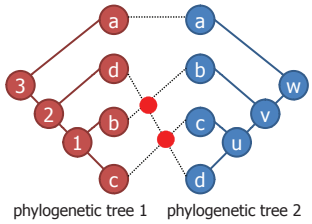
Distributed Modified Extremal Optimization using Island Model for Reducing Crossovers in Reconciliation Graph

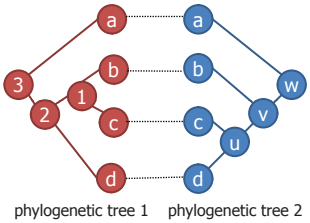
Keiichi Tamura, Hajime Kitakami, and Akihiro Nakada

***Abstract*—To determine the mechanism of molecular evolution, molecular biologists need to carry out reconciliation work. In reconciliation work, they compare the relation between two heterogeneous phylogenetic trees and the relation between a phylogenetic tree and a taxonomic tree are compared. Phylogenetic trees and taxonomic trees are referred to as ordered trees and a reconciliation graph is constructed from two ordered trees. In the reconciliation graph, the leaf nodes of the two ordered trees face each other. Furthermore, leaf nodes with the same label name are connected to each other by an edge. To carry out reconciliation work efficiently, it is necessary to find the state with the minimum number of crossovers of edges between leaf nodes. Reducing crossovers in a reconciliation graph is the combinatorial optimization problem that finds the state with the minimum number of crossovers. In this paper, we propose a novel bio-inspired heuristic called distributed modified extremal optimization (DMEO) using the island model. This heuristic is a hybrid of population-based modified extremal optimization (PMEO) and the distributed genetic algorithm using the island model that is used for reducing crossovers in a reconciliation graph. We have evaluated DMEO using actual data sets. DMEO shows better performance compared with PMEO.**

***Index Terms*—extremal optimization, distributed genetic algorithm, island model, evolutionary computation, reconciliation graph**



(a) Reconciliation graph with two crossovers.



(b) Reconciliation graph with no crossovers.

Fig. 1. Examples of reconciliation graphs ((a) shows a reconciliation graph that has two crossovers, and (b) shows a reconciliation graph that has no crossovers).

I. Introduction

MOLECULAR biologists need to carry out reconciliation work [1], [2], [3], [4] in order to determine the mechanism of molecular evolution. In reconciliation work, the relation between two heterogeneous phylogenetic trees and the relation between a phylogenetic tree and a taxonomic tree are compared. To compare two heterogeneous trees, a graph called a reconciliation graph that consists of two heterogeneous phylogenetic trees or a phylogenetic tree and a taxonomic tree are constructed. In a reconciliation graph, phylogenetic trees and taxonomic trees are referred to as ordered trees. The leaf nodes of these ordered trees face each other and leaf nodes with the same label name are connected to each other by an edge.

To carry out reconciliation work efficiently, it is necessary to find the state with the minimum number of crossovers of edges between leaf nodes in the reconciliation graph. For example, in Fig. 1, phylogenetic tree 1 and phylogenetic tree 2 are inferred from different molecular sequences with four identical species "a," "b," "c," and "d." The leaf nodes of phylogenetic tree 1 and those of phylogenetic tree 2 face each other. Moreover, leaf nodes representing the same species are connected to each other. The reconciliation graph shown in Fig. 1(a) has two crossovers. If node "d" and node "d" are replaced, we can obtain the reconciliation graph shown in Fig. 1(b), which has no crossovers. Thus, to reduce crossovers in a reconciliation graph is called reducing crossovers in a reconciliation graph.

Reducing crossovers in a reconciliation graph is the combinatorial optimization problem that finds the state with the minimum number of crossovers. The number of combinations increases exponentially as the number of leaf nodes increases. Therefore, there are some heuristics [5], [6] that can be used for reducing crossovers in a reconciliation graph, and they use a genetic algorithm(GA) [7], extremal optimization (EO) [8], [9], [10], and modified EO (MEO) [11]. EO is a general-purpose heuristic inspired by the Bak-Sneppen model [12] of self-organized criticality from the field of statistical physics. MEO improves the methodology of generating the next generation. Although EO select a neighbor solution randomly at an alternation of generations, MEO selects the best solution in multiple neighbor solutions.

In our previous study [13], we proposed population-based modified extremal optimization (PMEO), which is a combination of a population-based approach and MEO. PMEO shows better performance compared with MEO. However, it

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is difficult to maintain diversity at the end of alternation of generations. To overcome this difficulty, this paper proposes a novel extremal optimization model called distributed modified extremal optimization (DMEO) for reducing crossovers in a reconciliation graph. DMEO is a hybrid of PMEO and the distributed genetic algorithm (DGA) [14], [15] using the island model [16]. In the island model, a population is divided into two or more sub-populations called islands and each island evolves individually. Each island can maintain different types of individuals at the end of alternation of generations. Therefore, DMEO can maintain diversity at the end of alternation of generations.

