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An Imanishism-Based Genetic Algorithm for Sampling Various Pareto-Optimal Solutions: An Application to the Multiobjective Resource Division Problem

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SUMMARY

For sampling various solutions from the entire Pareto front of the multiobjective resource division problem, a new Genetic Algorithm (GA) based on an evolutionary theory advocated by Kinji Imanishi is proposed. First, two types of distance between two individuals, namely, structural and functional distances, are introduced and used to define four types of relation between them, namely, homogeneous, heterogeneous, homologous, and analogous species. Then, for keeping a variety of species within a population as far as possible, a new generation alternation model with variable population size is presented. In order to find Pareto-optimal solutions effectively, a new genetic operation that combines conventional harmonic crossover with a local optimization algorithm is also proposed. Finally, the advantage of the Imanishism-based GA is demonstrated through computational experiments conducted on two- and three-objective problem instances. © 2002 Scripta Technica, Electr Eng Jpn, 139(2): 23–35, 2002; DOI 10.1002/eej.10010

Key words: Imanishi's evolutionary theory; habitat segregation; distance; multiobjective optimization.

1. Introduction

The Genetic Algorithm (GA) has been successfully applied to multiobjective optimization problems, which usually have several optimal solutions incomparable with one another, because GA can survey different parts of the search space simultaneously based on a population, a set of solutions called individuals. Incidentally, in order to choose a preferred solution suiting a personal taste from several optimal solutions found by the GA, the decision maker could use some traditional techniques, such as the satisficing trade-off method [1] and the Analytic Hierarchy Process (AHP) [2].

It has been said that humans are good at taking a broad view of situations from instinct, and are able to make a global decision based on experience. On the other hand, humans cannot recognize any difference less than the difference threshold nor manage immense data at one time [3]. Thus, the desirable function for the GA applied to multiobjective optimization problems is not to find as many optimal solutions as possible, but to sample typical solutions from the set of all nondominated solutions called Pareto-optimal solutions. In order to design such a practical GA, we have to consider a way to keep the diversity of the population steady without harming the dynamical process for seeking Pareto-optimal solutions.

Conventional GAs based on Darwinism mimic the process of natural selection and select some individuals from the current population based on their fitness, namely, superiority or inferiority. In order to maintain population diversity, several techniques have been proposed for conventional GAs. The sharing technique, which obtained its idea from the ecological niche, evaluates the fitness while taking the structural distance between individuals into account [4]. However, since the sharing technique reduces only the fitness for similar individuals gathering in a niche to decrease their survival chances, it cannot manage the fitness of individuals outside the niche. Another technique divides the objective function space into several regions and defines the fitness for individuals in each of the regions [5]. The technique aims to maintain population diversity in the objective function space. But population diversity should not be discussed only in the objective function space, because the performance of the GA depends on the distribution of individuals over the problem space. Besides these techniques, some creative methods have been reported [6, 7]; however, conventional GAs based on Darwinism have

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to control population diversity indirectly through adjustment of individual fitness.

Kinji Imanishi (1902–1992), emeritus professor of Kyoto University, denied Darwinism and proposed an alternative evolutionary theory. First, instead of competition among individuals in the struggle for existence, namely, natural selection, he advanced a law of coexistence, the habitat segregation principle derived from the morphogenetic principle of life form [8]. In his evolutionary theory, Imanishi contended that all individuals belonging to the same species have an equal possibility of leaving their offspring, and even different species are able to live together in the same world. He paid more attention to the spatial structure of species society than the temporal change of individuals. Furthermore, Imanishi denied the random change of individuals caused by mutation, because he neglected the differences between individuals belonging to the same species. He supported the Lamarckian theory and asserted the adaptive change of form on the level of species: all individuals belonging to the same kind alter their forms uniformly at the same time [9]. However, since Imanishi could not prove his theory by the scientific method, many biologists have not accepted his evolutionary theory. In any case, we think that Imanishi's evolutionary theory offers a simple but efficient analogy of evolution that is usable to design a practical GA and that contrasts with the Darwinism forming the metaphysical basis of conventional GAs.

In this paper, we propose an Imanishism-based GA and apply it to the multiobjective resource division problem [12]. Imanishi's evolutionary theory describes the mechanism of evolution for the species, not for the individual. Therefore, each individual in the population is regarded as a representative of its species in our proposed GA, while a bunch of similar individuals is usually used to define a species in conventional GAs [13]. In order to sample various species from a set of Pareto-optimal solutions efficiently, we have to clarify the difference between individuals not only in the objective function space but also in the problem space. Thus, we introduce two types of distance between individuals, namely, functional and structural distance, into the objective function space and the problem space, respectively. Then, measuring both distances between individuals, we classify their relations into four types: heterogeneous, homogeneous, analogous, and homologous species. According to the definition of four species, we propose a new generation alternation model for our GA that tries to hold many kinds of heterogeneous species in the population as far as possible. We also use the two types of distance between individuals in order to evaluate the performance of the generation alternation model theoretically and experimentally.

Besides the above generation alternation model that realizes the situation of habitat segregation among various species in a population, we employ a genetic local search method that mimics the process of adaptive evolution of respective species. Supposing that a new species is born from crossbreeding, or crossover between two different species, we combine the harmonic crossover operation proposed in our former work [14] with a local optimization algorithm. The improved harmonic crossover optimizes the children in several objective functions selected randomly, and spreads them over the entire Pareto front of the multiobjective optimization problem, that is, the range of Pareto-optimal solutions in the objective function space [7]. Furthermore, we prove that children generated by the improved harmonic crossover inherit structural characters from their parents.

2. Imanishi's Evolutionary Theory

First, we briefly explain the habitat segregation principle that is the starting point of Imanishi's evolutionary theory. The form of living things is decided through interaction with the environment. Thus, the forms of living things differ from each other if they live in different ways. Imanishi called such an essential feature concerned with the forms of living things the "morphogenetic principle of life forms" [8]. If some living things take diverse forms, they may inhabit different places and avoid struggling for existence. Since the concept of species is ambiguous, there are several definitions of species: biological, genealogical, and so on [10]. In the habitat segregation principle, Imanishi adopted the morphological definition of species, namely, one species is distinguished from another according to their forms. Therefore, in the proposed Imanishisim-based GA, we also recognize different species by the distance between them. Incidentally, we can take the habitat segregation principle as a contraposition of the competitive exclusion principle, which asserts that similar species never coexist in the same place.

Imanishi's evolutionary theory insists that all individuals belonging to the same species should change their forms in a common direction rapidly and at the same time when they need to change. However, since Imanishi could not provide physical evidence, many biologists criticize that theory as unscientific or speculative. On the other hand, some scientists believe that an absolute principle for evolution, such as the natural selection of Darwinism, has never existed, because the mechanism of evolution is itself varied. Imanishi showed a tendency to shift his theory from adaptive evolution to orthogenesis in his last years [9, 11]. In any case, Imanishi's evolutionary theory does not admit random change of individuals. Therefore, we can employ a heuristic search procedure peculiar to each problem in the Imanishism-based GA without any contradiction in a grounded analogy of evolution, whereas conventional hybrid GAs combined with local optimization algorithms usually deviate from Darwinism.

