A New Genetic Algorithm based on Anti-Darwinism for Multi-Objective Part-Tool Grouping Problem

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Abstract- Grouping parts and tools is an essential problem that arises in the set-up of a Flexible Manufacturing System (FMS). In the Part-tool Grouping Problem (PGP), the process of assembling parts is assigned to several machines so as to optimize plural performance criteria. In this paper, the PGP is formulated as a multi-objective optimization problem. Then, for sampling various non-dominated solutions from along the entire Pareto-optimal front of the PTP, a new Genetic Algorithm (GA) based on the evolutionary theory advocated by Kinji Imanishi is proposed. While conventional GAs mimic the process of natural selection, the proposed GA realizes the situation of habitat segregation, i.e., a principle of coexistence. The Imanishism-based GA can find various Pareto-optimal solutions effectively, because it keeps the diversity of population in both of the objective and the problem spaces without harming the power of local search operations. The advantage of the Imanishism-based GA is confirmed quantitatively through computational experiments conducted on a practical problem instance of the PGP.

I. INTRODUCTION

A Flexible Manufacturing System (FMS) consists of a set of computer-controlled machines capable of performing a number of different operations. In the FMS, a bunch of related components are processed and assembled simultaneously. Processing a part may require several tools, and normally a tool can be used to process several parts. On the other hand, a tool may be used on several machines but it has to be loaded and unloaded holding their operations for a time. Therefore, grouping parts and associated tools in advance helps to make an efficient production planning for the FMS[1, 2].

The Part-tool Grouping Problem (PGP) concerned with the FMS usually requires the simultaneous optimization of multiple, and often competing, performance criteria. Concretely, for managing the entire system efficiently, not only the combination of parts and tools but also the number of available machines has to be considered. However, in order to apply conventional approaches for solving the PGP, it has to been reduced to a single-objective optimization problem such as a liner integer-programming formulation[1, 2]. With no doubt, it may be desirable that the PGP is formulated as a multi-objective optimization problem.

The multi-objective optimization problem has a set of alternative solutions called Pareto-optimal ones, which are optimal in the wider sense that no other solutions are superior to them when all objectives are considered. Furthermore, the number of the Pareto-optimal solutions can be extremely large for the PTP formulated as a multi-objective optimization problem. Therefore, from the production planner's point of view, it is desirable to sample various solutions from along the entire Pareto-optimal front. Hence, the goal of solving the PTP is to obtain a set of various solutions distributed uniformly on the Pareto-optimal front.

Genetic Algorithms (GAs)[12] seem particularly suitable to solve multi-objective optimization problems, because they deal simultaneously with a set of possible solutions so-called population. Actually, a lot of GA approaches have been proposed for multi-objective optimization problems, which are reviewed in several comprehensive works[3, 4, 5]. Regardless of the number of objective functions, traditional GAs emulate the process of natural selection thought by Charles Darwin[6]. However, the selection of only excellent individuals according to their fitness is likely to lose the diversity of population, which causes the undesirable phenomenon known as premature convergence. In order to find various Pareto-optimal solutions with such a Darwinism-based GA, several artificial techniques, namely, fitness sharing and ranking, need to be combined, and the performance of GA is highly dependent on an appropriate design of these techniques.

Kinji Imanishi (1902-1992), Emeritus Professor of Koto University, is a noted ecologist, a renowned mountaineer and explorer, and the recipient of Japan's Order of Culture First class. Instead of competition among individuals in the struggle for existence, namely, the natural selection, he contends the concept of habitat segregation that is a principle of coexistence[7, 8].

In this paper, a new GA based on the evolutionary theory asserted by Imanishi is proposed, because it seems that the weakness of conventional GAs essentially results from the concept of natural selection inspired by the Darwinism. Then, the Imanishism-based GA is applied to the PGP formulated as a multi-objective optimization problem. Keeping the diversity of population in both the objective and the problem spaces, the Imanishism-based GA can sample various solutions from along the entire Pareto-optimal front of the PTP.