The main contributions of this study are as follows:

- Distributed modified extremal optimization (DMEO) [17] is proposed. DMEO is a hybrid bio-inspired heuristic that combine PMEO and DGA using the island model. Many studies [8], [9], [10], [18], [19], [20], [21] have applied EO to combinatorial optimization problems such as the traveling salesman problem, graph partitioning problem, and image rasterization. Recently, some studies [22], [23], [24] have focused on integrating a population-based approach in EO. To the best of our knowledge, there is no study on population-based MEO involving the distributed genetic algorithm using the island model.
- To evaluate the proposed DMEO, we implemented DMEO for reducing crossovers in a reconciliation graph. Moreover, we evaluated DMEO using two actual data sets for experiments. Experimental results shows that DMEO outperforms PMEO. Moreover, we compared DMEO with another population-based heuristic based on genetic algorithm with minimal generation gap (MGG) [25], which is the one of the best generation alternation models. The performance of DMEO also is better than that of MGG.

The rest of the paper is organized as follows. In Section 2, the problem definition is presented. In Section 3, related work is reviewed. In Section 4, we explains MEO and PMEO. In Section 5, DMEO is proposed. In Section 6, experimental results are presented, and Section 7 is the conclusion of the paper.

II. Problem Definition

A reconciliation graph (RG) consists of two ordered trees, $OT_1 = (V_1, E_1)$ and $OT_2 = (V_2, E_2)$, where V_1 and V_2 are finite sets of nodes and E_1 and E_2 are finite sets of edges. A node that has no child nodes is a leaf node. The leaf node sets of OT_1 and OT_2 are denoted by $L_1 \in V_1$ and $L_2 \in V_2$, respectively. If the number of species is n, the number of leaf nodes is n. A leaf node has a label name, which is a species' name. The label name set is denoted by L_{leaf}.

In the reconciliation graph, OT_1 and OT_2 are located face to face. If a leaf node of OT_1 has the same label name as that of OT_2, then the two leaf nodes are connected to each other. In Fig.2, phylogenetic tree 1 is OT_1 and phylogenetic tree 2 is OT_2. The leaf node set L_1 has four nodes, v_{14}, v_{15}, v_{16}, and v_{17}. Similarly, L_2 has four nodes, v_{24}, v_{25}, v_{26}, and v_{27}. There are four label names in L_{leaf}, "a," "b," "c," and "d." Two leaf nodes v_{14} and v_{24} are connected because they have the same label name "a."

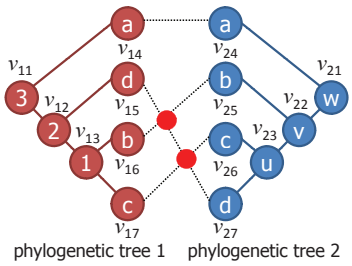


Fig. 2. Problem definition (OL_1 is given by $OL_1 = [v_{14}, v_{15}, v_{16}, v_{17}]$ and OL_2 is given by $OL_2 = [v_{24}, v_{25}, v_{26}, v_{27}]$).

Let OL_1 and OL_2 be the order lists of leaf nodes:

$$OL_1 = [ol_{1,1}, ol_{1,2}, \cdots, ol_{1,n}](ol_{1,i} \in L_1, \mathcal{L}(ol_{1,i}) \in L_{leaf}),$$
$$OL_2 = [ol_{2,1}, ol_{2,2}, \cdots, ol_{2,n}](ol_{2,i} \in L_2, \mathcal{L}(ol_{2,i}) \in L_{leaf}),$$

where function $\mathcal{L}$ returns the label name of an input node. The function $C(M)$ returns the number of crossovers:

$$C(M) = \sum m_{j,\beta} m_{k,\alpha} [1 \le j < k \le n, 1 \le \alpha < \beta \le n], \quad (1)$$

where $m_{i,j}$ is (i,j)th-element of the connection matrix M that is defined as

$$m_{i,j} = \begin{cases} 1 & if\ \mathcal{L}(ol_{1,i}) = \mathcal{L}(ol_{2,j}), \\ 0 & otherwise. \end{cases} \quad (2)$$

In Fig. 2, OL_1 is given by $OL_1 = [v_{14}, v_{15}, v_{16}, v_{17}]$. Similarly, there are four leaf nodes in phylogenetic tree 2, $ol_{2,1} = v_{24}$, $ol_{2,2} = v_{25}$, $ol_{2,3} = v_{26}$, and $ol_{2,4} = v_{27}$. Therefore OL_2 is given by $OL_2 = [v_{24}, v_{25}, v_{26}, v_{27}]$. For example, the $(0,0)$th-element $m_{0,0}$ is 1 because $\mathcal{L}(v_{14})$ equals $\mathcal{L}(v_{24})$. Similarly, the $(1,1)$th-element $m_{1,1}$ is 0 because $\mathcal{L}(v_{15})$ does not equal $\mathcal{L}(v_{25})$.