3. Multiobjective Resource Division Problem

In the multiobjective resource division problem [12], we consider an optimal way to divide n resources into several groups, where m kinds of relations exist among these resources. We are required to divide these resources into different groups as much as possible, and also to gather all resources related to each other in the same group. A problem instance of the multiobjective resource division problem can be represented by a graph $G = (V, E)$, in which each vertex $v_i \in V(i = 1 \sim n)$ corresponds to a resource and an edge $e \in E^j \subseteq E(j = 1 \sim m)$ connecting two vertexes denotes m kinds of relations among n resources. Then, as a solution for the problem instance, we consider a way to divide the set of vertexes V into k subsets as $\mathbf{s} = \{V_p | 1 \le p \le k\}$ including the number of subsets $k(k \le n)$. Thus, the multiobjective resource division problem is formulated as an $(m + 1)$-objective optimization problem.

$$\left[\begin{array}{l} \min_{\mathbf{s}} (f_1(\mathbf{s}),\ f_2(\mathbf{s}), \cdots,\ f_m(\mathbf{s}),\ f_{m+1}(\mathbf{s})) \\ \text{subject to} \\ \bigcup_{p=1}^{k} V_p = V, \quad V_p \cap V_q = \emptyset\ (p \ne q) \end{array}\right. \tag{1}$$

where

$$\left[\begin{array}{l} f_j(\mathbf{s}) = |E^j| - \sum_{p=1}^{k} |E_p^j|, \quad (j = 1 \sim m) \\ f_{m+1}(\mathbf{s}) = \max_{1 \le p \le k} \{|V_p|\} \end{array}\right.$$

the set of vertexes is also composed of m subsets: $E = E^1 \cup \cdots \cup E^m$; $E_p^j \subseteq E^j (j = 1 \sim m)$ denotes a subset of edges $e \in E^j$ both endpoints of which are included in the same subset $V_p (p = 1 \sim k)$.

For solving the multiobjective resource division problem, we may choose the number of subsets k arbitrarily. Therefore, we can reduce the value of the objective function $f_{m+1}(\mathbf{s})$ by increasing the number of subsets k. On the other hand, the other objective functions become worse with a large number of subsets, because many edges' endpoints are assigned to different subsets. Furthermore, if all vertexes are connected to each other by m kinds of edges, we cannot minimize all of the objective functions in Eq. (1) simultaneously. Consequently, a huge Pareto front exists in the objective function space of the multiobjective resource division problem.

4. Imanishism-Based Genetic Algorithm

In this section, we describe an Imanishism-based GA for sampling various solutions from the entire Pareto front of the multiobjective resource division problem in Eq. (1).

4.1 Phenotype and genotype of solution

We define a phenotypic representation of a solution of the multiobjective resource division problem as a way to divide the set of vertexes V into k groups. The phenotypic representation, or the phenotype, is also a synonym of the individual. Thus, we encode such a phenotype $\mathbf{s} = \{V_p | 1 \le p \le k\}$ into a string of $n = |V|$ integers $A = (a_1, \ldots, a_n)$ called a genotype. Each element $a_i \in A$ denotes the subscript $p(a_i = p)$ of the subset V_p in which the corresponding vertex $v_i \in V$ is included. Although such an encoding of phenotype into genotype seems natural enough, it does not give a unique representation: instead, $k!$ different genotypes exist for a phenotype. For example, a phenotype in Fig. 1, where seven vertexes are divided into $k = 3$ groups, can be represented by six different genotypes $A^x (x = 1 \sim k!)$ as shown in Eq. (2), because we do not distinguish the subsets $V_p (p = 1 \sim 3)$:

$$\left[\begin{array}{lcl} A^1 & = & (1,\ 1,\ 2,\ 3,\ 3,\ 2,\ 2) \\ A^2 & = & (1,\ 1,\ 3,\ 2,\ 2,\ 3,\ 3) \\ A^3 & = & (2,\ 2,\ 1,\ 3,\ 3,\ 1,\ 1) \\ A^4 & = & (2,\ 2,\ 3,\ 1,\ 1,\ 3,\ 3) \\ A^5 & = & (3,\ 3,\ 1,\ 2,\ 2,\ 1,\ 1) \\ A^6 & = & (3,\ 3,\ 2,\ 1,\ 1,\ 2,\ 2) \end{array}\right. \tag{2}$$

All of the genotypes $A^x (x = 1 \sim k!)$ that represent the same phenotype can be regarded an equivalence class. Since a set of isomorphic genotypes $[A] = \{A^x | x = 1 \sim k!\}$ is equivalent to a phenotype $\mathbf{s}$, we can replace the phenotype $\mathbf{s}$ by the corresponding $[A]$ in case of need.

4.2 Structural and functional distances

We introduce two types of distance between two individuals. Structural distance is defined on the problem space, the whole set of phenotypes. On the other hand, functional distance is defined on the objective function space, the range of objective functions.

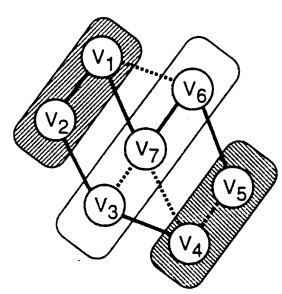

Fig. 1. Phenotype ($n = 7$; $m = 2$; $k = 3$).

First, the traditional Hamming distance is adopted as the genotypic distance between two genotypes $A = (a_1, \ldots, a_n)$ and $B = (b_1, \ldots, b_n)$ as follows:

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

where $h(a_i, b_i) = 0$(iff $a_i = b_i$), and $h(a_i, b_i) = 1$(iff $a_i \neq b_i$).

Then, we define the structural distance between phenotypes $[A]$ and $[B]$ by the least genotypic distance between corresponding sets of isomorphic genotypes $A \in [A]$ and $B \in [B]$:

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

From Eqs. (3) and (4), we find that the genotypic distance and the structural distance satisfy the inequality in Eq. (5) below. From Eq. (5), we can say that if the two genotypes are close to each other, the corresponding phenotypes should be similar, too. However, the reverse is not always true:

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

The following Theorems 1 and 2 justify the structural distance defined in Eq. (4).

[Theorem 1] The structural distance satisfies the metric axiom.

Condition 0: $[A] = [B] \Leftrightarrow \delta_p([A], [B]) = 0$

Condition 1: $\delta_p([A], [B]) \geq 0$

Condition 2: $\delta_p([A], [B]) = \delta_p([B], [A])$

Condition 3: $\delta_p([A], [B]) + \delta_p([B], [C]) \geq \delta_p([A], [C])$

[Proof] See the Appendix of Ref. 14. □

[Theorem 2] The structural distance can be evaluated in polynomial time complexity $O(n + k^3)$, where k is the larger number of groups with $[A]$ and $[B]$.

