol{p}^{(2)} = \left[p_1^{(2)}(t), p_2^{(2)}(t), \ldots, p_k^{(2)}(t+1), p_{k+1}^{(1)}, \ldots, p_K^{(1)}(t)\right]$.

The polynomial mutation operator is as follows.

$$\left\{\begin{array}{l} p_k(t+1) = p_k(t) + \delta(u_k - l_k) \\ \delta = \begin{cases} \left[2u + (1-2u)(1-\delta_1)^{\eta_m}\right]^{\frac{1}{\eta_m+1}} - 1, & if\ u \le 0.5 \\ 1 - \left[2(1-u) + 2(u-0.5)(1-\delta_2)^{\eta_{m+1}}\right]^{\frac{1}{\eta_m+1}}, & else \end{cases} \\ \delta_1 = \dfrac{(p_k(t) - l_k)}{(u_k - l_k)} \\ \delta_2 = \dfrac{(u_k - p_k(t))}{(u_k - l_k)} \end{array}\right. \tag{11}$$

where, $\eta_m = 20$, u_k and l_k separately are the upper and lower bound of the kth gene.

In the regularization, for each individual: (1) if the kth $(l+1 \le k \le K)$ gene p_k representing the fault free component is out of the tolerance range after the crossover and mutation operations, it is reset into the tolerance range; (2) if the number of faulty components is larger than 2, $\sum_{i=1}^{l} b_i > 2$, we reset the $\sum_{i=1}^{l} b_i - 2$ randomly selected genes that out of the tolerance range back into the tolerance range.

C. SECTIONALIZATION

The new generated population D is combined with the parent set P to generate a combine set C. Hence, there are totally $2n$ individuals in C. Individuals that have the same faulty parameters belong to one category. The number of potential fault sources is l; hence, there are at most l single fault and $C_l^2 = \frac{l(l-1)}{2}$ double-fault categories. The h= $l + \frac{l(l-1)}{2}$ fault categories are classified by algorithm 2. Lines 5 and 7 find the faulty parameters. Lines 4, 6 and 8 put the individuals into the corresponding categories.

D. ENVIRONMENTAL SELECTION

To keep diversity and avoid local convergence, individuals are selected from each category alternately in lines 4 to 11 of algorithm 3. In each category, the individual that has the smallest E is selected in each round, see line 6 to 7. In line 6, the $E^{(k)}$ is calculated by using formula (6). The superscript

Algorithm 2 Sectionalization

Input: C
Output: $\boldsymbol{S} = [S_0, S_1, S_2, \cdots S_h]$
1: $S_0 = S_1 = S_2 = \cdots = S_h = \emptyset$
2: **For** $j = 1$ to $2n$
3: **If** $\sum_{l=1}^{L} b_l^{(j)} = 0$
4: $S_0 = S_0 \cup \{\boldsymbol{p}^{(j)}\}$
5: **Else If** $\sum_{q=1}^{l} b_q^{(j)} = 1$ and $b_i^{(j)} = 1$
6: $S_i = S_i \cup \{\boldsymbol{p}^{(j)}\}$
7: **Else If** $\sum_{q=1}^{l} b_q^{(j)} = 2$ and $b_{i_1}^{(j)} = b_{i_2}^{(j)} = 1$
8: $S_k = S_k \cup \{\boldsymbol{p}^{(j)}\}$,
where $k = l + \frac{[(l-1)+(l-i_1+1)]\times(i_1-1)}{2} + (i_2 - i_1)$
9: **End**
10: **End**

k indicates the kth individual in set S_i. This step find the best solution in set S_i. This solution is moved from set S_i into set P in line 7.

Algorithm 3 Environmental Selection

Input: $\boldsymbol{S} = [S_0, S_1, S_2, \cdots S_h]$
Output: P
1: $P = \emptyset$
3: **While** $|P| < n$
4: **For** $i = 0$ to h
5: **If** $S_i \neq \emptyset$
6: $j = arg\left(E^{(k)} = \left\|\dot{U}_o\left(\boldsymbol{p}^{(k)}\right) - \boldsymbol{M}\right\|\right)$
where $\boldsymbol{p}^{(k)} \in S_i$
7: $P = P \cup \{\boldsymbol{p}^{(j)}, S_i = S_i - \boldsymbol{p}^{(j)}$
8: **If** $|P| \ge n$
9: break;
10: **End**
11: **End**
12: **End**
13: **End**

Once the iterations are finished, the best one $\boldsymbol{p}^*$ is selected from population P in line 10 of algorithm 1.

IV. EXPERIMENTS

The MATLAB is used for implementation of fault diagnosis framework. Due to that the slope technique [16] and the circle method [17] can model and diagnose CPS fault, they are selected as the comparison methods.

$$h^{(1)}(j\omega, \boldsymbol{p}) = -\frac{j\omega R_2R_3R_4R_5C_2}{R_1R_2R_6 + j\omega R_1R_3R_4R_5C_2 + (j\omega)^2 R_1R_2R_3R_4R_5C_1C_2} \tag{12}$$

$$h^{(2)}(j\omega, \boldsymbol{p}) = -\frac{R_2R_3R_6}{R_1R_2R_6 + j\omega R_1R_3R_4R_5C_2 + (j\omega)^2 R_1R_2R_3R_4R_5C_1C_2} \tag{13}$$

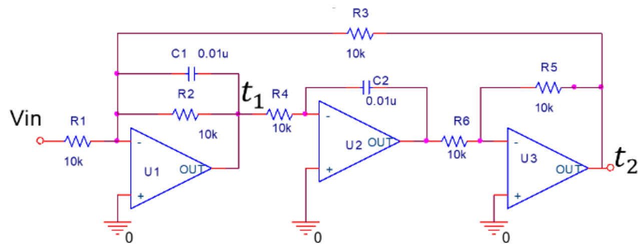

FIGURE 1. Tow–Thomas filter.