$$M = \begin{array}{c} \\ a \\ d \\ b \\ c \end{array} \begin{array}{c} \begin{array}{cccc} a & b & c & d \end{array} \\ \begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \end{pmatrix} \end{array}$$

The task of reducing crossovers in the reconciliation graph is defined as follows:

$$\begin{array}{ll} \textbf{min}: & C(M), \\ \textbf{subject to}: & (1)\ M \text{ is the connection matrix of the } RG, \\ & (2) \text{ There are no crossovers on edges} \\ & \text{between non-leaf nodes in the } RG. \end{array}$$

There should be no crossovers on edges between non-leaf nodes in the reconciliation graph. For this constraint, we need to change order of leaf nodes by changing the order of child nodes in intermediate nodes. We cannot change the order between v_{15} and v_{17} (Fig. 2) because it will lead to the presence of crossovers on edges between non-leaf nodes. If we want to change the order between v_{15} and v_{17}, it is necessary to replace v_{15} and v_{13}, which are child nodes of v_{12}. If we replace v_{15} and v_{13}, the number of crossovers in the reconciliation graph becomes zero, and OL_1 is changed to $OL_1 = [v_{14}, v_{16}, v_{17}, v_{15}]$.

III. Related Work

Molecular biologists used to perform reducing crossovers in reconciliation graphs manually. However, with increase in the number of nodes in a reconciliation graph, it is very difficult to make it manually. Hence, some computational solvers to reduce crossovers automatically in a reconciliation graph have been proposed. The most simplest computational heuristic was proposed in [5]. This simplest heuristic could obtain only a local optimal solution with a kind of local search. To improve the performance, a GA-based heuristic was proposed in [6]. There are two steps in the GA-based heuristic. First, the GA-based heuristic searches quasi-optimal solutions with simple GA. Second, the GA-based heuristic finds more better solutions from quasi-optimal solutions by using local search.

The GA-based heuristic has some performance issues, because it is difficult to design efficient crossover functions. One of the performance issue is that the speed of convergence slow. Therefore it need huge computation time to get optimal solutions. To overcome this difficulty, We have proposed modified Extremal Optimization (MEO) [11], which is a EO-based solver. The EO mechanism[8], [9], [10] follows the spirit of the Bak-Sneppen model, updating variables that have among the worst values in a solution and replacing them by random values without ever explicitly improving them. In other word, EO evolves a single individual by making local modifications to the worst components in the individual. Modified EO improved the methodology of generating the solution of next generation and making local modification. The experimental results show that MEO outperforms EO. Moreover, MEO is good performance compared with the GA-based heuristic.

In our previous study [13], we proposed population-based modified extremal optimization (PMEO), which is a combination of a population-based approach and MEO. Recently, there are some studies [22], [23], [24] on population-based EO algorithm. These algorithm is based on EO. Our approach uses MEO for changing state of individual. Multiple individuals are only used in [22], [23]. In our approach, not only multiple individuals are used but also restrictive crossover is performed between individuals. Our approach is most similar with the approach of [24]. However, [24] is a hybrid of partial swam optimization (PSO) and EO. This hybrid approach is only performing EO as mutation. However, our approach repeats a change of generation by PMEO.

IV. Population-based Modified Extremal Optimization

EO [8], [9], [10] follows the spirit of the Bak-Sneppen model, updating variables that have one of the worst values in a solution and replacing them by random values without ever explicitly improving them. Algorithm 1 shows the details of processing steps of EO. In EO, an individual I consists of n components O_i $(1 \leq i \leq n)$. Let λ_i be the fitness value of O_i. First, EO selects O_{worst}, which has the worst fitness value. Second, the state of component O_{worst} is changed at random. Henceforth, selection and change state of a component are repeated. The component with the worst fitness value has a high possibility that the fitness value of it will become better by changing state. Consequently, the fitness value of the individual also gets better because the fitness value of the component with worst fitness value gets better.

Algorithm 1 EO

```
Generate initial individual I at random.
I_best ← I
m ← 0
while m < max_of_generations do
    Evaluate fitness value λ_i of each component O_i.
    Select O_worst with the worst fitness value.
    Change the state of O_worst at random.
    if F(I) > F(I_best) /* The function which returns the
    fitness value of an individual is denoted as F. */ then
        I_best ← I
    end if
    m ← m + 1
end while
```

Algorithm 2 MEO

```
Generate initial individual I at random.
I_best ← I
m ← 0
while m < max_of_generations do
    Evaluate fitness value λ_i of each component O_i.
    Candidates ← φ
    n ← 0
    while n < num_of_candidates do
        Select O_selected with roulette selection (selection
        rates are the reciprocal of fitness values with com-
        ponents).
        Generate new individual I' from I by changing the
        state of O_selected.
        Candidates ← Candidates ∪ I'
        n ← n + 1
    end while
    I ← BEST(Candidates)
    if F(I) > F(I_best) then
        I_best ← I
    end if
    m ← m + 1
end while
```

Modified EO (MEO) [11] generates two or more neighbor individuals as candidates for the next generation individual. The best neighbor individual among the candidates is selected as the next generation individual. Moreover, MEO uses roulette selection to select a component. Algorithm 2 shows the details of processing steps of MEO. First, MEO selects $O_{selected}$ with roulette selection. The selection rates of roulette selection are reciprocals of fitness values with components. Second, MEO generates new individual I' from I by changing the state of $O_{selected}$. Third, the generated I' is stored into $Candidates$. Finally, MEO selects the best individual from $Candidates$.