In the sequel, the PGP is formulated as a multi-objective optimization problem in which three objective functions ought to be minimized in Section II. The proposed Imanishism-based GA and underlying principles are described in Section III. First of all, three types of distances, namely, genotypic, phenotypic and functional ones, between two individuals are introduced and used to realize the situation of habitat segregation in the population. The phenotypic distance is also employed in the Improved Harmonic-Crossover operation that is an improved version of the Harmonic-Crossover proposed in our previous papers[9, 10]. Through computational experiments conducted on a practical problem instance of the PTP, the merits of the proposed GA are confirmed quantitatively in Section IV. Finally, conclusions are drawn in Section V.

II. PROBLEM FORMULATION

We formulate the PTP concerned with the FMS as a multi-objective optimization problem. Let suppose that a fixed number of parts are going to be processed and then connected to each other with an appropriate tool. By using some machines, these operations are executed in parallel. The processing time spent on each part is the same, and the number of machines is a decision to be made by the production planner. In order to minimize the total operation time of the FMS, all parts should be distributed equally to a large number of machines. However, since different kinds of tools are used to assemble these parts, associated parts should be assigned into the same machine as much as possible. Obviously, trade-off exists in the objectives.

Supposing that two types of tools are necessary to assemble all parts, the relation between parts and tools can be represented by a graph as shown in Fig.1: a vertex corresponds to a part, and each edge between two parts denotes the type of tool used to connect them. Therefore, a problem instance of the PGP is given by a graph $G = (V,\ E)$: $E = E^{\alpha} \cup E^{\beta}$; $E^{\alpha} \cap E^{\beta} = \emptyset$. A feasible solution of the PTP, which is denoted by s, is a partition of $v_i \in V$ into k subsets: $V = V_1 \cup \cdots \cup V_p \cup \cdots \cup V_k$; $V_p \cap V_q = \emptyset$ $(p \neq q)$; k corresponds to the number of available machines. Fig.1 also shows a partition of V into three subsets. $E_p^{\alpha} \subseteq E^{\alpha}$ and $E_p^{\beta} \subseteq E^{\beta}$ denote subsets of edges both endpoints of which are included in the same subset $V_p \subseteq V$. Thereby, we try to minimize the following three objective functions simultaneously.

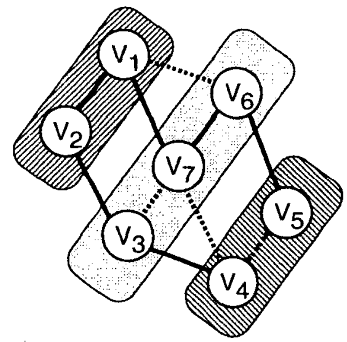

Fig. 1. Graphical representation of a problem instance of the PGP and its feasible solution, or phenotype.

$$\left[\begin{array}{lcl} f_1(s) & = & \max\limits_{1\leq p\leq k}\{\ |V_p|\ \} \\ f_2(s) & = & |E^{\alpha}| - \sum\limits_{p=1}^{k} |E_p^{\alpha}| \\ f_3(s) & = & |E^{\beta}| - \sum\limits_{p=1}^{k} |E_p^{\beta}| \end{array}\right. \qquad (1)$$

Mathematically, the Pareto-optimal solution of the PTP, which is optimal in the sense that no improvement can be achieved in any objective without degradation in others, is defined as follow: a feasible solution s^1 is said to dominate s^2, iff $\forall j \in \{1, \cdots, 3\}$ $f_j(s^1) \leq f_j(s^2)$ and $\exists j \in \{1, \cdots, 3\}$ $f_j(s^1) < f_j(s^2)$; s is Pareto-optimal, iff there doesn't exist any solution that dominates s.