[Proof] Computation of the structural distance is transformable to a $k \times k$-size optimal assignment problem in polynomial time complexity $O(n)$, because these problems are equivalent [14]. The optimal assignment problem is also solvable in $O(k^3)$. As a result, the total time for computing the structural distance has polynomial time complexity $O(n + k^3)$. □

Finally, in the objective function space of the multiobjective resource division, we define the functional distance between two points $\mathbf{f}([A])$ and $\mathbf{f}([B])$ by using the Manhattan distance:

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

where

$$\mathbf{f}([A]) = (f_1([A]), \cdots, f_{m+1}([A])), \text{ and}$$

$$\mathbf{f}([B]) = (f_1([B]), \cdots, f_{m+1}([B])).$$

4.3 Definition of species and analogy homology principle

The subject of the Imanishi evolutionary theory is not individuals but species, which are distinguished from one another on the basis of their form, or structure, and function. Therefore, according to their structural and functional distances, we classify the relations between two individuals into four types, namely, heterogeneous, homogeneous, analogous, and homologous species. Biologically, two homologous species are similar in form but not necessarily in function. For example, since both the dolphin and bat are mammals, they are recognized as homologous. On the contrary, analogous species are similar in function but not in embryological form. For example, the killer whale and shark are analogous, because the killer whale is a mammal, while the shark is a fish.

In this paper, we define four types of species by evaluating two kinds of distance. We introduce the structural distance threshold L_p and functional distance threshold L_f. Then, if two individuals $[A]$ and $[B]$ satisfy both conditions (7) and (8), they are regarded as homogeneous. If they satisfy neither condition, they are heterogeneous. Furthermore, if they satisfy condition (7) alone, they are regarded as homologous. If they satisfy only condition (8), they are analogous. The four types of relations between two individuals are illustrated in Fig. 2.

$$\delta_p([A], [B]) \leq L_p \tag{7}$$

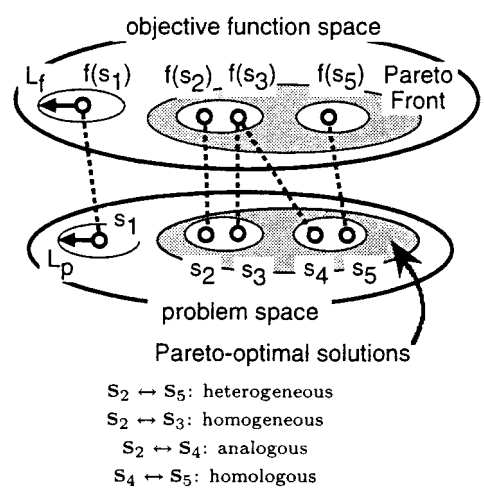

Fig. 2. Definition of species by distances.

$$\delta_f(\mathbf{f}([A]), \mathbf{f}([B])) \leq L_f \tag{8}$$

The functional distance threshold L_f is a desirable interval between individuals spread over the Pareto front in the objective function space. We decide an appropriate value for L_f by considering variable quantities: the estimated size of the Pareto front, the population size for the GA, the desirable variety of Pareto-optimal solutions, and so on. However, in order to obtain much better results, we have to adjust the value of L_f by trial and error in the same way as we usually decide the sharing radius.

On the other hand, since the structural distance threshold L_p dominates the performance of the GA, we coordinate it with the functional distance threshold L_f. Namely, we choose a suitable value for $L_p (L_p \geq 0)$ so that it satisfies the following relation for a given $L_f (L_f \geq 0)$:

$$\delta_p([A], [B]) \leq L_p \quad \Rightarrow \quad \delta_f(\mathbf{f}([A]), \mathbf{f}([B])) \leq L_f \tag{9}$$

[Theorem 3] The structural distance between any two individuals $[A]$ and $[B]$ always satisfies the following condition with an appropriate positive integer $\alpha (\alpha \geq 1)$:

$$\delta_f(\mathbf{f}([A]), \mathbf{f}([B])) \leq \alpha \delta_p([A], [B]) \tag{10}$$

[Proof] See Appendix 1. □

From Theorem 3, relation (9) can be derived by taking the value of L_p as $L_p = L_f/\alpha$, where the minimum value of α is unknown. In order to maintain population diversity, we wish to choose the value of L_p as large as possible. Therefore, assuming $\alpha = 1$, we set the initial value of the structural distance threshold as $L_p = L_f$ in our generation alternation model described later. Then we decrease the value of L_p little by little whenever we find a pair of individuals that does not satisfy relation (9). Taking the value of L_p as $L_p = 0$, relation (9) is always satisfied by any pair of individuals $[A]$ and $[B]$, because the equality $[A] = [B]$ holds from Theorem 1.

Incidentally, every individual ought to attribute its function to its structure. Furthermore, since we are able to choose any values for the structural distance threshold L_p, we can transform homologous species into heterogeneous ones by decreasing the value of L_p. On the other hand, we cannot determine the structure of an individual uniquely from its function, because deciding an exact structure from a desirable function constitutes a kind of inverse problem [16]. In other words, since the analogous relation is essential, we cannot change the relation by adjusting the value of L_f. From now on, we call the above characteristics of species the "analogy homology principle."

4.4 Improved harmonic crossover

In order to find Pareto-optimal solutions effectively for the multiobjective resource division problem, we propose a new genetic operation called improved harmonic crossover, which is a combination of the conventional harmonic crossover proposed by the authors [14] and a local optimization procedure that minimizes the values of several objective functions simultaneously.

First, we remark that an individual $[D]$ is superior to another individual $[C]$, namely, $[D]$ dominates $[C]$, if and only if they satisfy the condition

$$\left(\begin{array}{lll} & \forall j \in J & f_j([D]) \leq f_j([C]) \\ \wedge & \exists j \in J & f_j([D]) < f_j([C]) \end{array} \right. \tag{11}$$

where $J = \{1, \ldots, m + 1\}$ is a subscript set of the objective functions.

In improved harmonic crossover, we generate a single child C from two parents A and B with conventional harmonic crossover. Then, applying a local optimization method to child C, we transform it into a new individual D improved in some objective functions $f_j([D])(j \in I \subseteq J)$. However, the new individual $[D]$ may be degraded in other objective functions $f_j([D])(j \in J - I)$. Although we cannot guarantee that $[D]$ is always better than $[C]$ as shown in relation (11), $[D]$ is never dominated by $[C]$. Furthermore, we can expect the improved harmonic crossover to spread all the individuals in the population over the entire Pareto front in the objective function space. The procedure of improved harmonic crossover can be described as follows.

