INVESTIGATION OF THE GENETIC ALGORITHM IN THE DIAGNOSIS OF THE COUPLED CAVITY CHAIN*

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Abstract

The application of the genetic algorithm in the diagnosis of the coupled cavity chain is investigated in this paper. One program named GANL2 has already been developed based on the genetic algorithm at Tsinghua University. The cell frequencies, quality factors, and coupling between the cells can be estimated by GANL2 if the pass-band reflection curve is known. This method has been applied in the diagnosis of the S-band and X-band standing-wave linac cavities. In this paper we present the preliminary investigation of the genetic algorithm in the diagnosis of the L-band 9-cell superconducting copper The result of the calculation and cavity model. measurement are compared. Not all the cells are diagnosed well. More precise measurement is needed for further study.

INTRODUCTION

Accurate diagnosis of the coupled cavity chain is necessary to tune the accelerator cavity properly. A pair of probes is often adopted to measure the individual cells separately for the medical accelerator tubes. In the pretuning process of the superconducting cavities, the tuning of the cavities is guided commonly by the bead-pull method. In the above two methods, perturbing objects are needed to be inserted into the cavities. It will be timeconsuming for the tuning of long cavities and technically difficult for the tuning of sealed cavities. Haebel has developed a method of measuring the field-distribution and tuning the cavity accordingly under operating conditions without introducing an object in the cavity, based on the lumped-circuit model [1]. At Tsinghua University the modified genetic algorithm has been applied to diagnose the individual cell frequencies in a coupled cavity chain for the S-band and X-band standingwave linac cavities [2]. And the corresponding program named GANL2 has been developed by Y. Ni [3].

In this paper we present the preliminary investigation of the genetic algorithm in the diagnosis of the L-band 9-cell superconducting ICHIRO copper cavity model, which is made by KEK [4]. We measure the reflection curve $|\Gamma(f)|$ and use the code of GANL2 to obtain the individual cell parameters. A pair of probes has been machined to measure the individual cells to verify the result of the genetic algorithm. The results of the code GANL2 and experimental measurement are compared.

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EQUIVALENT CIRCUIT MODEL AND THE GENETIC ALGORITHM

The equivalent circuit of a *N*-cell coupled cavity chain is shown in Fig. 1, where f_i and Q_i are the resonant frequency and quality factor respectively for the *i*th cell (*i* =1, 2, ...N).



Figure 1: Equivalent circuit of a coupled cavity chain.

From the circuit theory we can obtain the matrix as [2]

$$\begin{bmatrix} a_{1} & \frac{k_{01}}{2} & \frac{k_{11}}{2} & 0 \\ \frac{k_{01}}{2} & a_{2} & \frac{k_{02}}{2} & . \\ \frac{k_{01}}{2} & \frac{k_{02}}{2} & a_{3} & . \\ . & . & 0 \\ . & . & a_{N-1} & \frac{k_{0N-1}}{2} \\ 0 & ... & 0 & \frac{k_{1N-1}}{2} & \frac{k_{0N-1}}{2} & a_{N} \end{bmatrix} \begin{bmatrix} X_{1} \\ X_{2} \\ X_{3} \\ . \\ . \\ . \\ . \\ X_{N} \end{bmatrix} = \begin{bmatrix} I_{1} \\ I_{2} \\ I_{3} \\ . \\ . \\ . \\ . \\ X_{N-1} \\ I_{N} \end{bmatrix}$$
(1)

where k_{0i} (*i* =1, 2, ...*N*-1) and k_{1i} (*i* =1, 2, ...*N*-2) are the nearest and next-nearest-neighbor couplings between cells, I_i is the excitation source and X_i is proportional to the current in the *i*th cell. If f_i , Q_i , k_{0i} , k_{1i} , and input coupling β_1 are known, the reflection coefficient $|\Gamma(f)|$ can be obtained by solving (1).

The genetic algorithm is just a reverse problem. It is adopted to calculate the cell parameters (f_i , Q_i , k_{0i} , k_{1i} , and β_1) based on the measured curve of $|\Gamma(f)|$. Therefore inserting the perturbing objects can be avoided in the diagnosis process.

The genetic algorithm starts its calculation by generating a number of populations from the beginning. Therefore it can find the global optimum and does not entirely depend on the initial values. Moreover, the code GANL2 developed by Y. Ni has been combined with the nonlinear least-squares method to speed up the

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convergence [2]. In the original GANL2 code the fitness function for each population is defined as [2]

$$\varepsilon = \sum_{i=1}^{M} \left(\left| \Gamma_{ci} \right| - \left| \Gamma_{mi} \right| \right)^2 \tag{2}$$

where *M* is the point number of the $|\Gamma(f)|$ curve, Γ_c and Γ_m refer to the calculated and measured values, respectively. Appropriate regions of the cell parameters $(f_i, Q_i, k_{0i}, k_{1i}, \text{ and } \beta_1)$ must be provided for the code. The code will not terminate until the pre-defined generation number or the required fitness function has been reached.

