OPTIMIZATION OF CHROMATIC SEXTUPOLES IN ELECTRON STORAGE RINGS USING GENETIC ALGORITHMS *

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Abstract

In order to suppress the head-tail instability, strong chromatic sextupoles are used in modern electron storage rings to correct large chromaticities due to small emittance or strong insertion quadrupoles to squeeze the bunch size at some places. However, the introduction of strong chromatic sextupoles also brings severe nonlinearity and might reduce dynamic aperture drastically. In the case of several sextupole families, the genetic algorithms are applied to find suitable configurations of sextupole strengths, directly maximizing dynamic aperture. A GeneRepair operator [1] is introduced into the algorithm to correct chromaticities and optimize the dynamic aperture simultaneously in electron storage rings.

INTRODUCTION

As a conventinal and indispensable step, dynamic aperture of a designed lattice should always be optimized with some methods to get a suitable congfiguration of chromatic sextupoles. Among these methods, the first one is to set up a systematic theorectical framework to evaluate nonlinear perturbation in the storage rings. The driving terms for structural resonances, general chromaticities [2], tune shift with amplitude, etc, are well controlled. The HARMON code [3] is a well-known example of this kind. However, there is no direct relation between the nonlinear perturbation strengths and the dynamic aperture, and there are no obvious criteria on how to control each of the driving terms. Moreover, as it uses local optimizer as its engine, the results are thus strongly affected by the initial conditions.

The second approach works very well for the noninterleaved sextupole configuration [4], such as the case of the KEKB storage rings. The nonlinearities of chromatic sextupoles are canceled efficiently so that chromatic effects and geometric aberrations can be separately dealt with. They can apply the so-called finite-bandwidth chromaticity correction and finite-amplitude matching methods sequently, controlling the nonlinearity in longitudinal and transverse directions, respectively. However, in the case of interleaved sextupoles configuration, transverse and longitudinal nonlinear effects are coupled together, and it becomes difficult to apply this method to solve the problem.

Another approach was proposed by E. Levichev and P. Pimimov [5]. In this treatment, the chromaticities are corrected to the goal by N small steps, while at each step a single pair of focusing and defocusing sextupoles (SF and SD) are used to correct the chromaticities. All the combination of (SD, SF) are tested and the best pair with the largest dynamic aperture is kept at this step. Then, the final dynamic aperture may be optimized. However, if the lattice is working very close to a strong resonance, e.g., a particle factory working nearly at the half integer as its transverse tune, the off-momentum particle might fall into the half integer resonance during the process of chromaticity correction step by step, and the dynamic aperture optimization for off-momentum particles might be difficult to achieved!

To overcome the limitations of these methods, a global optimization method of directly maximizing the dynamic aperture is needed. In this paper, we try to adopt the genetic algorithms (GA) to optimize the chromatic sextupoles.

OPTIMIZING BY USING GA

Genetic algorithm(GA) is a heuristic search alogrithm, that mimics the process of natural evolution. It has been used in the optimization of harmonic sextupoles of third generation synchrotron light sources [6, 7, 8] recently, with the aim of maximizing dynamic aperture. Moreover, in these storage rings, two families of very strong chromatic sextupoles are used to correct chromaticities, and several families of harmonic sextupoles are used to compensate the harmonics of the strong nonlinearity mainly induced by the chromatic sextupoles. However, in the case of a compact ring with several families of chromatic sextupoles, especially when there are no harmonic sextupoles installed, the chromaticity correction and dynamic aperture optimization are strongly crosstalk to each other.

The optimization of chromatic sextupoles is actually a problem of nonlinear optimization with linear constraints of variables. We try to introduce here a GeneRepair operator in the GA to fulfill the constraints. The GeneRepair operator works in this way: set the chromatic sextupole strengths into the lattice, and calculate the corrected chromaticities. If the corrected chromaticities satisfy the requirement, then no modification is done. Otherwise, the chromaticities are corrected to the required values with all the chromatic sextupoles, based on the current values. Since there are more variables than constraints, and the solution of the correction relies on the initial variables, the genetic diversity of the population is still kept to some extent. However, if a chromosome is mutated not too much, the GeneRepair operator would probably recover its original values, and cancel out the effect of mutation. It thus accelerates the convergence of the algorithm. Actually, the effect of the GeneRepair operator and mutation operator can be combined, i.e., the ”effective mutation rate” should include the counteraction of the GeneRepair operator. Moreoever,

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an Extinction and Immigration operator is introduced and could also make up for this shortcoming.