[Improved harmonic crossover]

Step 1: Transform one of the parents $B \in [B]$ to an isomorphic genotype $B^Z \in [B]$ so that the genotypic distance $\delta_g(A, B^Z)$ becomes minimal, and $\delta_g(A, B^Z) = \delta_p([A], [B])$.

Step 2: Apply an ordinary uniform crossover to the parents A and B^Z, generating a new child C.

Step 3: Select some objective functions $f_j(j \in I \subseteq J, I \neq \phi)$ randomly.

Step 4: As long as corresponding elements between parents $a_i \in A$ and $b_i \in B$ have different values $(a_i \neq b_i)$, change the value of $c_i \in C$ inherited from one of the parents randomly. Then, find a genotype D that differs from C in an element $c_i \in C$ and satisfies the condition

$$\left(\begin{array}{lll} & \forall j \in I \subseteq J & f_j([D]) \leq f_j([C]) \\ \wedge & \exists j \in I \subseteq J & f_j([D]) < f_j([C]) \end{array} \right.$$

Step 5: If such a genotype D can be found in the neighborhood of C, replace C by D $(C = D)$ and return to Step 4. Otherwise, output the current C as an improved child and end this procedure. □

[Theorem 4] When a child D is generated from parents A and B by improved harmonic crossover, phenotypes corresponding to these genotypes satisfy the relation

$$\delta_p([A],[B]) \geq \max\{\delta_p([A],[D]),\ \delta_p([B],[D])\} \qquad (12)$$

[Proof] It can be proved in a similar way as shown in the appendix of Ref. 14. □

The behavior of individuals concerned with improved harmonic crossover is shown schematically in Fig. 3. Harmonic crossover generates a child C from parents A and B, then the local optimization procedure transforms C into D in the search space, the whole set of available genotypes. At that time, from Theorem 4, phenotype $[D]$ corresponding to the improved child D always exists in the dark-shaded area between parents $[A]$ and $[B]$ in the problem space. Therefore, it is evident that improved harmonic crossover, as well as conventional harmonic crossover, transfers the structural character of parents, which is common to them, to their child successfully.

4.5 Generation alternation model of habitat segregation

In order to maintain population diversity, we propose a new generation alternation model that realizes the situation of habitat segregation among various species in a population. The proposed generation alternation model generates a single child from two parents every generation in the same way as the traditional steady-state model, but, the number of individuals (i.e., the population size) increases and decreases. We have to set three parameters for the GA: the functional distance threshold L_f, the upper limit of population size P_{max}, and the terminal generation T. The structural distance threshold L_p is controlled automatically

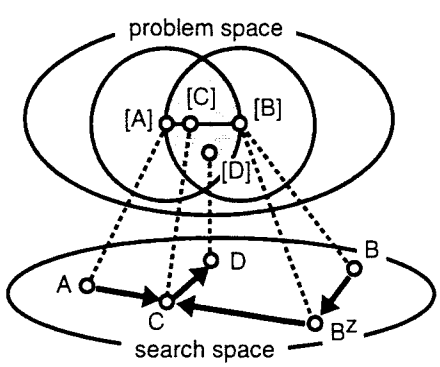

Fig. 3. Improved harmonic crossover.

according to a rule based on the analogy and homology principle as mentioned above. By checking both conditions (7) and (4) with thresholds L_f and L_p, a species type is determined for every child $[D]$, namely, heterogeneous, homogeneous, analogous, or homologous. In order to evaluate the goodness of fit for each individual in the population, we adopt Goldberg's ranking [17] and call individuals assigned to rank 1 Pareto individuals. Our proposed generation alternation model can be described as follows.

[Generation alternation model]

Step 1: Randomly generate P_{max} individuals in the genotypic representation as an initial population $P(0)$. Set generation $t = 0$ and an initial value of distance threshold L_p as $L_p = L_f$.

Step 2: Select parents A and B ($A \neq B$) from the current population $P(t)$ randomly. If they are homogeneous, eliminate the dominated one and go to Step 10; otherwise, go to Step 3.

Step 3: Applying improved harmonic crossover to parents A and B, generate a new child D.

Step 4: Find the individual $E \in P(t)$ that is the closest one to the child $[D]$ in the objective function space. If $\delta_f(\mathbf{f}([D]), \mathbf{f}([E])) > L_f$, go to Step 7.

Step 5: If $[D]$ and $[E]$ are homogeneous, eliminate the dominated one, and go to Step 10.

Step 6: If $[D]$ and $[E]$ are analogous and the population size is less than P_{max}($|P(t)| < P_{max}$), add the child D to $P(t)$; otherwise, eliminate the dominated one, and go to Step 10.

Step 7: Find the individual $F \in P(t)$ that is the closest one to the child $[D]$ in the problem space, where they have already satisfied $\delta_f(\mathbf{f}([D]), \mathbf{f}([F])) > L_f$ in the objective function space.

Step 8: If $[D]$ and $[F]$ are heterogeneous: if $|P(t)| < P_{max}$, add child D to $P(t)$; otherwise, replace the worst individual with the largest rank in $P(t)$ by D, and go to Step 10.

Step 9: If $[D]$ and $[F]$ are homologous: decrease the value of L_p as $L_p = \max\{L_p - 1, 0\}$. If $|P(t)| < P_{max}$, add child D to $P(t)$; otherwise, replace the worst one by D.

Step 10: If $t = T$ or $|P(t)| = 1$, output all of the Pareto individuals in $P(t)$ and terminate the algorithm. Otherwise, increase the current generation as $t = t + 1$ and return to Step 2. □

We now summarize the characteristics of the proposed generation alternation model and the behavior of individuals in a population accompanying evolution. If parents A and B are homogeneous, Theorem 4 asserts that their child generated by improved harmonic crossover always belongs to the same species as they. Therefore, for maintaining population diversity, we have prohibited a pair of homogeneous species from making a new child in Step 2. In order to determine the species type for a child $[D]$,

namely, heterogeneous, homogeneous, analogous, or homologous species, we have to find the closest individual to child [D] in both the problem and the objective function spaces. Thus, by arranging the order of evaluation of the structural and functional distances, we have successfully reduced the total number of computations to $|P(t)|(|P(t)| \leq P_{max})$ or less.

When we find a pair of individuals classified as homologous in population, we cut down the value of L_p in Step 9. The existence of such a pair of individuals suggests that the value of L_p is too large for them to satisfy condition (9) with a given L_f. However, if we decrease the value of L_p suddenly in the early stage of evolution, it may cause a reduction of population diversity. Therefore, for gradual transformation of homologous species into heterogeneous species, we reduce the value of L_p one by one in Step 9. As a result, we expect that the landscape of the objective function space will be reflected in the distribution of individuals in the problem space. Incidentally, we need more consideration of the method used to control the value of L_p. For example, we can adopt a schema based on population diversity and introduce learning mechanisms.