Population-based MEO (PMEO) [13] involves a population-based approach. There are two or more individuals in a population. Alternation of generation is repeatedly performed for every individual by using MEO. To improve the search efficiency, individuals copy a sub-structure of an individual that has good sub-structures at

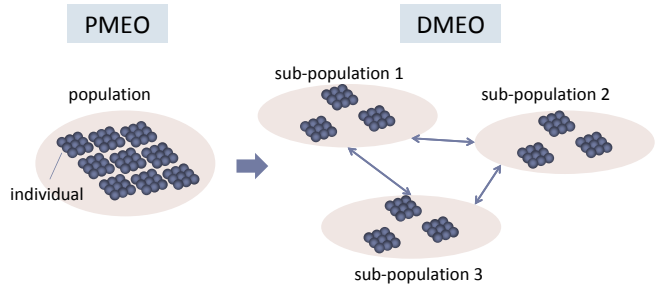


Fig. 3. Distributed modified extremal optimization (DMEO divides the entire population into two or more sub-populations, as many islands. Each island has a sub-population and the sub-population evolves individually by PMEO.).

each alternation of generations. This operation resembles the crossover operation in genetic programing (GP). However, one side only copies a sub-structure of another side. Copying of good sub-structures leads to a high probability of generation of a good individual.

V. Distributed Modified Extremal Optimization

This section explains the main concept of DMEO and the algorithm of DMEO for reducing crossovers in a reconciliation graph.

A. Main Concept

DMEO is a hybrid of PMEO and DGA using the island model. DMEO divides the entire population into two or more sub-populations, as many islands. Each island has a sub-population and the sub-population evolves individually by PMEO. In the island model, from each island, some individuals are selected and transferred to another island. In return, the same number of migrants are received from another island. Each sub-population in a island converges to the separate best solution. Each island evolves individually, the island model can maintain diversity at the end of alternation of generations.

DMEO repeats the following two steps:

(1) Sub-populations in islands should be made to evolve through one or more generations by using PMEO.
(2) Some individuals in islands are migrated to other islands.

B. Individual and Component

A reconciliation graph is defined as an individual. A component of an individual is defined as a pair of leaf nodes with the same label name:

$$O_i = \{ol_{1,i}, ol_{2,\delta(i)}\} \quad (\mathcal{L}(ol_{1,i}) = \mathcal{L}(ol_{2,\delta(i)})). \tag{3}$$

Let $ol_{1,i}$ be a leaf node of OL_1 and $ol_{2,\delta(i)}$ be a leaf node of OL_2. The function $\delta(i)$ returns the subscript number of an element of OL_2 whose label name is the same as the label name of $ol_{1,i}$. To change the state of O_i, it is necessary to change the order of child nodes of ancestor nodes of $ol_{1,i}$ or $ol_{2,\delta(i)}$. Here, $\mathcal{AS}(T, lname)$ is a set of ancestor nodes of a leaf node in T that has the label name $lname$. For example, $\mathcal{AS}(I, T_1, O_2)$ returns $\{v_{12}, v_{11}\}$ in Fig. 2.

Algorithm 3 DMEO

1: Generate initial population P_{init} at random.
2: $I_{best} \leftarrow \mathbf{BEST}(P_{init})$
3: Divide P_{init} into p sub-populations $SubP_i$.
4: Store sub-populations $SubP_i$ into island $ISLND_i$.
5: **for** $i = 1$ to $max\_generations/m$ **do**
6: **(Evolution Step)** For each $ISLND_i$, sub-population $SubP_i$ should be made to evolve through m generations by using the function $\mathbf{PMEO}(SubP_i, m)$.
7: **(Migration Step)** For each $ISLND_i$, migrate some individuals of a sub-population in the island to another island.
8: **if** $\mathbf{F}(\mathbf{BEST}(SubP_1 \cap \cdots \cap SubP_p)) > \mathbf{F}(I_{best})$ **then**
9: $I_{best} \leftarrow \mathbf{BEST}(SubP_1 \cap \cdots \cap SubP_p)$
10: **end if**
11: **end for**