A. ILLUSTRATIVE EXAMPLE

This example is mainly used to further illustrate the proposed method. TheCUT is shown in Fig. 1. The transfer functions on test points $\boldsymbol{t}_1$ and $\boldsymbol{t}_2$ are shown at the bottom of the previous page, where, $\boldsymbol{p} = [p_1, p_2, p_3, p_4, p_5, p_6, p_7, p_8,] = [R_1, R_2, R_3, R_4, R_5, R_6, C_1, C_2,]p[p_1, p_2, p_3, p_4, p_5, p_6, p_7, p_8,] = [R_1, R_2, R_3, R_4, R_5, R_6, C_1, C_2,]$. The nominal parameters are shown in figure 1, R = 10kΩ, C = 10nF. The tolerance range of resistances and capacitances is ±5%. According to the method in [21], on test point t_2, the eight components fall into four ambiguity sets: {R1}, {R2}, {R4, R5, R6, C2}, {R3, C1}. Any component in each set can be chosen as representative fault. Hence, R1, R2, R3 and R4 are selected in this example, $l = 4$. There are totally $h = l + \frac{l(l-1)}{2} = 10$ fault categories including single and double faults, viz., four single faults $\{R_1\}$, $\{R_2\}$, $\{R_3\}$, $\{R_4\}$ and six double faults $\{R_1, R_2\}$, $\{R_1, R_3\}$, $\{R_1, R_4\}$, $\{R_2, R_3\}$, $\{R_2, R_4\}$, $\{R_3, R_4\}$. We randomly set the faulty parameter vector $\boldsymbol{p}_f = [10.1888k\Omega\ 6.7821k\Omega\ 1.6858k\Omega\ 10.3917k\Omega\ 10.2555k\Omega\ 9.8787k\Omega\ 10.1016nF\ 10.4416nF]$. Obviously, the faulty components are $\{R_2, R_3\}$.

The excitation (input) signal is a 1V sinusoidal wave with frequency 1k. Hence, the total number of response is T×1 = 2 × 1 = 2. Taking the inputs as reference phasor, the faulty responses are $\boldsymbol{M} = [-0.0233 - 0.1223j, -0.1728+0.0329j]$V.

Our task is to find the faulty components by using the proposed method.

- ***Initialization***

The population size, crossover and mutation rate, maximum generation separately are $n = 10 * h = 100$, $p_c = 1$, $p_m = 1/k\ G_{max} = 100$, where $k = 8$ is the length of chromosome. Initially, all genes are randomly set within the tolerance range. Table 1 lists 10 individuals of the initial population. The genotypes of the first two individuals shown in the 3rd and 4th lines separately are

$$\boldsymbol{p}^{(1)} = [9.63, 9.60, 9.87, 10.17, 10.39, 9.82, 10.15, 9.68]$$
$$\boldsymbol{p}^{(2)} = [9.75, 9.83, 10.08, 10.43, 9.65, 9.55, 10.11, 10.21].$$

- ***Sectionalization***

Any gene can be chosen as crossover point. The first two individuals shown in Table 1 are taken as example. If the 3rd gene is chosen. Then we use formula (10) to calculate the new gene. Besides, the 4th to 8th genes are switched. After crossover, the new genotypes are as follows.

TABLE 1. The 10 individuals in the initial population.

	Resistance (UNIT: kΩ)						Capacitance(UNIT: nF)	
	R_1	R_2	R_3	R_4	R_5	R_6	C_1	C_2
$\boldsymbol{p}^{(1)}$	9.63	9.60	9.87	10.17	10.39	9.82	10.15	9.68
$\boldsymbol{p}^{(2)}$	9.75	9.83	10.08	10.43	9.65	9.55	10.11	10.21
$\boldsymbol{p}^{(3)}$	9.88	10.06	9.55	10.32	10.20	10.04	10.03	10.28
$\boldsymbol{p}^{(4)}$	9.50	10.29	9.75	10.15	9.94	9.52	9.67	10.40
$\boldsymbol{p}^{(5)}$	9.54	9.63	10.23	10.35	10.18	10.43	10.14	9.55
$\boldsymbol{p}^{(6)}$	9.77	9.58	9.92	10.09	10.46	10.35	10.36	9.79
$\boldsymbol{p}^{(7)}$	9.84	9.88	9.75	9.64	9.60	10.17	10.36	9.99
$\boldsymbol{p}^{(8)}$	10.03	10.46	10.39	10.12	10.17	10.41	10.35	9.66
$\boldsymbol{p}^{(9)}$	9.59	10.16	10.17	10.43	10.20	9.74	9.92	10.21
$\boldsymbol{p}^{(10)}$	9.97	10.39	10.21	10.24	10.09	9.93	10.45	10.13
…	…	…	…	…	…	…	…	…

$$\boldsymbol{p}^{(1)} = [9.63, 9.60, 10.11, 10.43, 9.65, 9.55, 10.11, 10.21]$$
$$\boldsymbol{p}^{(2)} = [9.75, 9.83, 9.85, 10.17, 10.39, 9.82, 10.15, 9.68]$$