4.6 Discussion of population diversity

In the proposed generation alternation model, since heterogeneous species gradually take the place of homogeneous ones in a population, we can expect that all individuals in a population scatter in both the problem and the objective function spaces. In the following, by using the average of the functional distances among individuals in the objective function spaces, we try to gain further insight into the population diversity, which fluctuates from the replacement of species and the variation of population size. Similarly, we can also analyze the population diversity in the problem space based on the average of the structural distance among individuals.

Obviously, if all individuals in a population are heterogeneous with one another, the average of the functional distances among them $\bar{\delta}_f$ becomes larger than a given L_f. Furthermore, we can derive the following theorems concerned with population diversity, where population $P(t)$ is regarded as a set of phenotypes $\mathbf{s} \in P(t)$ for convenience.

[Theorem 5] Although an individual is replaced by a homogeneous species in the population, the variation $\nabla\bar{\delta}_f$ of the average distance $\bar{\delta}_f$ is limited as follows:

$$-\frac{2L_f}{|P(t)|} \leq \nabla\bar{\delta}_f \leq \frac{2L_f}{|P(t)|} \tag{13}$$

[Proof] See Appendix 2. □

[Theorem 6] When an individual $\mathbf{s}_r$ ($r = |P(t)|$) is eliminated from a population $P(t) = \{\mathbf{s}_1, \ldots, \mathbf{s}_r\}$, the variation $\nabla\bar{\delta}_f$ of the average distance $\bar{\delta}_f$ becomes

$$\nabla\bar{\delta}_f = \frac{2\left(\sum_{i=1}^{|P(t)|-1}\left(\bar{\delta}_f - \delta_f(\mathbf{f}(\mathbf{s}_i), \mathbf{f}(\mathbf{s}_r))\right)\right)}{(|P(t)|-1)(|P(t)|-2)} \tag{14}$$

[Proof] See Appendix 3. □

[Theorem 7] When an individual $\mathbf{s}_{r+1}(r = |P(t)|)$ is added to a population $P(t) = \{\mathbf{s}_1, \ldots, \mathbf{s}_r\}$, the variation $\nabla\bar{\delta}_f$ of the average distance $\bar{\delta}_f$ becomes

$$\nabla\bar{\delta}_f = \frac{2\left(\sum_{i=1}^{|P(t)|}\left(\delta_f(\mathbf{f}(\mathbf{s}_i), \mathbf{f}(\mathbf{s}_{r+1})) - \bar{\delta}_f\right)\right)}{(|P(t)|+1)|P(t)|} \tag{15}$$

[Proof] It can be proved in the same way as Theorem 6. □

From Theorem 5, the average distance $\bar{\delta}_f$ does not change drastically even if an individual is replaced by a homogeneous species in Step 5. Elimination of an individual in Step 2 also increases the average distance $\bar{\delta}_f$ if a bunch of homogeneous species is crowding around the individual, because the variation $\nabla\bar{\delta}_f$ of the average distance becomes positive from Theorem 6. Furthermore, adding a new individual to the population in Step 8 increases the average distance D as long as the individual is heterogeneous and far away from the others in the population, because the variation $\nabla\bar{\delta}_f$ of the average distance becomes positive from Theorem 7. Consequently, we can expect the proposed generation alternation model to maintain population diversity successfully even though it does not use the results of Theorems 6 and 7 explicitly.

5. Experimental Results

5.1 Two-objective problem instance

A two-objective problem instance of the multiobjective resource division problem is given by a complete graph $G = (V, E)$ including $n = 24$ vertexes connected to each other by the same kind of edges ($m = 1$). The problem instance has 24 Pareto-optimal solutions $\mathbf{s}_i^*(i = 1 \sim 24)$ which can be enumerated easily. Therefore, we can evaluate the performance of the proposed GA absolutely in the two-objective problem instance by comparing the obtained Pareto individuals with these Pareto-optimal solutions. Furthermore, we show that the distance between individuals should be considered not only in the objective function space but also in the problem space for sampling various Pareto-optimal solutions from the entire Pareto front in the objective function space.

In order to demonstrate the high performance of the proposed generation alternation model, we compared the

Imanishism-based GA with two types of Darwinism-based GA that maintain a constant population size: D-GA always replaces the worst individual in a population by a new child; ER-GA [18] eliminates the worst individual in a family, namely, a child and two parents. D-GA and ER-GA, as well as the proposed GA, employ improved harmonic crossover for generating a new child. For comparison, besides the proposed Imanishism-based GA (I-GA1), we also evaluate a modified version (I-GA2), in which we use only the functional distance to distinguish two types of species. Namely, if two individuals $[A]$ and $[B]$ satisfy only condition (8), they are regarded as homogeneous species; otherwise they are regarded as heterogeneous species. Therefore, the generation alternation model stated above has to be changed for I-GA2: Steps 6, 7, and 9 are ignored, and Steps 4 and 8 are altered as follows.

Step 4: Find the individual $E \in P(t)$ that is the closest one to child $[D]$ in the objective function space. If $\delta_f(\mathbf{f}[D], \mathbf{f}([E])) > L_f$, go to Step 8.

Step 8: If $[D]$ and $[E]$ are heterogeneous: if $P(t)| < P_{max}$ holds, add child D to $P(t)$; otherwise, replace the worst individual with the largest rank in $P(t)$ by D, and go to Step 10.

We compared the above four types of GA, namely, D-GA, ER-GA, I-GA1, and I-GA2, with the following parameter specifications: population size $P_{max} = 30$, terminal generation $T = 10^4$; we chose several values for the functional distance threshold, $L_f = 5$, 10, 15, 20, in both I-GA1 and I-GA2. Table 1 shows some performance criteria for the GA: $|S^*|$ is the number of Pareto-optimal solutions $\mathbf{s}_i^* \in S^*$ obtained by GA; $\bar{\delta}_f(S^*)$is the average functional distance among them; $|P(T)|$ is the population size at terminal generation T; and $\bar{\delta}_p^T$ is the average structural distance among $\mathbf{s} \in P(T)$, where these results are averaged over 10 runs. We can estimate the search ability of GA from $|S^*|$ and $\bar{\delta}_f(S^*)$. It should be noted that the proposed I-GA1 finds more various Pareto-optimal solutions than the others. Furthermore, from $|P(T)|$ and $\bar{\delta}_p^T$, we can confirm that I-GA1 maintains population diversity not only in the objective function space but also in the problem space without decreasing the number of individuals.