Algorithm 4 $\mathbf{PMEO}(\mathbf{P}, \mathbf{m})$

1: **for** $i = 1$ to m **do**
2: **for all** $I \in P$ **do**
3: Evaluate fitness value λ_i of each component O_i of I.
4: $C \leftarrow \phi$
5: $n \leftarrow 0$
6: **while** $n < num\_of\_candidates$ **do**
7: Select $O_{selected}$ by roulette selection (selection rates are the reciprocal of fitness values with components).
8: $C \leftarrow C \cup \mathbf{GNI}(I, O_{selected})$
9: $n \leftarrow n + 1$
10: **end while**
11: $I \leftarrow \mathbf{BEST}(C)$
12: **end for**
13: $\mathbf{CSS}(P)$
14: **end for**

C. Definition of Fitness

The number of crossovers between $ol_{1,i}$ and $ol_{2,\delta(i)}$ is denoted by $\mathcal{C}(M, i)$. The following are the definitions of $\mathcal{C}(M, i)$ and the fitness value λ_i of O_i:

$$\lambda_i = \frac{\mathcal{C}(M) - \mathcal{C}(M, i)}{\mathcal{C}(M)}, \tag{4}$$

$$\mathcal{C}(M, i) = \sum_{l=i+1}^{n} \sum_{m=1}^{\delta(i)-1} \frac{m_{l,m}}{2} + \sum_{l=1}^{i-1} \sum_{m=\delta(i)+1}^{n} \frac{m_{l,m}}{2}. \tag{5}$$

In Fig. 2, there are four components, $O_1 = \{ol_{1,1}, ol_{2,1}\}(= \{v_{14}, v_{24}\})$, $O_2 = \{ol_{1,2}, ol_{2,4}\}(= \{v_{15}, v_{27}\})$, $O_3 = \{ol_{1,3}, ol_{2,2}\}(= \{v_{16}, v_{25}\})$, and $O_4 = \{ol_{1,4}, ol_{2,3}\}(= \{v_{17}, v_{26}\})$, with $\delta(1) = 1$, $\delta(2) = 4$, $\delta(3) = 2$, and $\delta(4) = 3$. The fitness values of the components are $\lambda_1 = 1$, $\lambda_2 = 1/2$, $\lambda_3 = 3/4$, and $\lambda_4 = 3/4$.

D. Algorithm

The algorithm of DMEO for reducing crossovers in a reconciliation graph consists of two steps: (1) Evolution Step and (2) Migration Step (Algorithm 3). First, an initial population divided to p sub-populations (p is the number

Algorithm 5 CSS(P)

1: Select individual $SI \in P$ by roulette selection (selection rates are the fitness values of components).
2: **for all** $I \in P, I \neq SI$ **do**
3: **for** $i = 1$ to n **do**
4: Calculate the difference $diff_i$ between the fitness value of O_i in SI and the fitness value of O_j in I, where O_i and O_j have the same label name.
5: **end for**
6: Select $O_{selected}$ by roulette selection (selection rates are $diff_i$).
7: $A \leftarrow \mathcal{AS}(T_1, \mathcal{L}(O_{selected}))$ or $\mathcal{AS}(T_2, \mathcal{L}(O_{selected}))$
8: $C \leftarrow \phi$
9: **for all** $a \in A$ **do**
10: Generate a new individual I' from I by changing the order of child nodes in a.
11: $C \leftarrow C \cup I'$
12: **end for**
13: $I \leftarrow \mathbf{BEST}(C)$
14: **end for**

of sub-populations). Sub-population $SubP_i$ is located in an island $ILND_i$. In the Evolution Step (step 6), the sub-populations in all the islands are made to evolve through m generations by using the function $\mathbf{PMEO}(SubP_i, m)$ (m is migration interval). In Migration Step (step 7), some individuals of a sub-population in an island are migrated to another island. Finally, the best individual is selected from all the islands (step 8 and step 9).

E. Evolution Step

In the Evolution Step, each sub-population is in an island is made to evolve through m generations by using the function **PMEO** (Algorithm 4). First, for each individual, the state of the individuals in P is changed by using MEO. Second, the function **CSS** copies a good sub-structure of an individual to another individual.

In the MEO steps, for each individual, the following steps are executed. Initially, the function evaluates the fitness value λ_i (step 3). Next, the following three steps are repeated while n is less than $num\_of\_candidates$. First, component $O_{selected}$ in I is selected by using the roulette selection (step 7). Second, the function generates an neighbor individual from I with the function **GNI**. The function **GNI** generates a neighbor individual by changing the state of component $O_{selected}$. Third, the neighbor individual is stored in C (step 8). Finally, the best individual in C is selected and I is replaced by it (step 11).

The state of $O_{selected}$ is changed by changing the order of child nodes in an intermediate node, which is an ancestor node of $O_{selected}$. The processing steps of **GNI** are as follows. First, T_1 or T_2 is selected randomly and $\mathcal{AS}(T_1, \mathcal{L}(O_{selected}))$ or $\mathcal{AS}(T_2, \mathcal{L}(O_{selected}))$ are stored in the set $Ancestors$. Then, node a is selected at random from A. Finally, the order of the child nodes in a is changed.