DIAGNOSIS PROCESS AND RESULT

Numerical experiment has been carried out based on the 9-cell superconducting copper cavity model to search for the appropriate region of the cell parameters. Firstly the cell parameters calculated by the MAFIA code [5] are used to obtain the curve of $|\Gamma(f)|$, with f_i =1289.4 MHz (middle cells) and 1294.3 MHz (end cells), k_{0i} =0.016 and Q_i =25000. Fig. 2 gives the curve of $|\Gamma(f)|$ calculated directly from the above cell parameters. This curve is provided to the code of GANL2. After calculation for a number of generations, the cell parameters can be obtained when the fitness function decreases to a tolerable value. To check the results, $|\Gamma(f)|$ is recalculated based on the result of GANL2. Fig. 2 shows that the two curves of $|\Gamma(f)|$ agree well and the fitness is about 10⁻⁶.



Figure 2: Numerical experiment result for the 9-cell superconducting copper cavity model.

To determine the appropriate searching region of the cell frequencies, as an example, we choose the generation number to be 10^4 . Fig. 3 presents the relationship between the convergence percentage and the searching region of the cell frequency for the GANL2 code. We should keep the region as large as possible to include the unknown frequency of the detuned cell. But if the region is larger than 18 MHz, it will be difficult for the GANL2 code to obtain a convergent result. Therefore we choose the frequency region to be 14 MHz for the subsequent calculation.



Figure 3: Convergence percentage vs the searching region of the cell frequency for the GANL2 code.

In the following calculation, the searching regions are chosen as: f_i : [1287, 1301] (end cells) and [1282, 1296] (middle cells), Q_i : [10000, 30000], k_{0i} : [0.015, 0.017], k_{1i} : [0.0, 0.0]. The next-nearest-neighbor coupling k_{1i} has been considered to be zero at present.

The reflection measurement and diagnosis system of the L-band 9-cell copper cavity model has been set up at Tsinghua University, as shown in Fig. 4. The reflection curves of $|\Gamma(f)|$ have been obtained by the Network Analyzer (HP8720B), one of which is shown in Fig. 5.



Figure 4: Reflection measurement and diagnosis system of the L-band 9-cell copper cavity model.



Figure 5: Measured reflection curve $|\Gamma(f)|$.

Though the measurement port has been calibrated carefully, the base line of $|\Gamma(f)|$ deviates from 1.0, as shown in Fig. 5. In fact the troughs should have larger effect on the fitness function. The fitness function plays an important role in the genetic operations (reproduction, crossover and mutation) and stopping rules [2]. To apply the GANL2 code on the experimental data the fitness function is modified to

$$\varepsilon = \sum_{i=1}^{M} w_i \left(\left| \Gamma_{ci} \right| - \left| \Gamma_{mi} \right| \right)^2$$
(3)

where w_i is the weight factor.

Fig. 6 gives the comparison of the curve $|\Gamma(f)|$ between the measurement and genetic algorithm result. As we can see from Fig. 6, the curve $|\Gamma(f)|$ derived by GANL2 based on its individual cell parameter results is consistent with the measured curve at the eight troughs. As expected, the fitness is 4×10^{-2} , not as good as the result of above numerical experiment.



Figure 6: Comparison of the curve $|\Gamma(f)|$ between the measurement and genetic algorithm result.

As shown in Fig. 7, a pair of probes with the diameter of 60 mm made by aluminium and Teflon has been prepared and adopted to measure the individual cells. The measured cell parameters are compared with the genetic algorithm result of GANL2.



Figure 7: A pair of probes for the diagnosis of the individual cells.

Fig. 8 gives the cell frequencies for the individual nine

07 Accelerator Technology T06 Room Temperature RF cells calculated by the code GANL2. The error bars come from the measurement results by the pair of probes for four consecutive times. Though the calculated and measured frequencies of the last four cells are consistent, there is some deviation in the results of the first five cells.



Figure 8: Cell frequencies for the nine cells calculated by the code GANL2.

CONCLUSIONS

Preliminary study has been carried out to apply the genetic algorithm on the diagnosis of the L-band 9-cell superconducting copper cavity model (not pre-tuned) without introducing an object in the cavity. The reflection curve $|\Gamma(f)|$ is measured and provided to the code GANL2 to calculate the individual cell parameters. The weight factor has been adopted in the fitness function of GANL2 to make the code more efficient. A pair of probes has been machined to measure the individual cells to test the result of GANL2. The comparison of the calculated and measured cell frequencies shows that though the genetic algorithm result of $|\Gamma(f)|$ agrees with the measurement at the troughs, not all the cells are diagnosed well. This is mainly because there exist some experiment errors when acquiring the reflection curve. We will make further measurement more precisely. Moreover, more points (for example 801) of the reflection curve will be tried instead of 401 points at present.

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