III. GENETIC ALGORITHM

In this section, we describe the proposed Imanishism-based GA, i.e., a new approach to the PTP formulated as a multi-objective optimization problem.

A. Phenotype and Genotype

In the application of GA to the PGP, we regard each partition of V, a feasible solution of the PGP, as an individual so-called phenotype. Then, in order to apply genetic operations, we encode such a partition of V into a string of integer $A = (a_1, \cdots, a_n)$ $(n = |V|)$ so-called genotype. Each element $a_i \in A$ $(i = 1 \sim n)$ denotes the subscript p $(p = 1 \sim k)$ of the subset V_p in which the corresponding vertex $v_i \in V$ is included.

Although the encoding of phenotype into genotype seems natural enough, it does not give unique representation. For example, a phenotype of the PGP in Fig.1 can be represented by $k!$ $(k = 3)$ different genotypes A^x $(x = 1 \sim 6)$ as shown in (2), because we have not to distinguish respective subsets $V_p \subseteq V$ $(p = 1 \sim k)$.

$$\begin{cases} A^1 &= (1,\ 1,\ 2,\ 3,\ 3,\ 2,\ 2) \\ A^2 &= (1,\ 1,\ 3,\ 2,\ 2,\ 3,\ 3) \\ A^3 &= (2,\ 2,\ 1,\ 3,\ 3,\ 1,\ 1) \\ A^4 &= (2,\ 2,\ 3,\ 1,\ 1,\ 3,\ 3) \\ A^5 &= (3,\ 3,\ 1,\ 2,\ 2,\ 1,\ 1) \\ A^6 &= (3,\ 3,\ 2,\ 1,\ 1,\ 2,\ 2) \end{cases} \tag{2}$$

Let $[A]$ be a set of isomorphic genotypes A^x $(x = 1 \sim k!)$ which represent the same phenotype. We adopt such a set of isomorphic genotypes $[A]$ as the mathematical expression of the corresponding phenotype.

B. Metric Functions

We introduce metric functions to the search space of genotypes, the problem space of phenotypes and the objective space respectively. First of all, we define a genotypic distance between two genotypes $A = (a_1, \cdots, a_n)$ and $B = (b_1, \cdots, b_n)$ by the Hamming distance as,

$$\delta_g(A, B) = \sum_{i=1}^{n} h(a_i, b_i) \tag{3}$$

where, if $a_i = b_i$, $h(a_i, b_i) = 0$; if $a_i \neq b_i$, $h(a_i, b_i) = 1$.

Then, we define a phenotypic distance between two phenotypes $[A]$ and $[B]$ by the least genotypic distance between the sets of isomorphic genotypes.

$$\delta_p([A], [B]) = \min\{\delta_g(A, B) \mid A \in [A],\ B \in [B]\} \tag{4}$$

From (3) and (4), the following relation holds.

$$\delta_p([A], [B]) \leq \delta_g(A, B) \leq n \tag{5}$$

where, $A \in [A]$, $B \in [B]$.

The phenotypic distance defined in (4) is justified by the following Theorem 1 and Theorem 2[10].

Theorem 1: δ_p in (4) satisfies the metric axiom.

$$\begin{cases} [A] = [B] & \Leftrightarrow & \delta_p([A], [B]) = 0 \\ \delta_p([A], [B]) & \geq & 0 \\ \delta_p([A], [B]) & = & \delta_p([B], [A]) \\ \delta_p([A], [C]) & \leq & \delta_p([A], [B]) + \delta_p([B], [C]) \end{cases}$$

□

Theorem 2: The phenotypic distance can be evaluated in a polynomial time complexity: $O(n + k^3)$. □

Finally, in the objective space of the PTP, we define a functional distance between two points $\mathbf{f}([A])$ and $\mathbf{f}([B])$ by using the Manhattan distance as,

$$\delta_f(\mathbf{f}([A]), \mathbf{f}([B])) = \sum_{j=1}^{3} \mid f_j([A]) - f_j([B]) \mid \tag{6}$$

where, $\mathbf{f}([A]) = (f_1([A]),\ f_2([A]),\ f_3([A]))$.