After the crossover, mutation and regularization operations, we got the new generated population D. In each chromosome, the first four genes represent the four representative fault sources R1, R2, R3 and R4. They can randomly vary within the faulty range $(0, \infty)$. The other genes represent the other fault free components, viz. R5, R6, C1 and C2. They vary within the tolerance range. The population D is merged with the original population P to form a combine set C. The individuals in this set are grouped into 11 subsets according to the different fault sources. They are shown in Table 2. Subset S_0 saves the sole fault free condition, $\boldsymbol{p}^{(1)} = \{9.6k\Omega, 10k\Omega, 10.28k\Omega, 9.54k\Omega, 10.5\Omega, 10.5k\Omega, 10.5nF, 9.5nF\}$. Its responses are $\dot{\boldsymbol{U}}_{\boldsymbol{o}} = [-0.4962-0.5202j, -0.9136+0.8713j]$V by using (12) and (13), as shown at the bottom of the previous page. Then the value of objective function (6) is

$$E = \sqrt{\begin{matrix}\|(-0.4962 - 0.5202j) - (-0.0233 - 0.1223j)\|^2 + \\ \|(-0.9136 + 0.8713j) - (-0.1728 + 0.0329j)\|^2\end{matrix}} = 1.28$$

The objective function value of each individual is listed in the last column of the Table 2. In subset S_1, the R_1 of every individual is out of the tolerance range while the other components are within the tolerance range. This set represents the R_1 single fault. Subsets S_1 to S_4 save the single fault individuals, viz., respectively R_1, R_2, R_3 and R_4. In subset S_5, the R_1 and R_2 are simultaneously out of the tolerance range. This set represent the double fault $\{R_1, R_2\}$ situation. Due to the page limitation, only two individuals in each subset are shown. In each subset, the individuals are sorted in ascending order based on the objective value E. A smaller E value is desirable.

- ***Environmental Selection***

Table 3 lists part of the selected individuals.

We alternatively move the best individuals from the 11 subsets into set P until the P contains n = 100 individuals. In the first round of selection, the first individuals in all subsets are

TABLE 2. The 11 subsets in the initial population.

	Resistance (UNIT: kΩ)						Capacitance (UNIT: nF)		E
	R_1	R_2	R_3	R_4	R_5	R_6	C_1	C_2	
S_0	9.60	10.00	10.28	9.54	10.50	10.50	10.50	9.50	1.28
S_1 $\{R_1\}$	12.21	10.40	10.24	10.05	10.50	9.50	10.50	9.50	1.02
	10.53	9.62	10.33	9.86	10.50	9.50	10.50	9.50	1.16
	…	…	…	…	…	…	…	…	…
S_2 $\{R_2\}$	9.77	7.00	10.41	10.14	9.50	10.50	10.50	9.51	1.03
	10.13	8.72	10.16	10.45	10.50	10.50	10.46	9.58	1.12
	…	…	…	…	…	…	…	…	…
S_3 $\{R_3\}$	10.08	9.66	5.48	10.25	9.50	9.50	10.50	9.50	0.54
	9.99	10.05	6.20	10.47	9.50	10.50	10.50	10.50	0.67
	…	…	…	…	…	…	…	…	…
S_4 $\{R_4\}$	9.59	9.88	9.75	8.04	9.50	10.50	9.50	9.50	1.09
	10.37	9.71	9.97	12.11	10.50	9.50	9.50	10.50	1.13
	…	…	…	…	…	…	…	…	…
S_5 $\{R_1, R_2\}$	13.26	5.54	9.69	10.24	9.50	9.50	10.50	9.50	0.42
	13.97	6.02	10.43	10.20	10.50	9.50	10.50	10.50	0.55
	…	…	…	…	…	…	…	…	…
S_6 $\{R_1, R_3\}$	73.81	9.65	10.99	9.81	10.50	9.52	9.62	10.50	0.16
	13.79	9.66	5.40	10.21	9.50	9.50	10.50	9.50	0.31
	…	…	…	…	…	…	…	…	…
S_7 $\{R_1, R_4\}$	10.62	9.88	9.90	8.04	9.50	10.50	9.50	9.50	0.44
	11.66	9.72	9.89	6.77	10.50	9.50	9.50	9.50	0.45
	…	…	…	…	…	…	…	…	…
S_8 $\{R_2, R_3\}$	10.17	6.02	0.27	9.64	9.56	9.50	9.50	10.50	0.18
	10.11	14.17	7.23	9.80	9.50	9.50	9.50	10.44	0.45
	…	…	…	…	…	…	…	…	…
S_9 $\{R_2, R_4\}$	10.17	6.02	10.49	8.86	9.50	10.00	9.50	10.50	0.78
	9.68	5.44	9.93	8.96	10.50	9.50	10.50	10.50	0.82
	…	…	…	…	…	…	…	…	…
S_{10} $\{R_3, R_4\}$	9.60	10.00	6.50	13.01	9.78	10.50	9.50	9.50	0.46
	10.01	9.76	6.21	9.32	9.50	9.50	10.50	9.50	0.51
	…	…	…	…	…	…	…	…	…

TABLE 3. The first 20 selected individuals in the first generation.

