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Physics Procedia 27 (2012) 244 – 247

Physics Procedia

ISS2011

Parametric analysis of flux creep-flow model by using genetic algorithm

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Abstract

The pinning parameters for numerical calculation based on the flux creep-flow model are determined by using genetic algorithm (GA), which has been applied to many practical determination for parameters. Several estimation functions which describe the distance between the experimental and calculated results by GA were proposed, and the difference between the results were calculated. It is found that the pinning parameters of the flux creep-flow model are successfully deduced by GA. The difference between the calculated and experimental results and the calculation time are found to be largely depended on the estimation functions.

Keywords: genetic algorithm (GA); flux creep-flow model; *E-J* characteristics; cuprate high temperature superconductor

1. Introduction

Many kinds of applications using cuprate high temperature superconductors such as Bi based and Rare Earth (RE) based are expected for electric power devices, since the operation temperature is high and the superconductor is thermally more stable than conventional metric superconductors [1]. It is desired to describe the characteristics of critical current density at high temperatures and/or high magnetic fields, since the effect of flux creep becomes serious. However, it is known that it is difficult to use convectional scaling law such as Kramer model [2] for cuprate superconductors at high temperatures. On the other hand, it is well known that the flux creep-flow model is effective to describe the characteristics of electric field vs current density especially at high temperatures [3]. However, it is difficult to determine the pinning parameters to fit the experimental and calculated results, since the number of fitting parameters is 4 to 5. In this study, genetic algorithm (GA) is used to determined the pinning parameters of the flux creep-flow model.

GA is proposed by John Henry Holland of Michigan University on 1975, which is an emergent optimization algorithm [4]. GA is widely used for determination and calculation of parameters in many scientific

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 doi:10.1016/j.phpro.2012.03.456

fields. The operations such as a selection, a crossover and a mutation which are an analogy of transmission of living things are performed to find the optimum solution.

In this study, several evaluation functions are proposed and the pinning parameters of the flux creep-flow model are deduced by GA. The result of difference among the evaluation functions is discussed.

2. Calculation

The characteristics of critical current density of cuprate high temperature superconductors were successfully explained by the flux creep-flow model [3]. The temperature and magnetic field dependences of the critical current density for the case of the virtual flux-creep free is assumed as

$$J_{c0} = A\left(1 - \frac{T}{T_c}\right)^m B^{\gamma-1}\left(1 - \frac{B}{B_{c2}}\right)^2, \tag{1}$$

where A, m and γ are pinning parameters. In practical superconductors, it is well known that the flux pinning strength is widely distributed. Here, it is simply assumed that the pinning strength parameter A is distributed as

$$f(A) = K\exp\left[-\frac{(\log A - \log A_m)^2}{2\sigma^2}\right], \tag{2}$$

where A_m is the most probable value of A, σ^2 is a parameter representing a distribution width and K is a normalization constant. The pinning potential U_0 which determines the flux creep property is described in terms of J_{c0} as

$$U_0 = \frac{0.835 g^2 k_B J_{c0}^{1/2}}{(2\pi)^{3/2} B^{1/4}}, \tag{3}$$

where g^2 is the number of flux lines in a flux bundle. The detail theoretical calculation of E-J characteristics is reported elsewhere [5]. In the above, it is necessary to determined the parameters, A_m, σ^2, γ, m and g^2 for the analysis. In present study, these parameters are determined by Genetic Algorithm (GA) and E-J characteristics are calculated.

Furthermore, Distributed Genetic Algorithm (DGA) is used for determined the parameters, since DGA is knows to be more effective than original GA [7]. The total population in DGA is divided in to sub-population which is often called "island" as shown in Fig. 1. In each sub-population, normal GA operations

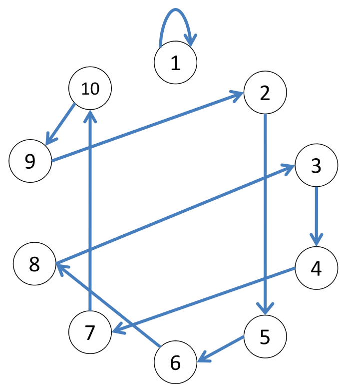

Fig. 1. Migration in Distributed Genetic Algorithm (DGA). After certain generation, some individuals are selected and migrated to other sub-population ("island"). The arrow indicates the direction of the migration. There is no migration for the case of island 1.