C. Harmonic Crossover

In the design of GA to the PGP, encoding solution as a string allows the application of one-point (1X), two-point (2X) and uniform (UX) crossovers[11]. We could enhance the performance of these traditional crossovers by using a new crossover technique named the Harmonic crossover (H-crossover)[9, 10]. In order to preserve the common characteristics of parents in their child, the H-crossover considers the phenotypic distance between them in genetic recombination process. Assuming that every crossover creates one child from two parents, C is created from A and B in the following procedure.

[H-crossover]

Step 1: Transform one of the parents $B \in [B]$ to an isomorphic genotype $B^z \in [B]$ so that the genotypic distance $\delta_g(A, B^z)$ turns to the minimum, i.e., $\delta_g(A, B^z) = \delta_p([A], [B])$ holds.

Step 2: Applying one of the traditional crossovers, namely, 1X, 2X and UX, to the parents A and B^z, create a new child C. □

For example, let's apply the uniform crossover (UX) to A and B in (7), where $\delta_g(A, B) = 6$ holds initially. Specifying random cut points with an arbitrary bit mask $M = (m_1, \cdots, m_n)$ of set $\{0,\ 1\}$, a child C is created from A and B as shown in (8).

$$\begin{cases} M &= (0,\ 1,\ 0,\ 1,\ 0,\ 1,\ 0) \\ A &= (1,\ 1,\ 2,\ 2,\ 3,\ 3,\ 2) \\ B &= (1,\ 2,\ 3,\ 4,\ 2,\ 2,\ 4) \end{cases} \tag{7}$$

$$C = (1,\ 2,\ 2,\ 4,\ 3,\ 2,\ 2) \tag{8}$$

where, if $m_i = 0$, $c_i = a_i$; if $m_i = 1$, $c_i = b_i$.

On the other hand, let's apply the Harmonic uniform crossover (H-UX) to the same parents in (7). In Step 1 of the H-crossover, we transform $B \in [B]$ to $B^z \in [B]$ as shown in (9), where the genotypic distance is minimized such as $\delta_g(A, B^z) = \delta_p([A], [B]) = 2$.

$$B^z = (1,\ 3,\ 4,\ 2,\ 3,\ 3,\ 2) \tag{9}$$

In Step 2, applying the traditional UX to A and B^z, a new child is obtained as shown in (10).

$$C = (1,\ 3,\ 2,\ 2,\ 3,\ 3,\ 2) \tag{10}$$

The next theorem says that the child $[C]$ created by the H-crossover always comes to a point on the segment between its parents $[A]$ and $[B]$ in the problem space[10]. Consequently, we can conclude that the characteristic of parents is preserved in their child.

Theorem 3: Employing the H-crossover, the following holds among child $[C]$ and its parents $[A]$, $[B]$.

$$\delta_p([A], [C]) + \delta_p([B], [C]) = \delta_p([A], [B]) \tag{11}$$

□

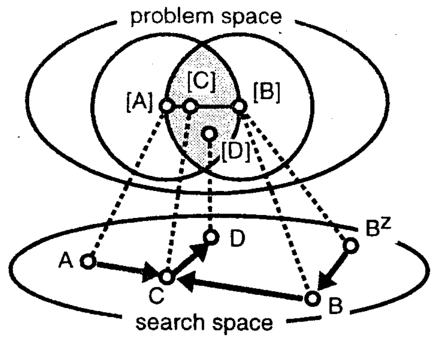

Fig. 2. Behavior of children and parents according to the Harmonic and the Improved Harmonic crossovers.