Suppose that the selected component is O_2 in Fig. 2. The function $\mathcal{AS}(T_1, \mathcal{L}(O_2))$ returns $\{v_{12}, v_{11}\}$ and $\mathcal{AS}(T_2, \mathcal{L}(L_2))$ returns $\{v_{22}, v_{21}\}$. If $Ancestors = \{v_{12}, v_{11}\}$ and v_{12} is selected as a, the order of child nodes in v_{12} is changed. In this case, order of node v_{15} and v_{13} are changed. As a result, a new individual I' is obtained by the change state.

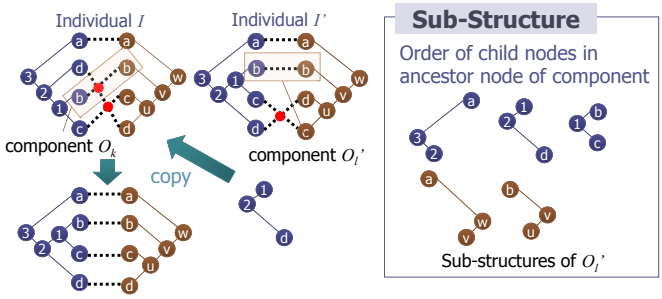


Fig. 4. Example of copy sub-structure (The component O_l' has five sub-structures. If individual I copies the 2-th sub-structure, then, the number of crossovers of I becomes zero.).

Algorithm 5 shows the function **CSS**. At the beginning, an individual SI in P is selected by roulette selection (step 1). Each individual of P copies a sub-structure of SI by the following steps. First, the function calculates the difference $diff_i$ between the fitness value of O_i of SI and the fitness value of O_j of I, where O_i and O_j have the same label name (steps 3, 4, and 5). Second, $O_{selected}$ is selected by roulette selection (step 6). Next, $\mathcal{AS}(T_1, \mathcal{L}(O_{selected}))$ or $\mathcal{AS}(T_2, \mathcal{L}(O_{selected}))$ is stored in A (step 7). Then, for all $a \in A$, a new individual I' is generated from I by changing the order of child nodes in a, and I' is stored in C (steps 9, 10, 11, and 12). Finally, the function selects the best individual from C (step 13).

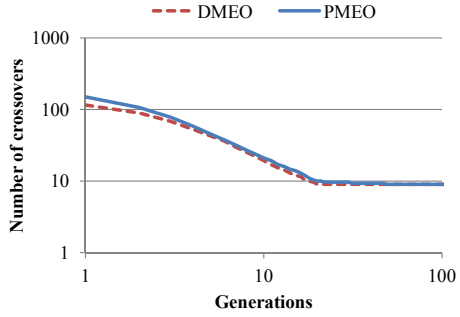
The fitness value of a component is depend on order of child nodes in its ancestor nodes. In other words, it is very likely that a component with a good fitness value has good ancestor nodes. Here, we define order of child nodes of a ancestor node as a sub-structure. Fig. 4 shows an example of copy sub-structure. In this example, there are two individuals I and I'. The component O_l' in I' is good component compared with component O_k in I. The component O_l' has five sub-structures. If individual I copies the 2-th sub-structure, then, the number of crossovers of I becomes zero.

F. Migration Step

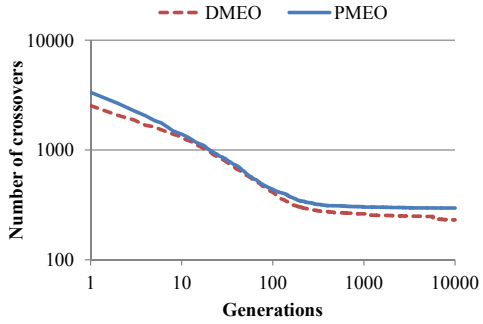
In the Migration Step, some individuals in each island are migrated to another island. The island model requires $number\ of\ sub-populations$, $migration\ rate$, $migration\ interval$, and $migration\ model$. The first three items are user-given parameters. The last item consists of two things: $selection\ method$ and $topology$. The method used for the selection of individuals for migration is referred as $selection\ method$. The structure of the migration of individuals between sub-populations is referred as $topology$. In this study, we use uniform random selection as the $selection\ method$. In the Migration step, some individual are selected from a sub-population in each island according to $migration\ rate$. Moreover, the proposed algorithm uses the random ring migration topology. In this topology, the ring includes all islands, and the order of the islands is determined randomly every Migration step. Each island transfers some individuals to the next inland based on the direction of the ring.