	Resistance (UNIT: kΩ)						Capacitance (UNIT: nF)		E
	R_1	R_2	R_3	R_4	R_5	R_6	C_1	C_2	
$\boldsymbol{p}^{(1)}$	9.60	10.00	10.28	9.54	10.50	10.50	10.50	9.50	1.28
$\boldsymbol{p}^{(2)}$	12.21	10.40	10.24	10.05	10.50	9.50	10.50	9.50	1.02
$\boldsymbol{p}^{(3)}$	9.77	7.00	10.41	10.14	9.50	10.50	10.50	9.51	1.03
$\boldsymbol{p}^{(4)}$	10.08	9.66	5.48	10.25	9.50	9.50	10.50	9.50	0.54
$\boldsymbol{p}^{(5)}$	9.59	9.88	9.75	8.04	9.50	10.50	9.50	9.50	1.09
$\boldsymbol{p}^{(6)}$	13.26	5.54	9.69	10.24	9.50	9.50	10.50	9.50	0.42
$\boldsymbol{p}^{(7)}$	73.81	9.65	10.99	9.81	10.50	9.52	9.62	10.50	0.16
$\boldsymbol{p}^{(8)}$	10.62	9.88	9.90	8.04	9.50	10.50	9.50	9.50	0.44
$\boldsymbol{p}^{(9)}$	10.17	6.02	0.27	9.64	9.56	9.50	9.50	10.50	0.18
$\boldsymbol{p}^{(10)}$	10.17	6.02	10.49	8.86	9.50	10.00	9.50	10.50	0.78
$\boldsymbol{p}^{(11)}$	9.60	10.00	6.50	13.01	9.78	10.50	9.50	9.50	0.46
$\boldsymbol{p}^{(12)}$	10.53	9.62	10.33	9.86	10.50	9.50	10.50	9.50	1.16
…	…	…	…	…	…	…	…	…	…

moved into P. The first individual in Table 3 comes from the set S_0. The 2nd individual is the first individual in set S_1. Then, the set P contains 11 individuals and $S_0 = \emptyset$. In the second round of selection, the empty set are not considered. Hence the 12$^{\text{th}}$ individual in P is the 2nd individual in set S_1.

- ***Result***

After 100 iterations, the individuals in set S are listed in Table 4.

TABLE 4. The individuals in set in the last generation.

	Resistance (UNIT: kΩ)						Capacitance (UNIT: nF)		E
	R_1	R_2	R_3	R_4	R_5	R_6	C_1	C_2	
S_0	10.50	9.50	9.50	9.50	9.50	10.50	9.50	9.50	0.9745
	…	…	…	…	…	…	…	…	…
S_1 $\{R_1\}$	64.06	10.49	9.50	9.52	9.50	10.50	9.50	9.50	0.0872
	…	…	…	…	…	…	…	…	…
S_2 $\{R_2\}$	10.50	0.27	9.50	9.53	9.50	10.50	9.50	9.50	0.2102
	…	…	…	…	…	…	…	…	…
S_3 $\{R_3\}$	10.50	9.5	1.71	9.97	10.50	9.52	10.50	10.44	0.0105
	…	…	…	…	…	…	…	…	…
S_4 $\{R_4\}$	10.50	9.50	9.50	0.1	9.5	10.50	9.50	9.50	0.7452
	…	…	…	…	…	…	…	…	…
S_5 $\{R_1, R_2\}$	86.43	55.66	9.50	10.40	10.50	9.50	9.50	9.57	0.0025
	…	…	…	…	…	…	…	…	…
S_6 $\{R_1, R_3\}$	11.75	9.50	1.89	9.94	10.50	9.52	10.50	10.50	0.0070
	…	…	…	…	…	…	…	…	…
S_7 $\{R_1, R_4\}$	57.66	10.49	9.50	6.63	9.50	10.50	9.50	9.50	0.0709
	…	…	…	…	…	…	…	…	…
S_8 $\{R_2, R_3\}$	9.79	6.52	1.62	9.78	10.50	9.5	10.50	10.41	0.0001
	…	…	…	…	…	…	…	…	…
S_9 $\{R_2, R_4\}$	10.50	0.21	9.50	5.73	9.53	9.5	9.50	10.43	0.2101
	…	…	…	…	…	…	…	…	…
S_{10} $\{R_3, R_4\}$	10.50	9.50	1.71	10.88	10.50	9.50	10.50	9.55	0.0105
	…	…	…	…	…	…	…	…	…

This table shows that every subset converges to a best solution with respect to the faulty category. For example, the subset S_0 represents the fault free category. The individual with parameter $\boldsymbol{p}^{(1)} = \{10.5k\Omega, 9.5\text{k}\Omega, 9.5\text{k}\Omega, 9.5\text{k}\Omega, 9.5\Omega, 10.5\text{k}\Omega, 9.5\text{nF}, 9.5\text{nF}\}$ generates the response that most close to the measured faulty response $\boldsymbol{M}$. Hence, all faulty free individuals converge to $\boldsymbol{p}^{(1)}$. Similarly, if only R_1 is the fault source, the individual with parameter $\{64.06\text{k}\Omega, 10.49\text{k}\Omega, 9.5\text{k}\Omega, 9.52\text{k}\Omega, 9.5\Omega, 10.5\text{k}\Omega, 9.5\text{nF}, 9.5\text{nF}\}$ can generate the best response. Therefore, all individuals in set S_1 converge to this individual. Obviously, within Table 4, the individual $\boldsymbol{p}^* = \{9.79k\Omega, 6.52\text{k}\Omega, 1.62\text{k}\Omega, 9.78\text{k}\Omega, 10.5\text{k}\Omega, 9.5\text{k}\Omega, 10.5\text{nF}, 10.41\text{nF}\}$ in subset S_8 has the minimal objective value $E = 0.0001$. Thus, it is the best solution.