It is showed in [9] that the diversity of the population tends to decrease after some generations, and the algorithm is likely to converge before the desired optimization goal is achieved. We can either restart the GA or else re-establish the diversity. The latter approach is chosen in our implementation through the so called Extinction and Immigration operator [10]. It works in the following way: if the best fitness in the population ceases to increase for several successive generations, all but the best chromosome in the current generation are eliminated(extinction), and the same number of new chromosomes are generated randomly to fill the vacancy of the population(immigration).

Since the variables we are dealing with are the strengths of chromatic sextupoles, a continuous GA dealing with real parameters [11] is adopted. Compared with the binary encoding GA, it's more straightforward and easier to implement. A chromosome is a vector of strengths of chromatic sextupole families, with each of its gene corresponding to a specified sextupole family. The detailed algorithm can be referred to [12]. Besides, the best individual is always passed down to the next generation without changes. And the algorithm terminates if the optimization goal is obtained, or the loop has been repeated a certain number of times. The flow chart of the algorithm is shown in Fig. 1.

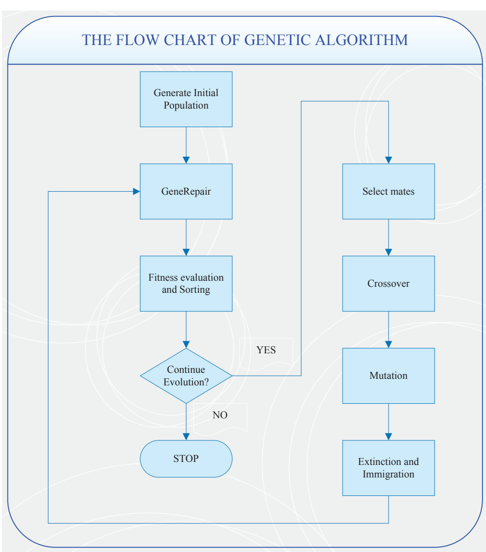

Figure 1: Flow chart of the algorithm

ALGORITHM APPLICATION

We apply here the algorithm to optimize the chromatic sextupoles in BEPCII. BEPCII is a symmetric double-ring particle factory-like e^+e^- collider, composed of quasi-FODO cells and insertions of IR and injection, and optimized at the beam energy of 1.89GeV. In either the electron ring or the positron ring of BEPCII there are in total 36 chromatic sextupoles placed in a 4-fold symmetric manner, with 5 defocusing sextupoles and 4 focusing sextupoles arranged alternatively in each arch. Since 18 power supplies are used in each ring, two SDs and SFs placed symmetrically in north and south half rings are in series powered. Thus, there are at most 18 independent variables of sextupole strengths. Moreover, due to the limited space in the interaction region, no harmonic sextupole is used in BEPCII. The main parameters are summarized in Table 1.

Table 1: Parameters of BEPCII storage rings

Parameter	Value
Beam energy	1.89 GeV
Design luminosity	$1.0 \times 10^{33}\mathrm{cm}^{-2}\mathrm{s}^{-1}$
Circumference	237.53 m
Tunes (x/y/s)	6.510/5.580/0.035
Natural chromaticities (x/y)	-11.06/-20.63
Natural emittance	154 nm-rad
Energy spread	5.21×10^{-4}
Momentum compaction factor	0.0243
β_x/β_y at IP	1/0.015 m
RF bucket height	0.0068

We implement the algorithm using a SADScript programming language [13]. With the built-in shared memory parallel algorithm, the fitness of individuals of the population which is time consuming, is evaluated in parallel, and the other process in the GA is done in serial. In SAD, the full six-dimensional tracking can be reduced into a two-dimensional case, by setting the initial coordinates $p_x = p_y = z = 0$, and tracking along a certain direction of J_y/J_x in the transverse plane with a certain momentum offset. The number of surviving particles with different amplitudes at a two-dimension grid point $(J_x, dp/p)$ is recorded as the score of the dynamic aperture. We do the tracking for 2000 turns, with synchrotron motion but without radiation damping or quantum excitation, off-momentum particles within $\pm 0.68\%$, say $\pm 13\sigma_e$, are also tracked to check the momentum aperture. Since the beams before being injected into BEPCII storage rings are round beams, we maximize the worst score and the total score of different momentum offsets, along the line $J_y/J_x = 1:1$, to obtain a good enough acceptance.