D. Improved Harmonic Crossover

We propose a new genetic operation so-called the Improved Harmonic Crossover (IH-crossover), which combines the above-mentioned H-crossover with a local optimization algorithm. First of all, a new child C created by using the H-crossover. Then a local optimization algorithm is employed to improve the initial solution $[C]$ intensively. The local optimization algorithm transforms $[C]$ into another individual $[D]$ by changing the values of respective elements $c_i \in C$ randomly as long as $[C]$ is dominated by $[D]$, and ends when no further improvement can be made. At that time, in order to keep the parents' characteristics acquired by the H-crossover, the alteration of $c_i \in C$ is prohibited on the common elements included in both parents A and B^z.

The next theorem says that the child $[D]$ created by the IH-crossover always comes to a point in the area between its parents $[A]$ and $[B]$ in the problem space. Consequently, we can conclude that the characteristic of parents is preserved even after the application of the local optimization algorithm.

Theorem 4: Employing the IH-crossover, the following holds among child $[D]$ and its parents $[A]$, $[B]$.

$$\max\{\delta_p([A],[D]),\ \delta_p([B],[D])\} \leq \delta_p([A],[B]) \quad (12)$$

Proof: See appendix. □

A schematic of Theorem 3 and Theorem 4 is shown in Fig.2 for the case where the H-crossover creates a new child C from parents A and B, after that the restricted local optimization algorithm transforms C into D in the search space. According to Theorem 4, it is guaranteed that the child $[D]$ created by the IH-crossover always exists in the dark-shaded area in the problem space.

E. Habitat Segregation

In order to keep the diversity of population, we propose a new generation alternation model inspired by the principle of habitat segmentation. Instead of individuals, Imanishi pays attention to interaction between species, and contends that there is no struggle to survive among different species. Therefore, we try to hold various species in the population as much as possible.

First of all, in order to distinguish between species, we compare two individuals based on their structural and functional differences. Namely, we introduce two kind of species-radiuses L_p and L_f. The structural species-radius L_p is given by phenotypic distance measure in the problem space. On the other hand, the functional species-radius L_f is given by functional distance measure in the objective space. Thereby, if two individuals $[A]$ and $[B]$ satisfy both of the following conditions, they are regarded as the same species.

$$\left[\begin{array}{rcl} \delta_f(\mathbf{f}([A]),\mathbf{f}([B])) & \leq & L_f \\ \delta_p([A],[B]) & \leq & L_p \end{array}\right. \quad (13)$$

The IH-crossover creates a new child D from two parents A and B selected randomly. Then, an individual $[E]$ that belongs to the same species with $[D]$ is selected from the current population. If $[E]$ is dominated by $[D]$, $[E]$ is replaced by $[D]$. In the case that such an individual of the same kind does not exist in the population, the worst one assigned the largest rank is eliminated. In order to evaluate the dominance property for each individual in the population, we adopt the ranking method[12]. This method assigns the rank 1 to the non-dominated individuals in a population and ignore them, and then assigns the rank 2 to the non-dominated individuals in the rest of the population, and so on.

In the following generation alternation model of the proposed GA, we need to decide three GA-parameters, namely, population size $|P|$, terminal generation T, and functional species-radius L_f. The structural species-radius L_p is controlled automatically.

[Generation Alternation Model]

Step 1: Create a set of genotypes randomly as an initial population $P(0)$. Set generation $t = 0$. Set structural species-radius $L_p = |V|$ initially.

Step 2: Select two parents A and B ($[A] \neq [B]$). Employing the IH-crossover, create a new child D.

Step 3: If $\exists E \in P(t)$ satisfies $\delta_f(\mathbf{f}([E]),\mathbf{f}([D])) \leq L_f$, then go to Step 4, else go to Step 7.

Step 4: If $\delta_p([E],[D]) \leq L_p$ holds, then go to Step 5, else go to Step 6.

Step 5: If $[D]$ is dominated by $[E]$, then eliminate D, else eliminate E. Go to Step 10.