It is easy to verify that the response of the CUT with parameters $\boldsymbol{p}^*$ is $\dot{\boldsymbol{U}}_{\boldsymbol{o}} = [-0.0232 - 0.1221\text{j}, -0.1728 + 0.0328\text{j}]$. Then the value of objective function (6) is

$$E = \sqrt{\begin{array}{l}\|(-0.0233 - 0.1222\text{j}) - (-0.0233 - 0.1223\text{j})\|^2 + \\ \|(-0.1728 + 0.0328\text{j}) - (-0.1728 + 0.0329\text{j})\|^2\end{array}} = 0.0001.$$

The 2$^{\text{nd}}$ and 3$^{\text{rd}}$ elements in vector $\boldsymbol{p}^*$ is out of their tolerance ranges, hence, the double fault $\{R_2, R_3\}$ is correctly diagnosed. Besides, the proposed method deduce that the faulty parameters of R_2, R_3 are 6.52kΩ and 1.62kΩ which are very close to the actual faulty parameters 6.7821kΩ and 1.6858kΩ. Obviously, the proposed method can realize not only fault location but also faulty parameter identification.

The average running time is 0.5 seconds for each diagnosis.

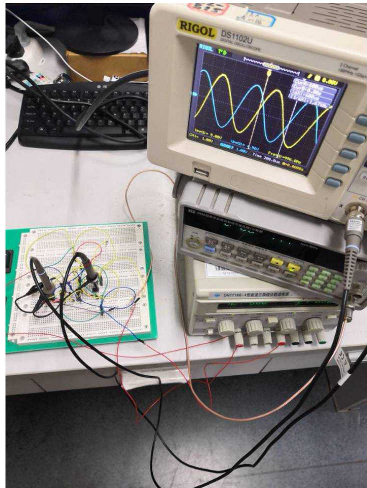

FIGURE 2. Experimental setup.

B. ACTUAL EXAMPLE

We use an actual CUT to verify the effectivity of the propose method. The experimental setup and the CUT are shown in Fig. 2.

The structure and parameters of the CUT are the same as those of the circuit shown in figure 1. The DC source is $\pm 12V$. The excitation (input) signal are 1V sinusoidal waves with frequencies 500Hz, 1kHz and 5kHz respectively. How to choose the test frequency is out of the range of this paper. Hence, the total number of responses is $2\times 3 = 6$. We randomly set the R_1 to a faulty value 15kΩ, with the three different test frequencies, the actual measured responses on the two test points are $\boldsymbol{M}$=[−0.08−0.22j, −0.69+0.25j, −0.39−0.34j, −0.53+0.61j, −0.06+0.20j, 0.06+0.02j]V. Based on the actual responses $\boldsymbol{M}$, the proposed method is used to find the fault source. The size of the population is 400 and the maximum generation is 200. The final best individual is $\boldsymbol{p}^*$=[14.3624kΩ, 9.8779kΩ, 10.1157kΩ, 9.6694kΩ, 10.5000kΩ, 10.4472kΩ, 10.5000nF, 10.5000nF] and the corresponding responses are $\dot{\boldsymbol{U}}_{\boldsymbol{o}}$ = [−0.0819−0.2227j, −0.6948+0.2554j, −0.3909−0.3406j, −0.5313+0.6097j, −0.0707+0.2089j, 0.0652+0.0221j]. Obviously, the fist component in $\boldsymbol{p}^*$ is the fault source. Fault diagnosis result is right. The fault diagnosis time is 0.9 seconds.

C. ACTUAL STATISTICAL EXPERIMENT

The GA parameter setting is same as that in the illustrative example. For each fault category (including the fault free), we randomly adjust the resistances that within this category for 100 cases. Then the 100 responses are saved for fault diagnosis. Table 5 lists the diagnosis results. For the fault free category, all the 8 components vary within the tolerance range. It is correctly diagnosed by 97 cases. While it is also improperly partitioned into set $\{R_4\}$ for 3 cases. The reason is that some peculiar small parameter faults may induce the same responses as the fault free scenario. Here below is an example.

TABLE 5. Actual fault diagnosis results.

	Fault free	R_1	R_2	R_3	R_4	R_1, R_2	R_1, R_3	R_1, R_4	R_2, R_3	R_2, R_4	R_3, R_4
Fault free	97	0	0	1	3	0	1	0	0	0	0
R_1	0	94	0	0	0	2	0	0	0	0	0
R_2	0	0	95	0	0	1	0	0	1	2	0
R_3	0	0	0	94	0	0	0	0	1	0	1
R_4	3	0	0	0	96	0	0	1	0	1	0
R_1, R_2	0	1	0	0	0	97	0	0	0	0	0
R_1, R_3	0	0	0	0	0	0	96	3	0	0	0
R_1, R_4	0	5	0	0	0	0	2	96	0	0	0
R_2, R_3	0	0	0	0	0	2	1	0	98	0	0
R_2, R_4	0	0	5	0	1	0	0	0	0	97	0
R_3, R_4	0	0	0	5	0	0	0	0	0	0	99

TABLE 6. Statistical experimental results.