To suppress the head-tail instability, the chromaticities are generally corrected to positive values. However, the larger the corrected chromaticities are, the stronger the strengths of sextupoles will be, and thus probably the smaller dynamic aperture. As a result, the corrected chromaticities are chosen to be small positive values in general. In the case of BEPCII, chromaticities equal to or larger than $(0.3, 0.3)$ are acceptable. Considering the chromaticity requirement to the GeneRepair operator, we can either assign the corrected chromatities to be fixed values, say $(0.5, 0.5)$, or just require the corrected chromaticities to be larger than (0.3,0.3). The latter case is prefered, because those chromosomes with corrected chromaticities larger than (0.3, 0.3) but not equal to $(0.5, 0.5)$ are allowed to breed. Therefore, the solution space is enlarged, and it reduces the effect of GeneRepair operator on the "effective mutation rate".

Generally speaking, the population of a generation is chosen to be 100, and a multi-gene mutation is applied with a high rate of 0.1 0.2, to assure a reasonable "effective mutation rate". Besides, the Extinction and Immigrantion operator is applied if no increase in the best fitness is detected for seven successive generations. The optimization is done on an 8-core workstation, and typically it takes 20 generations to converge. With the Extinction and Immigration operator, the process can keep running, and better results can be expected within 200 generations, which takes about 12 hours.

With this method, the optimized dynamic aperture (new result) is compared with theprevious results, which were obtained with HARMON code, with 4 families or 18 families of chromatic sextupoles, respectively. Particles with momentum offset

$$dp/p = \sigma_\epsilon \times i, i = -13, -12, \cdots, 12, 13, \qquad (1)$$

are tracked along the line $J_y/J_x = 1 : 1$, as displayed in Fig. 2.

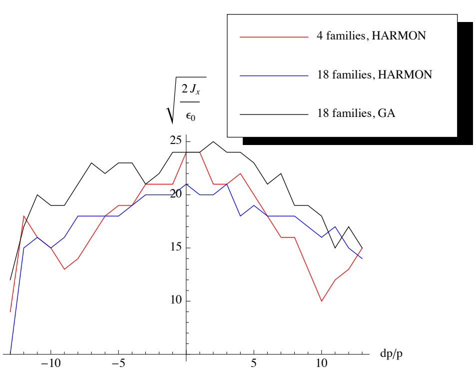

Figure 2: Comparision of dynamic aperture

The new results of dynamic aperture are also shown in transverse plane in Fig. 3. Since beam-beam interaction might cause beam blow-up, the tracking results are normalized with the full coupling emittances, i.e, $(\epsilon_x, \epsilon_y) = (\epsilon_0, \epsilon_0/2)$. Moreover, the general chromaticities of β functions at the IP and tunes are depicted in Fig. 4.

CONCLUSION

The present work discusses a modified genetic algorithm for optimizing the multi-families of chromatic sextupoles, by introducing a GeneRepair operator into the algorithm, and a better result is obtained, compared with the traditional methods. This algorithm can naturally be applied to simultaneous optimization of chromatic and harmonic sextupoles in light sources. The application to the 3rd generation light source like Beijing Advanced Photon Source is under way.

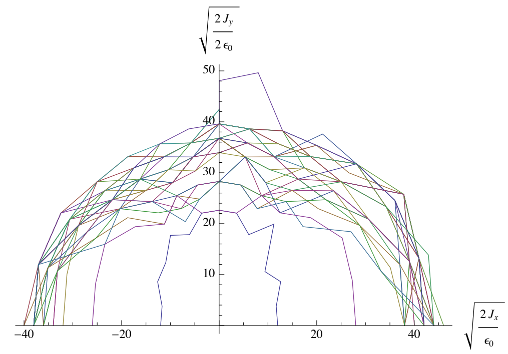

Figure 3: Dynamic aperture got with the method of GA

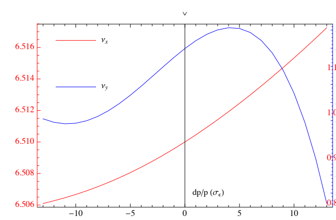

Figure 4: Tunes versus dp/p

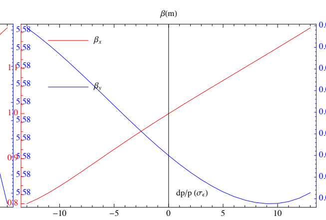

Figure 5: β^* versus dp/p

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