TABLE I
DATA SETS

	Taxonomic tree		Phylogenetic tree	
	Number of nodes	Number of leaf nodes	Number of nodes	Number of leaf nodes
Housekeeping	241	40	79	40
Moss	290	207	394	207

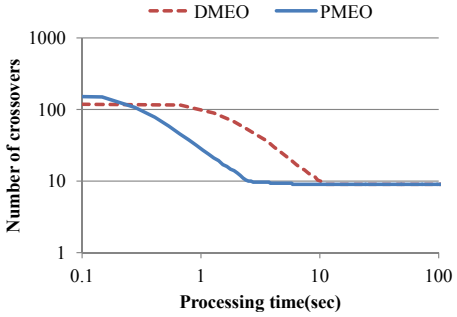


(a) *Housekeeping* data set

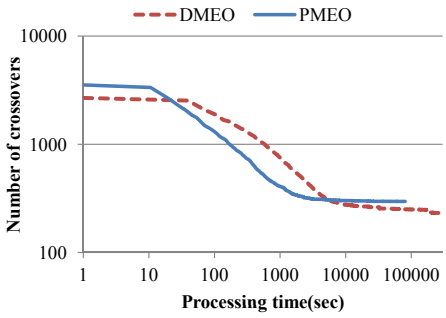


(b) *Moss* data set

Fig. 5. Experiment 1 ((a) and (b) shows the number of crossovers of the best individual) .



(a) *Housekeeping* data set



(b) *Moss* data set

Fig. 6. Experiment 2 ((a) and (b) shows the number of crossovers of the best individual).

VI. Experimental Results

We performed five experiments for evaluating the performance of DMEO. This section shows the experimental results.

A. Setup

In the experiments, the two data sets listed in Table I are used. The *Housekeeping* data set consists of a phylogenetic tree of the housekeeping gene and its taxonomic tree. The *Moss* data set consists of a phylogenetic tree of the rps4 gene and its taxonomic tree. The number of species in the *Housekeeping* data set is 40 and that in the *Moss* data set is 207.

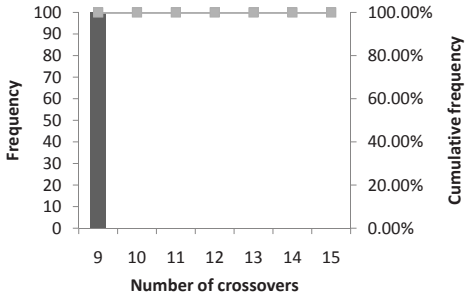
Experiment 1 measured the number of crossovers of the best individual at each generation to compare DMEO and PMEO. Experiment 2 also measured the number of crossovers of the best individual at each elapsed time to compare DMEO and PMEO. Experiment 3 measured frequency of the number of crossovers of best individuals in fixed generations. Experiment 4 measured the number of crossovers of the best individual at each generation by changing the number of sub-populations. Experiment 5 compares PMEO with MGG.

In PMEO and DMEO, the number of individuals in the population was set to 100. The user parameter $num\_of\_candidates$ was set to 100 and m was set to 10000 in PMEO. In DMEO, the user parameter $num\_of\_candidates$, $migration\_interval(m)$, $number\ of\ sub{-}populations(p)$, and $migration\ rate$ were set to be 100, 10, 5 and 0.05, respectively. The number of individuals in a sub-population is 20. The number of crossovers was the average of three trials.

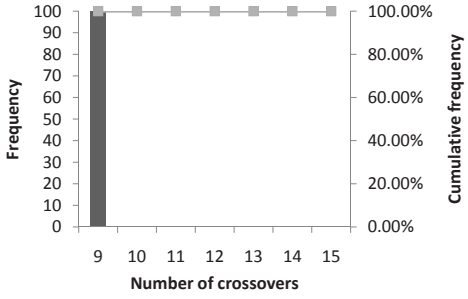
B. Experiment 1

In Experiment 1, we measured the number of crossovers of the best individual in each generation. Figure5(a) and Figure5(b) show the number of crossovers (vertical axis: the number of crossovers, horizontal axis: generations). Fig. 5(a) and Fig. 5(b) show that the number of crossovers of DMEO in each generation was smaller than that in the case of PMEO. DMEO showed better performance compared with PMEO.

The number of crossovers in PMEO is converging into around 300 when we use *Moss* data set. On the other hand, in DMEO, the number of crossovers is converging into around 250. The diversity of PMEO is small, because the number of sub-populations is one. Therefore, the fitness value of a individual will not be improved in the end of alternation of generations.

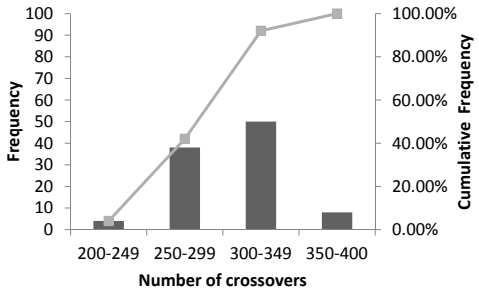


(a) PMEO

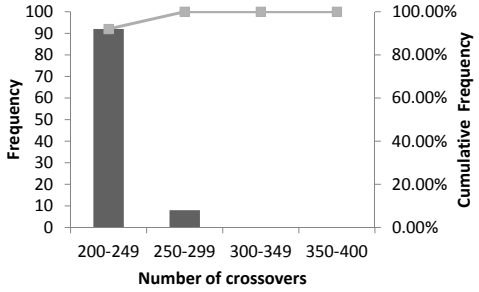


(b) DMEO

Fig. 7. Experiment 3 ($Housekeeping$ data set).