	Fault free	R_1	R_2	R_3	R_4	R_1, R_2	R_1, R_3	R_1, R_4	R_2, R_3	R_2, R_4	R_3, R_4
Fault free	961	0	10	2	27	0	0	0	0	0	0
R_1	6	915	2	0	0	23	20	34	0	0	0
R_2	4	0	954	0	0	7	1	0	11	23	0
R_3	7	3	0	921	0	2	15	0	19	0	33
R_4	23	0	2	0	855	0	0	1	0	55	64
R_1, R_2	0	11	6	0	0	874	7	1	101	0	0
R_1, R_3	1	8	0	9	0	5	868	44	65	0	0
R_1, R_4	0	25	0	0	2	0	23	945	0	2	3
R_2, R_3	0	0	7	9	0	5	7	2	966	4	0
R_2, R_4	0	0	23	0	10	1	0	3	9	954	0
R_3, R_4	0	0	0	47	13	0	1	34	0	0	905

The fault free parameters are $\boldsymbol{p}$=[10.0081kΩ, 10.0972kΩ, 10.2285kΩ, 10.2852kΩ, 10.1046kΩ, 9.5713kΩ, 9.7506nF, 9.8522nF]. The responses are $\boldsymbol{M}$=[−0.12−0.33j, −0.99+0.37j, −0.58−0.49j, −0.74+0.87j, −0.11+0.31j, 0.09+0.03j]V. The faulty parameter $\boldsymbol{p}$=[10.2721kΩ, 10.3629kΩ, 10.4983kΩ, 10.7682kΩ, 9.8980kΩ, 9.5000kΩ, 9.5000nF, 9.5347nF] can generate almost the same responses. Obviously, the $R_4 = 10.7682k\Omega$ is out of its tolerance a little. Hence, we conclude that R_4 is faulty.

For the single fault $\{R_4\}$, we randomly adjust its value out of the tolerance rang for 100 cases. It is correctly diagnosed by 96 cases and improperly partitioned into category {fault free } for 3 cases and $\{R_2, R_4\}$ for 1 case.

D. SIMULATED STATISTICAL EXPERIMENT

Besides the actual experiments, we examine it on Monte Carlo simulations. The GA parameter setting is same as that in the illustrative example. For each fault category, 1000 Monte Carlo simulations are executed. Totally, there are 11∗1000 sets of simulated results. Not only the tolerance but also measurement error e= ±5% is taken into consideration. The Monte Carlo simulations are automatically accomplished by using MATLAB. The 11∗1000 sets of results are analyzed by using the proposed GA method. Table 6 shows that in most cases the accuracy is above 90 percent. The slope method [16] needs at least two test points to diagnose single fault and three points to diagnosis double faults. Hence, with the selected two test points,

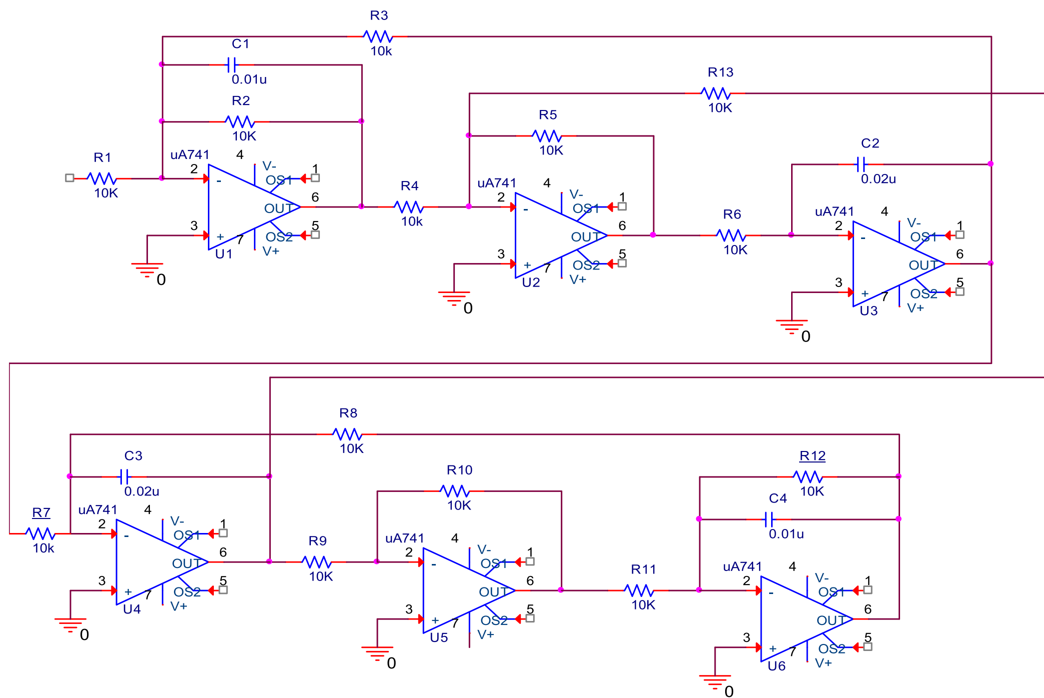

FIGURE 3. Leapfrog filter.