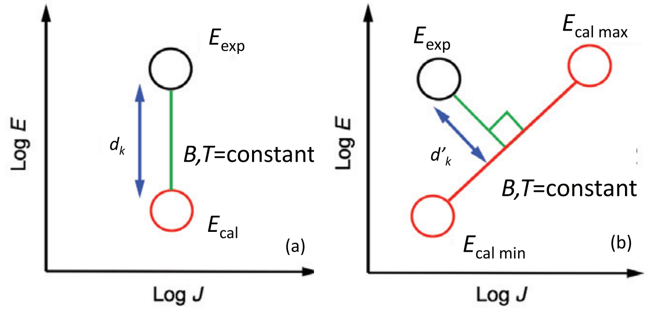

Fig. 2. Definition of distances (a) d_k and (b) d'_k for the evaluation function.

Table 1. Pinning parameters of the experimental values and best deduced values by DGA for each evaluation functions, P_1, P_2, P_3.

	A_m [A/m^2]	σ^2	γ	m
exp.	3.8×10^{11}	0.0072	0.65	2.4
P_1	3.8×10^{11}	0.0071	0.65	2.4
P_2	3.1×10^{11}	0.0049	0.64	2.4
P_3	3.9×10^{11}	0.0074	0.65	2.4

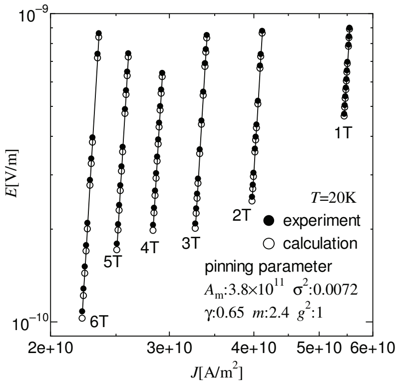

Fig 3. Best fit result of E-J by GA.

are performed for several generations. Then after the certain generation, some of the individuals are chosen and are moved to the another island. This operation is called "migration". In DGA, the problem of the convergence in the same population can be avoid by the operation of migration, resulting in the fast determination of parameters.

The estimation function determines the level of the adaptation of an individual. Therefore, the results of GA and the calculation time are seems to be largely depended on the estimation function. In present study, three following estimation functions are proposed and used for the calculations.

The first and second estimation functions, P_1 and P_2, are determined as

$$P_1 = \sum_{k=1}^{N} d_k, \quad P_2 = \sum_{k=1}^{N} d'_k, \tag{4}$$

where d_k is the distance between the k-th experimental and the calculated values at same value of current density, J, as shown in Fig. 2(a). And d'_k is determined as the distance between E_{cal} and the line of minimum and maximum values of E_{exp} as shown in Fig. 2(b). It is expected that the calculation speed becomes high using P_2, since the number of calculation of E_{cal} is reduced.

The third estimation function, P_3 is determined as

$$P_3 = \sum_{k=1}^{N} d_k \sum_{l=1}^{M} \frac{|n_{\mathrm{exp}} - n_{\mathrm{cal}}|}{n_{\mathrm{exp}}}, \tag{5}$$

where d_k is shown in Fig. 2(a) and is same to the first estimation function. In the above n-value is the parameter represents the sharpness of superconductivity transition described as $E \propto J^n$, where n_{exp} and n_{cal} are the n-value for experimental and calculated values.