(a) PMEO



(b) DMEO

Fig. 8. Experiment 3 ($Moss$ data set).

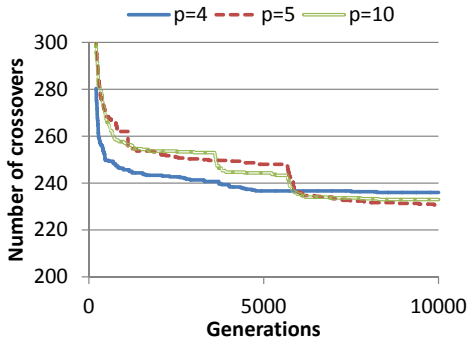


Fig. 9. Experiment 4 ($Moss$ data set).

C. Experiment 2

In Experiment 2, we measured the number of crossovers of the best individual at different time instants. The computation time of DMEO was longer than that in the case of PMEO because the former included the Migration Step. Therefore, it was necessary to compare the number of crossovers for the same computation time.

Fig. 6(a) and Fig. 6(b) show the number of crossovers at different time instants (vertical axis: the number of crossovers, horizontal axis: processing time). At the end of the processing, DMEO have fewer crossovers than PMEO. This result indicates DMEO performs better with fewer crossovers than PMEO.

D. Experiment 3

The number of crossovers of the best individual was measured 100 times for the 10,000th alternation generation. Figure7(a) and Figure7(b) show frequency of the number of crossovers when $Housekeeping$ data set is used. The number of crossovers of the optimal solution of $Housekeeping$ data set is 9. Both of them can obtain the best solution by 100%. Fig. 8(a) and Fig. 8(b) show the frequency of the number of crossovers for the $Moss$ data set. In DMEO, all the numbers of crossovers of optimal solutions were between 200 and 299. On the other hand, they were distributed between 200 and 400 for PMEO. Above all, although 90% of optimal solutions were between 200 and 249 in the case of DMEO, only a few optimal solutions were obtained between 200 and 249 in the case of MEO.

E. Experiment 4

In Experiment 4, we changed the number of sub-populations in DMEO. Fig. 9 shows the results of Experiment 4 using $Moss$ data set. When the number of sub-populations is four, it has fallen into the local optimal solutions. On the other hand, when the number of sub-populations is five or ten, convergence is not early. Therefore, they can obtain better solutions.

F. Experiment 5

In Experiment 5, we compared PMEO with MGG, which is the one of the best generation alternation models. In DMEO, the number of individuals in the population was set to 100. The user parameter $num\_of\_candidates$ was set to 100 and m was set to 30000. In DMEO, the user parameter $num\_of\_candidates$, $migration\_interval(m)$, $number\ of\ sub{-}populations(p)$, and $migration\ rate$ were set to be 100, 10, 5 and 0.05, respectively. The number of individuals in a sub-population is 20. In MGG, the number of individuals is 100, the number of children is 100, and the rate of mutation is 5%.The number of crossovers was the average of three trials.

Figure10 show the number of crossovers (vertical axis: the number of crossovers, horizontal axis: generations). The performance of DMEO also is better than that of MGG. In

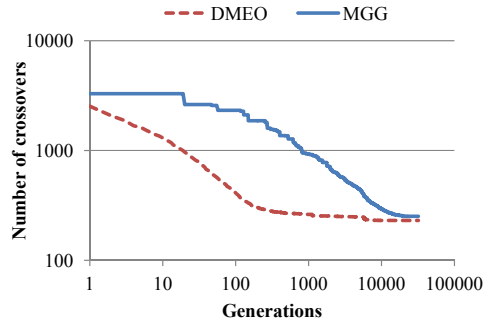


Fig. 10. Experiment 5 ($Moss$ data set).

particular, the speed of convergence in DMEO is faster than that in MGG.

VII. Conclusion

This paper proposes distributed modified extremal optimization (DMEO) for reducing crossovers in a reconciliation graph. DMEO is a hybrid of population-based modified extremal optimization (PMEO) and the distributed genetic algorithm using the island model that is used for reducing crossovers in a reconciliation graph. In the island model, a population is divided into two or more sub-populations called islands and each island evolves individually. Each island can maintain different types of individuals at the end of alternation of generations. Therefore, DMEO can maintain diversity at the end of alternation of generations. We have evaluated DMEO by using actual data sets. Experimental results show that DMEO is better performance compared with PMEO. Moreover, experimental results show that DMEO can maintain diversity and performs better than PMEO. In the future work, we will develop extended DMEO for making it applicable to other combination optimization problems.

Acknowledgment

This work was supported in part by a Grant-in-Aid for Young Research (B) (No.23700124) from the Ministry of Education, Culture, Sports, Science and Technology in Japan and a Grant-in-Aid for Scientific Research (C) (2) (No.20500137) from the Japanese Society for the Promotion of Science, Japan.

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