Table 1. Experimental performance of GAs

GA(L_f)	$\lvert S^*\rvert$	$\bar{\delta}_f(S^*)$	$\lvert P(T)\rvert$	$\bar{\delta}_p^T$
I-GA1(5)	20.2	95.0	30.0	13.6
I-GA1(10)	17.7	99.1	30.0	14.0
I-GA1(15)	15.8	95.1	30.0	13.1
I-GA1(20)	15.1	87.9	30.0	13.4
I-GA2(5)	13.9	72.7	19.9	9.9
I-GA2(10)	11.7	77.8	12.9	8.7
I-GA2(15)	9.8	80.1	9.8	8.0
I-GA2(20)	4.8	59.5	4.8	5.6
D-GA	11.8	55.7	30.0	11.2
ER-GA	14.5	70.1	30.0	11.6

Figure 4 plots the values of the objective function for all of the individuals $\mathbf{s}_i \in P(T)$ in the final population, which are obtained by I-GA1 and I-GA2 with $L_f = 5$ and $L_f = 10$, respectively. As can be seen in Fig. 4, I-GA1 samples various Pareto-optimal solutions uniformly, while I-GA2 cannot find some solutions that take small values for the second objective function f_2. Now, we assign subscripts to the Pareto-optimal solutions $\mathbf{s}_i^*(i = 1 \sim 24)$ in increasing order of the value of f_2. Table 2 shows the structural distance from each Pareto-optimal solution $\mathbf{s}_i^*$ to the nearest one $\mathbf{s}_j^*(i \neq j)$. From Table 2, we find that I-GA2 is unable to find solutions $\mathbf{s}_1^*$ to $\mathbf{s}_7^*$ that are distant from the others in the problem space, because I-GA2 neglects the structural distance between individuals.

5.2 Three-objective problem instance

A three-objective problem instance of the multiobjective resource division problem is given by a graph $G = (V, E)$, $E = E^1 \cup E^2$ including $n = 64$ vertexes arranged as an 8×8 torus network. These vertexes are connected to each

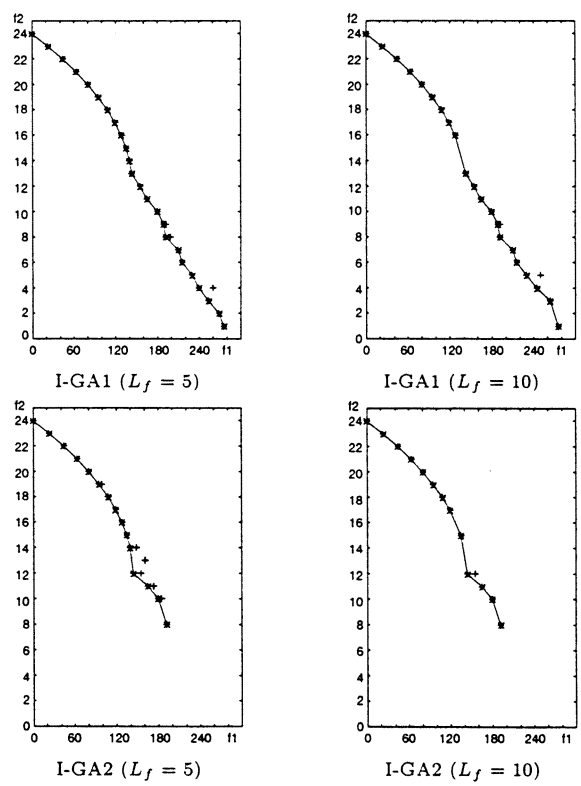

Fig. 4. Pareto front and $\mathbf{f}(\mathbf{s}_i)$ ($\mathbf{s}_i \in P(T)$).

Table 2. Nearest structural distance

s_1^*	12	s_5^*	6	s_9^*	3	s_{13}^*	1	s_{17}^*	1	s_{21}^*	1
s_2^*	8	s_6^*	6	s_{10}^*	3	s_{14}^*	1	s_{18}^*	1	s_{22}^*	1
s_3^*	8	s_7^*	6	s_{11}^*	3	s_{15}^*	1	s_{19}^*	1	s_{23}^*	1
s_4^*	6	s_8^*	3	s_{12}^*	1	s_{16}^*	1	s_{20}^*	1	s_{24}^*	1

Table 3. Experimental performance of GAs

GA(L_f)	$\lvert S\rvert$	$\bar{\delta}_f(S)$	$\lvert\hat{S}\rvert$	$\lvert P(T)\rvert$	$\bar{\delta}_p^T$
I-GA1(10)	48.3	41.3	28.0	50.0	37.9
I-GA3(10)	19.1	9.3	9.9	49.9	22.9
D-GA	48.8	24.5	35.1	50.0	29.5
ER-GA	29.4	27.5	2.9	50.0	32.5

other by two kinds of edges ($m = 2$). To be exact, row lines are linked by one kind of edge $e \in E^1$ ($|E^1| = 64$), and column lines are linked by the other kind of edge $e \in E^2$ ($|E^2| = 64$). Consequently, the problem instance has a vast expanse of the Pareto front, which includes four points $(f_1, f_2, f_3) = (0, 0, 64)$, $(0, 64, 8)$, $(64, 0, 8)$, and $(64, 64, 1)$ in the three-dimensional objective function space, and also has various Pareto-optimal solutions in the problem space.

Instead of I-GA2, we evaluate another modified version of the Imanishism-based GA (I-GA3), in which we change the improved harmonic crossover at Step 3 to select all objective functions $f_j (j \in J)$ every time. Then, we compare four types of GA, namely, D-GA, ER-GA, I-GA1, and I-GA3, with the following parameter specifications: population size $P_{max} = 50$, and terminal generation $T = 10^4$, choosing the functional distance threshold as $L_f = 10$ for I-GA1 and I-GA3. Figure 5 plots the values of objective function $\mathbf{f}(\mathbf{s})$ ($\mathbf{s} \in P(T)$) at the terminal generation for each of the above four types of GA. From Fig. 5, we can confirm that I-GA1 spreads the points of $\mathbf{f}(\mathbf{s})$ ($\mathbf{s} \in P(T)$) in the objective function space more widely than the others. On the other hand, the variety of individuals obtained by I-GA3 is very small, and all of the points of $\mathbf{f}(\mathbf{s})$ ($\mathbf{s} \in P(T)$) gather around the center of the Pareto front. As a result, we can say that the proposed improved harmonic crossover is fully justified in selecting some objective functions $f_j (j \in I \subseteq J)$ to be optimized randomly.

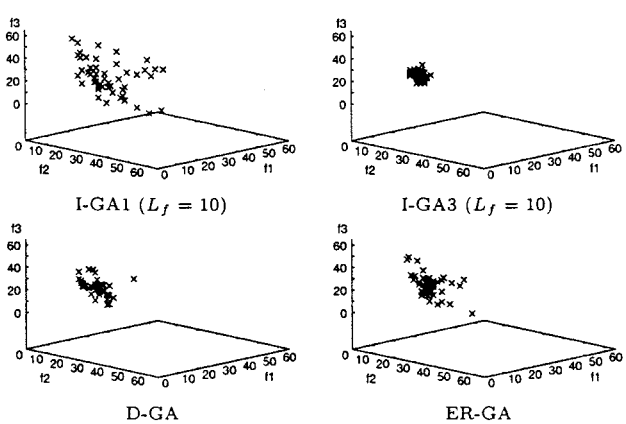

Fig. 5. $\mathbf{f}(\mathbf{s}_i)$ ($\mathbf{s}_i \in P(T)$) in objective space.