Step 6: If $[D]$ ($[E]$) is dominated by $[E]$ ($[D]$), then eliminate D (E); otherwise, compare them for the margin of the structural species-radius, and eliminate one (D or E) that has the closer phenotype in the current population. Go to Step 10.

Step 7: If $\exists G \in P(t)$ satisfies $\delta_p([G],[D]) \leq L_p$, then go to Step 8, else go to Step 9.

Step 8: If $[D]$ ($[G]$) is dominated by $[G]$ ($[D]$), then eliminate D (G) and go to Step 10; otherwise, let $L_p = \delta_p([G],[D])$ and go to Step 9.

Step 9: Eliminate an individual that is assigned the largest rank from the current population $P(t)$.

Step 10: Let $t = t + 1$. If $t = T$, then output all non-dominated individuals in the final population $P(T)$, else go to Step 2. □

IV. COMPUTATIONAL RESULTS

In this section, the computational results are described which have been carried out using the proposed Imanishisim-based GA for solving a practical problem instance of the PTP.

The problem instance $G = (V, E^{\alpha} \cup E^{\beta})$ consists of 64 parts ($|V| = 64$) and 56×2 edges ($|E^{\alpha}| = 56$ and $|E^{\beta}| = 56$). For the Imanishism-based GA, we fix GA-parameters as $T = 10^4$ and $|P| = 50$ except the functional species-radius L_f, and employ the Improved Harmonic uniform crossover (IH-UX) to create a new child. The Imanishism-based GA was programmed in C-language and run on a personal computer (CPU: intel Pentium III; 400[MHz]).

At first, we chose the functional species-radius as $L_f = 5$. Fig.3 plots the values of objective functions $\mathbf{f} = (f_1, f_2, f_3)$ evaluated for individuals included in the initial and the final populations respectively. Comparing the distribution of them, we can confirm that all of the individuals have made rapid progress without losing the diversity of population.

Next, we decreased the functional species-radius to $L_f = 0$. Fig.4 plots the values of objective functions in the same way with Fig.3. Comparing the result of Fig.4 with that of Fig.3, the final population in Fig.4 has been converged in the objective space. Actually, the final population in Fig.4 ($L_f = 0$) contains 6 non-dominated solutions, whereas the final population in Fig.3 ($L_f = 5$) contains 8 non-dominated solutions.

In order to evaluate the performance of the generation alternation model inspired by the principle of habitat segregation, we observed the average distance between individuals in each population $P(t)$ ($t = 0 \sim T$). Fig.5 shows the mean value of functional distance against to the generation, where the results are averaged over 10 runs. Similarly, Fig.6 shows the mean value of phenotypic distance. From the results of Fig.5 and Fig.6, we can confirm that the diversity of population is preserved in both of the objective and the problem spaces by choosing an appropriate functional species-radius L_f.

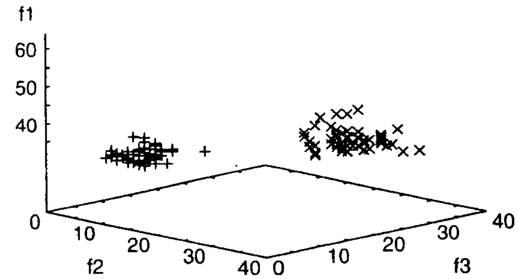

Fig. 3. Initial (denoted by $\times$) and final (denoted by $+$) populations in the objective space ($L_f = 5$).

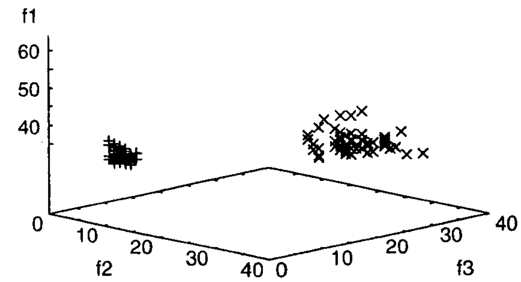

Fig. 4. Initial (denoted by $\times$) and final (denoted by $+$) populations in the objective space ($L_f = 0$).