it can diagnose only single fault. This method partitions all the components into only two sets $\{R_1, R_2, R_3, C_1\}$ and $\{R_4, R_5, R_6, C_2\}$. If $\{R_1\}$ and $\{R_4\}$ is selected as reprehensive components, the slope method can diagnose only two single fault categories, viz., $\{R_1\}$ and $\{R_4\}$. With the same test points, the proposed method and the circle method [17] can diagnose ten fault categories, viz., $\{R_1\}$, $\{R_2\}$, $\{R_3\}$, $\{R_4\}$, $\{R_1, R_2\}$, $\{R_1, R_3\}$, $\{R_1, R_4\}$, $\{R_2, R_3\}$, $\{R_2, R_4\}$ and $\{R_3, R_4\}$. Hence, the performance of the proposed method and the circle method overwhelm the slope method.

The advantage of the proposed method over the circle model is that the proposed method can realize both fault location and fault parameter identification while the circle model realize only fault location. Hence, the proposed method can be used to monitor the state of CUT to carry out the Condition Based Maintenance (CBM). Another shortage of the circle model is that it is a SBT based method and there is no explicit expression of double fault signature. Therefore, to realize the double fault diagnose, we have to do tremendous Monte Carlo simulations to cover all possible parameter shift. But it is known that the analog component has continuous parameter value. It is impossible to exhaustively simulate and save all the parameter shifting faults. Hence, the circle model can not actually diagnose the double or multiple faults. The proposed method do not need simulations before test and fault dictionary that saves all the possible fault signatures. But it can realize all the possible single or double parameter shift faults.

E. LEAPFROG FILTER EXAMPLE

The second statistical experiment is carried out on the leapfrog filter shown in figure 3. There are 17 potential fault components. Hence, the length of chromosome is $k = 17$. The output ports of the 1st, 3rd and 6th amplifiers are set as test points. The 11 representative faults are $R_1, R_2, R_3, R_4, R_5, R_7, R_8, R_{12}, C_1, C_3, C_4$. There are $l = 11$ single fault and $\frac{l(l-1)}{2} = 55$ double fault. Hence, the amount of fault categories is 66. The population size, crossover and mutation rate, maximum generation separately are $n = 10*66 = 660, p_c = 1, p_m = 1/17, G_{max} = 200$. The DC source is $\pm 12V$. The excitation (input) signal are 1V sinusoidal wave with frequencies 500Hz, 1kHz and 5kHz respectively. The range of faulty parameters and frequencies are same as that in example 1. For each fault category, 100 Monte Carlo simulations are executed. The faulty responses are used to guide the GA. Due to the page limitation, we can not present a 66×66 table. Hence, a bar graph shown in figure 4 is used to illustrate the fault diagnosis results.

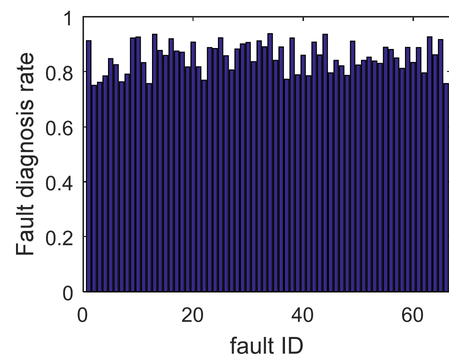

FIGURE 4. Leapfrog filter.

This figure shows that in most cases the fault diagnosis rate (FDR) is larger than 80%. The average FDR is 0.85. Considering that the proposed method can diagnosis the wide range of continues parameter fault (soft) and hard fault,

the proposed method is a competitive method. Besides, the accuracy can be improved by selecting proper frequency or adding test points. The average fault diagnosis time is 2.93 seconds.

V. CONCLUSION

Traditionally, analog circuit fault diagnosis has been carried out using simulation-before-test (SBT) strategies. The SBT method is easy to implement but this method can not elaborately characterize all possible continues parameter shift fault occur in analog circuit, let alone all possible combinations of different parameter shift from different fault components.

Whereas, the simulation-after-test (SAT) can theoretically diagnose all parameter shifting single and multiple faults. The proposed float encoding genetic algorithm can model all parameter shifting fault. Usually, the transfer function of linear CUT is obtainable. For the CUT without transfer function, to evaluate the fitness of an individual, the automatic simulation is an alternative method although it time complexity is higher than that of transfer function computation.

Different from the other selection operation, such as roulette wheel and tournament, the proposed method partitions the population into several groups based on the fault categories. Then, the best individuals in every group are selected alternatively. Obviously, it is a hybrid selection method which has the merits of both stochastic (ensuring diversity) and deterministic (ensuring convergence). To the best of our knowledge, it has not been researched.

The main advantage of the proposed method is that it can diagnosis all possible parameter shifting faults without any SBT requirement. In this paper, only the single and double faults are considered. Its disadvantage is that if the transfer function is not available, the fault diagnosis time will increase. We also should note that the transfer function is only valid for the small signal (linear) model.

REFERENCES

[1] J. Shi, Q. He, and Z. Wang, "GMM clustering-based decision trees considering fault rate and cluster validity for analog circuit fault diagnosis," *IEEE Access*, vol. 7, pp. 140637–140650, 2019.