We next evaluate the diversity and quality of the Pareto individuals obtained by the above four types of GA. Table 3 shows some performance criteria for the GA: $|S|$ is the total number of Pareto individuals $\mathbf{s} \in S$, and $\bar{\delta}_f(S)$ is the average functional distance among them; $|\hat{S}|$ is the total number of individuals $\mathbf{s} \in \hat{S} \subseteq S$ that have not been dominated by any other Pareto individuals obtained by the others; $|P(T)|$ denotes the population size at terminal generation T, $\bar{\delta}_p^T$ is the average structural distance among $\mathbf{s} \in P(T)$, where these results are averaged over 10 runs. We can estimate the relative search abilities of the GAs from $|\hat{S}|$. D-GA finds many Pareto individuals $\mathbf{s} \in \hat{S} \subseteq S$ of good quality, although their diversity is low from $\bar{\delta}_f(S)$. On the contrary, since the proposed I-GA1 takes a large value for $\bar{\delta}_f(S)$, we can say that I-GA1 finds a variety of individuals $\mathbf{f}(\mathbf{s})$ ($\mathbf{s} \in S$) spread over the entire Pareto front.

If we choose an appropriate value for the functional distance threshold L_f in the proposed generation alternation model, we can control the climax of habitat segregation, namely, the distribution of Pareto individuals in the objective function space $\mathbf{f}(\mathbf{s})$ ($\mathbf{s} \in S \subseteq P(T)$) at the terminal generation. By changing the value of L_f, we evaluated the performance of I-GA1 in the same manner as in Table 3. Table 4 shows the results of the experiments. From $|S|$ and $|\hat{S}|$ in Table 4, it appears that I-GA1 samples a variety of Pareto individuals from the entire Pareto front with a small value of L_f. Furthermore, since $|P(T)|$ and $\bar{\delta}_p^T$ take large values in any case, we can say that I-GA1 always maintains population diversity in the problem space. However, if the value of L_f is large relative to the population size, many

Table 4. Effect of threshold L_f on I-GA1

L_f	$\lvert S\rvert$	$\bar{\delta}_f(S)$	$\lvert\hat{S}\rvert$	$\lvert P(T)\rvert$	$\bar{\delta}_p^T$
5	49.0	32.3	40.4	50.0	34.5
10	48.6	42.7	33.5	50.0	38.0
20	32.5	29.4	13.2	50.0	34.6
30	22.5	28.7	4.1	49.9	36.0

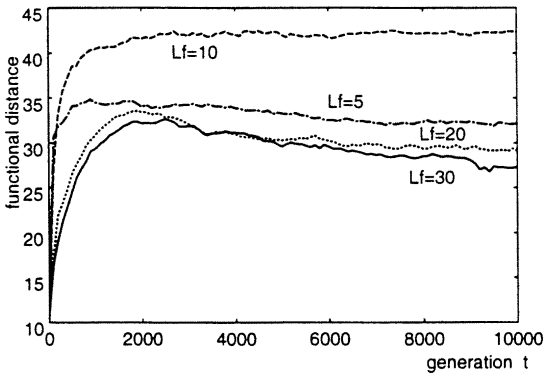

Fig. 6. Average of functional distance $\bar{\delta}_f$.

individuals are regarded as analogous species and they cannot be transformed into heterogeneous ones. Therefore, the value of $\bar{\delta}_f(S)$ does not always increase proportionally to the value of L_f. Comparing the values of $\bar{\delta}_f(S)$ in Table 4, we find that $L_f = 10$ is the best value in order to obtain a variety of Pareto individuals.

For all cases of I-GA1 shown in Table 4, Fig. 6 indicates the average functional distance $\bar{\delta}_f$ among individuals in each population $P(t)$ at generation t ($t = 0 \sim T$), where the results are averaged over 10 runs. Similarly, Fig. 7 shows the change of the average structural distance $\bar{\delta}_p$ by generation. The results in Figs. 6 and 7 confirm that $L_f = 10$ is suitable for I-GA1 to expand the population diversity in both the problem and objective function spaces with the renewal of generations, and retains a variety of individuals until the terminal generation.

In the proposed generation alternation model, we initialize the value of the structural distance threshold L_p as $L_p = L_f$ based on Theorem 3. In order to verify the suitability of such an initial value of L_p, we examine the performance of the Imanishism-based GA with several initial values of L_p, while the functional distance threshold takes a constant value $L_f = 10$. Table 5 shows the results of the experiments for the same criteria as in Table 3. As can be seen in Table 5, by choosing an initial value of L_p as $L_p = L_f = 10$, we can obtain the best results on all criteria. Incidentally, we could not extend the population diversity any further, even if we set the larger initial value to $L_p (L_p > 10)$. We estimate that since many individuals are regarded as homologous with a large initial value of L_p, the value of L_p declines rapidly in the beginning of evolution.

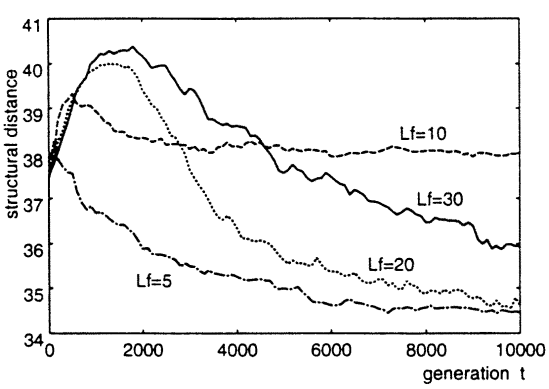

Fig. 7. Average of structural distance $\bar{\delta}_p$.

Table 5. Effect of threshold L_p on I-GA1

L_p	$\lvert S \rvert$	$\bar{\delta}_f(S)$	$\lvert \hat{S} \rvert$	$\lvert P(T) \rvert$	$\bar{\delta}_p^T$
5	48.1	40.4	23.6	50.0	37.4
10	48.6	42.7	25.3	50.0	38.0
20	48.4	41.8	25.3	50.0	37.9
30	48.3	40.7	25.0	50.0	37.8

6. Conclusions

In this paper, we have proposed a new Genetic Algorithm (GA) based on an evolutionary theory advocated by Kinji Imanishi and have applied it to the multiobjective resource division problem. Since the starting point of Imanishi's evolutionary theory is habitat segregation among various species, Imanishi paid much more attention to the spatial structure of species society than the temporal change of each individual. Therefore, by introducing two kinds of distance, namely, structural and functional distance, we have expanded both the problem and the objective function spaces into metric spaces. Furthermore, by evaluating these distances between two individuals, we have subdivided their relations into four types: heterogeneous, homogeneous, analogous, and homologous species. We have presented a new genetic operation that combines harmonic crossover with a local optimization algorithm, and a generation alternation model based on the habitat segregation principle. We have also analyzed the performance of the proposed techniques mathematically by using the structural and functional distances. Finally, we have conducted some computational experiments on several problem instances and have demonstrated that the proposed GA has the advantage of sampling various Pareto-optimal solutions effectively.