V. CONCLUSIONS

In this paper, the PGP has been formulated as a multi-objective optimization problem. Then a new GA based on an Ant-Darwinism, i.e., the evolutionary theory advocated by Kinji Imanishism, has been proposed and applied to the PGP successfully.

In order to sample various solutions from along the Pareto-optimal front of the PGP, the concept of habitat segregation was reflected in the design of the proposed GA. Concretely, two types of species-radiuses were introduced into the objective and the problem spaces respectively to keep the diversity of population. Furthermore, the Improved Harmonic Crossover, which contained a local optimization algorithm, was proposed and used to find a Pareto-optimal solution effectively. Finally, computational experiments were conducted on a practical problem instance of the PGP. As a result, we could confirm the advantage of the proposed GA.

In future works, we would like to apply the proposed Imanishism-based GA to many sort of multi-objective optimization problems which arise in the design of FMS.

ACKNOWLEDGMENT

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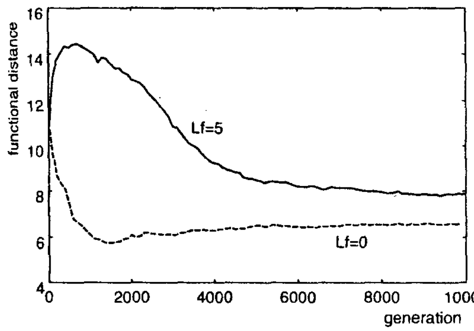

Fig. 5. Mean value of functional distance

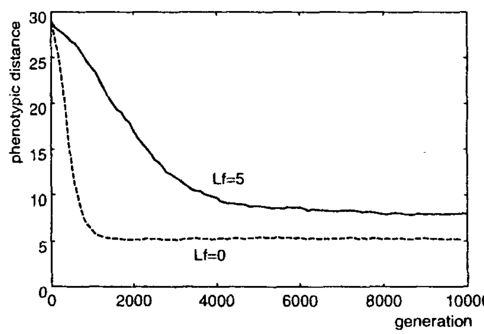

Fig. 6. Mean value of phenotypic distance

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APPENDIX

We can regard that each element a_i of genotype $A = (a_1, \cdots, a_n)$ indicates both its value $a_i \in \{1, \cdots, k\}$ and its position $i \in \{1, \cdots, n\}$. Hereafter, we call such an element a_i $(i = 1 \sim n)$ gene. Considering a genotype A as a set of gene, $A = \{a_1, \cdots, a_n\}$, we can describe the genotypic distance between A and B as follow.

$$\delta_g(A, B) = n - |A \cap B| \tag{14}$$

The IH-crossover is applied to genotypes $A \in [A]$ and $B^z \in [B]$ which satisfy the following equation.

$$\delta_p([A], [B]) = \delta_g(A, B^z) \tag{15}$$

Since the child D has common genes of its parents A and B^z, the following relation holds among them.

$$\left(\begin{array}{l} D \supseteq A \cap B^z \ \wedge \ A \supseteq A \cap B^z \\ \Rightarrow \ |A \cap D| \geq |A \cap B^z| \end{array} \right. \tag{16}$$

From (14) and (16),

$$\left(\begin{array}{lcl} \delta_g(A, D) & = & n - |A \cap D| \\ & \leq & n - |A \cap B^z| = \delta_g(A, B^z) \end{array} \right. \tag{17}$$

From (5), (15) and (17),

$$\left(\begin{array}{lcl} \delta_p([A], [D]) & \leq & \delta_g(A, D) \\ & \leq & \delta_g(A, B^z) = \delta_p([A], [B]) \end{array} \right. \tag{18}$$

Similarly, we can derive the following relation.

$$\delta_p([B], [D]) \leq \delta_p([A], [B]) \tag{19}$$