[2] X. Tang, A. Xu, and S. Niu, "KKCV-GA-based method for optimal analog test point selection," *IEEE Trans. Instrum. Meas.*, vol. 66, no. 1, pp. 24–32, Jan. 2017.

[3] G. Xu-Sheng, Q. Hong, M. Xiang-Wei, W. Chun-Lan, and Z. Jie, "Research on ELM soft fault diagnosis of analog circuit based on KSLPP feature extraction," *IEEE Access*, vol. 7, pp. 92517–92527, 2019.

[4] Y. He, C. Li, T. Wang, T. Shi, L. Tao, and W. Yuan, "Incipient fault diagnosis method for IGBT drive circuit based on improved SAE," *IEEE Access*, vol. 7, pp. 92410–92418, 2019.

[5] W. He, Y. He, B. Li, and C. Zhang, "Feature extraction of analogue circuit fault signals via cross-wavelet transform and variational Bayesian matrix factorisation," *IET Sci., Meas. Technol.*, vol. 13, no. 2, pp. 318–327, Mar. 2019.

[6] D. Binu and B. S. Kariyappa, "RideNN: A new rider optimization algorithm-based neural network for fault diagnosis in analog circuits," *IEEE Trans. Instrum. Meas.*, vol. 68, no. 1, pp. 2–26, Jan. 2019.

[7] C. Zhang, Y. He, L. Yuan, and S. Xiang, "Analog circuit incipient fault diagnosis method using DBN based features extraction," *IEEE Access*, vol. 6, pp. 23053–23064, 2018.

[8] X. Tang, A. Xu, R. Li, M. Zhu, and J. Dai, "Simulation-based diagnostic model for automatic testability analysis of analog circuits," *IEEE Trans. Comput.-Aided Design Integr. Circuits Syst.*, vol. 37, no. 7, pp. 1483–1493, Jul. 2018.

[9] M. Tadeusiewicz and S. Halgas, "A method for local parametric fault diagnosis of a broad class of analog integrated circuits," *IEEE Trans. Instrum. Meas.*, vol. 67, no. 2, pp. 328–337, Feb. 2018.

[10] Q. Luo, Y. He, and Y. Sun, "Real-time fault detection and diagnosis system for analog and mixed-signal circuits of acousto–magnetic EAS devices," *IEEE Design Test.*, vol. 33, no. 3, pp. 77–90, Jun. 2016.

[11] M. Khanlari and M. Ehsanian, "An improved KFCM clustering method used for multiple fault diagnosis of analog circuits," *Circuits Syst Signal Process.*, vol. 36, no. 9, pp. 3491–3513, Sep. 2017.

[12] X. Yuan, Z. Liu, Z. Miao, Z. Zhao, F. Zhou, and Y. Song, "Fault diagnosis of analog circuits based on IH-PSO optimized support vector machine," *IEEE Access*, vol. 7, pp. 137945–137958, 2019.

[13] Y. Yu, Y. Jiang, and X. Peng, "Multi-frequency test generation for incipient faults in analog circuits based on the aliasing measuring model," *IEEE Access*, vol. 6, pp. 34724–34735, 2018.

[14] Z. Liu, T. Liu, J. Han, S. Bu, X. Tang, and M. Pecht, "Signal model-based fault coding for diagnostics and prognostics of analog electronic circuits," *IEEE Trans. Ind. Electron.*, vol. 64, no. 1, pp. 605–614, Jan. 2017.

[15] Q. Z. Zhou, Y. Le Xie, X. F. Li, D. J. Bi, X. Xie, and S. S. Xie, "Methodology and equipments for analog circuit parametric faults diagnosis based on matrix eigenvalues," *IEEE Trans. Appl. Supercond.*, vol. 24, no. 5, pp. 1–6, Oct. 2014.

[16] Z. Longfu and S. Yibin, "A novel method of single fault diagnosis in linear resistive circuit based on slope," presented at the Int. Conf. Commun., Circuits Syst., 2008.

[17] S. Tian, C. Yang, F. Chen, and Z. Liu, "Circle equation-based fault modeling method for linear analog circuits," *IEEE Trans. Instrum. Meas.*, vol. 63, no. 9, pp. 2145–2159, Sep. 2014.

[18] C. Yang, J. Yang, Z. Liu, and S. Tian, "Complex field fault modeling-based optimal frequency selection in linear analog circuit fault diagnosis," *IEEE Trans. Instrum. Meas.*, vol. 63, no. 4, pp. 813–825, Apr. 2014.

[19] C. Yang, L. Zhen, and C. Hu, "Fault diagnosis of analog filter circuit based on genetic algorithm," *IEEE Access*, vol. 7, pp. 54969–54980, 2019.

[20] M. Tadeusiewicz and S. Hałgas, "A method for multiple soft fault diagnosis of linear analog circuits," *Measurement*, vol. 131, pp. 714–722, Jan. 2019.

[21] G. Fedi, S. Manetti, M. Piccirilli, and J. Starzyk, "Determination of an optimum set of testable components in the fault diagnosis of analog linear circuits," *IEEE Trans. Circuits Syst. I, Fundam. Theory Appl.*, vol. 46, no. 7, pp. 779–787, Jul. 1999.

[22] K. Deb and R. B. Agrawal, "Simulated binary crossover for continuous search space," *Complex Syst.*, vol. 9, no. 2, pp. 115–148, 1995.