Actually, the proposed Imanishism-based GA is applicable not only to the multiobjective resource division problem, but also to any other multiobjective optimization problem by introducing appropriate structural and func-

tional distances between individuals. In future work, we hope to form a theory to describe the high performance of the proposed GA, including the correspondence between the problem and objective function spaces. Furthermore, we need to investigate a more sophisticated way to adjust the structural distance threshold L_p for our GA.

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APPENDIX

1. Proof of Theorem 3

For $\delta_p([A], [B]) = 0$, since $[A] = [B]$ and $f([A]) = f([B])$, we have that $\delta_f(\mathbf{f}([A]), \mathbf{f}([B]) = 0$. Conversely, if $\delta_p([A], [B]) = \beta(\beta \geq 1)$, β denotes the number of vertexes $v_i \in \overline{V} \subseteq V$ distributed to different subsets between $[A]$ and $[B]$. Since $\beta = |\overline{V}|$, we must have

$$|f_{m+1}([A]) - f_{m+1}([B])| \leq \beta \tag{A.1}$$

Let $\mu_j(v_i)$ denote the degree of a vertex $v_i \in \overline{V}$, namely, the number of edges $e \in E^j$ connected to the vertex, and $\psi_j = \max\{\mu_j(v_i) | v_i \in \overline{V}\}$. Then we must have

$$|f_j([A]) - f_j([B])| \leq \beta\psi_j \quad (j = 1 \sim m) \tag{A.2}$$

From Eqs. (A.1), (A.2), and $\beta = \delta_p([A], [B])$, we find that

$$\begin{aligned} \delta_f(\mathbf{f}([A]), \mathbf{f}([B])) &= \sum_{j=1}^{m+1} \mid f_j([A]) - f_j([B]) \mid \\ &\leq \left(\sum_{j=1}^{m} \psi_j + 1\right) \beta = \alpha\delta_p([A], [B]) \end{aligned} \tag{A.3}$$

where $\alpha = \Sigma_{j=1}^{m} \psi_j + 1$.

2. Proof of Theorem 5

Supposing that an individual $\mathbf{s}_1 \in P(t)$ is replaced by the same kind $\acute{\mathbf{s}}$, we have

$$\delta_f(\mathbf{f}(\mathbf{s}_1), \mathbf{f}(\acute{\mathbf{s}}_1)) \leq L_f \tag{A.4}$$

Furthermore, from the metric axiom, any individual $\mathbf{s}_i \in P(t)$ satisfies

$$\left[\begin{array}{l} \delta_f(\mathbf{f}(\mathbf{s}_1), \mathbf{f}(\mathbf{s}_i)) - \delta_f(\mathbf{f}(\acute{\mathbf{s}}_1), \mathbf{f}(\mathbf{s}_i)) \\ \qquad \leq \delta_f(\mathbf{f}(\mathbf{s}_1), \mathbf{f}(\acute{\mathbf{s}}_1)) \\ \delta_f(\mathbf{f}(\acute{\mathbf{s}}_1), \mathbf{f}(\mathbf{s}_i)) - \delta_f(\mathbf{f}(\mathbf{s}_1), \mathbf{f}(\mathbf{s}_i)) \\ \qquad \leq \delta_f(\mathbf{f}(\acute{\mathbf{s}}_1), \mathbf{f}(\mathbf{s}_1)) \end{array}\right. \tag{A.5}$$

Let $\bar{\delta}_f^t (\bar{\delta}_f^t = \bar{\delta}_f)$ and $\bar{\delta}_f^{t+1}$ be the average distances among populations $P(t) = \{\mathbf{s}_1, \ldots, \mathbf{s}_r\}$ and $P(t+1) = \{\mathbf{s}_1, \ldots, \mathbf{s}_r\}$ respectively. Then we take the difference between them such that

$$\frac{\nabla \bar{\delta}_f}{2} = \frac{\bar{\delta}_f^{t+1} - \bar{\delta}_f^t}{2} = \frac{\sum_{i=2}^{|P(t)|} (\delta_f(\mathbf{f}(\acute{\mathbf{s}}_1), \mathbf{f}(\mathbf{s}_i)) - \delta_f(\mathbf{f}(\mathbf{s}_1), \mathbf{f}(\mathbf{s}_i)))}{|P(t)|(|P(t)| - 1)} \tag{A.6}$$

From Eqs. (A.4), (A.5), and (A.6), we find that

$$-\frac{2L_f}{|P(t)|} \leq \nabla \bar{\delta}_f \leq \frac{2L_f}{|P(t)|} \tag{A.7}$$

3. Proof of Theorem 6

Let $\bar{\delta}_f^t (\bar{\delta}_f^t = \bar{\delta}_f)$ and $\bar{\delta}_f^{t+1}$ be the average distances among populations $P(t) = \{\mathbf{s}_1, \ldots, \mathbf{s}_r\}$ and $P(t+1) = \{\mathbf{s}_1, \ldots, \mathbf{s}_{r-1}\}$, respectively. Then they are represented as

$$\frac{\bar{\delta}_f^t}{2} = \frac{\sum_{i=1}^{|P(t)|-2} \sum_{j=i+1}^{|P(t)|-1} \delta_f(\mathbf{f}(\mathbf{s}_i), \mathbf{f}(\mathbf{s}_j))}{|P(t)|(|P(t)| - 1)} + \frac{\sum_{i=1}^{|P(t)|-1} \delta_f(\mathbf{f}(\mathbf{s}_i), \mathbf{f}(\mathbf{s}_r))}{|P(t)|(|P(t)| - 1)} \tag{A.8}$$

where $r = |P(t)|$ and

$$\frac{\bar{\delta}_f^{t+1}}{2} = \frac{\sum_{i=1}^{|P(t)|-2} \sum_{j=i+1}^{|P(t)|-1} \delta_f(\mathbf{f}(\mathbf{s}_i), \mathbf{f}(\mathbf{s}_j))}{(|P(t)| - 1)(|P(t)| - 2)} \tag{A.9}$$

From Eqs. (A.8) and (A.9), we obtain the variation $\nabla \bar{\delta}_f$ of the average distance $\bar{\delta}_f$ as

$$\frac{\nabla \bar{\delta}_f}{2} = \frac{\bar{\delta}_f^{t+1} - \bar{\delta}_f^t}{2} = \frac{\sum_{i=1}^{|P(t)|-1} (\bar{\delta}_f - \delta_f(\mathbf{f}(\mathbf{s}_i), \mathbf{f}(\mathbf{s}_r)))}{(|P(t)| - 1)(|P(t)| - 2)} \tag{A.10}$$

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