In present study, a real data of E-J characteristics is not used, since the true pinning parameters are unknown. Instead of using real data, experimental data, $E_{\mathrm{exp}}(J)$, is calculated with given pinning parameters as shown in Table 1 using the flux creep-flow model. These parameters are from the result of the rare earth coated conductors at 20 K, 25 K and 30 K, and the value of g^2 is unity [6].

In the calculation of DGA, following numbers are used. The number of islands is 10, and the number of individuals is 20 in each island. The number of generation is 100, and the DGA calculation is tried for 50 times for each evaluation function. The migration between the islands is performed every 10 generations.

3. Results and Discussion

Fig. 3 shows the best fitted E-J characteristics of experimental and calculated results by using P_1. The obtained best values of pinning parameters by DGA is also shown in Table 1. It is found that DGA successfully deduces the pinning parameters.

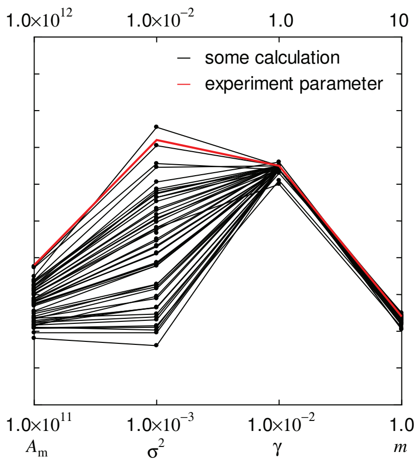

Fig. 4. Results of pinning parameters estimated by DGA for 50 trials. Each pinning parameters are connected for one trial.

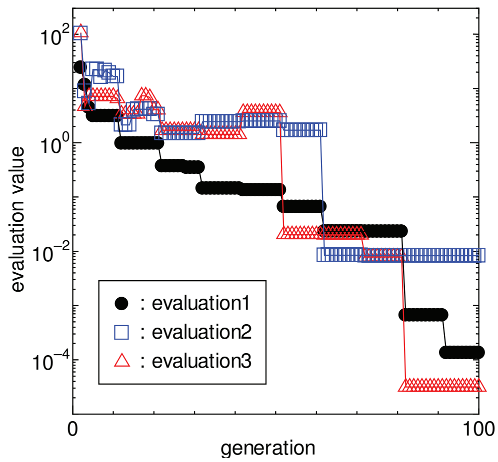

Fig. 5. Evaluation function P_1 as a function of generation with using different evaluation functions, P_1, P_2, P_3.

Fig. 4 shows the result of 50 trial calculations of pinning parameters obtained in DGA calculation using the evaluation function P_1. Each pinning parameters are connected for each one trial. It is found that the values of A_m and σ^2 are largely distributed, while the values of γ and m are almost the same in each trial. It is considered that the similar result of E is obtained with large A_m with large σ^2. In other words, there are many local optimal solutions for the sets of A_m and σ^2, and GA can be found nearly the optimal result.

Fig. 5 shows the comparison result of P_1 with using different evaluation functions of P_1, P_2, P_3 for DGA calculations as a function of generation. Since the migration between islands is performed each 10 generation, the decrease of P_1 is found at the migration. Therefore, DGA is useful way to avoid the convergence in GA calculation. The best result after 100 generations is obtained using evaluation function P_3 in which the n-value is taken into account. However, the best result at 50 generations is P_1. And P_2 and P_3 sometimes increase, while P_1 monotonically decreases with increasing generation. Therefore, it is difficult to determined the best evaluation function. The calculation time is shortest using P_2, since the calculation cost is smallest as shown in Eq. (1).

4. Conclusions

The Distributed Genetic Algorithm (DGA) is used to deduce the pinning parameters, A_m, σ, m, γ of flux creep-flow model with fitting the experimental result of E-J characteristics. Three evaluation functions which determine the adaptation of an individual are proposed. It is found that the pinning parameters are successfully obtained by DGA. The adaptation and calculation speed are largely depended on the evaluation function.

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