Island-Model-based Distributed Modified Extremal Optimization with Tabu Lists for Reducing Crossovers in Reconciliation Graph

Keiichi Tamura, Hajime Kitakami

***Abstract*—Molecular biologists need to reveal the difference between two heterogeneous phylogenetic trees and the between a phylogenetic tree and a taxonomic tree in order to determine the mechanism of molecular evolution. 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. It is difficult to compare two heterogeneous ordered trees, if there are many crossed edges between leaf nodes in the reconciliation graph. Therefore the number of crossovers in the reconciliation graph should be decreased; then 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 with tabu lists (DMEOTL). This heuristic is a hybrid of distributed modified extremal optimization (DMEO) and the tabu search mechanism. We have evaluated DMEOTL using actual data sets. DMEOTL shows better performance compared with DMEO.**

***Index Terms*—extremal optimization, distributed genetic algorithm, island model, tabu list, reconciliation graph**

I. Introduction

PHYLOGENETIC trees and taxonomic trees are evolutionary trees showing the inferred evolutionary relationships among various biological organisms. Molecular biologists need to reveal the difference between two heterogeneous trees for determining the mechanism of molecular evolution in organisms. In this task, comparing two heterogeneous trees, which consist of phylogenetic trees or a phylogenetic tree and a taxonomic tree is required [1], [2], [3], [4]. A phylogenetic tree is a branching tree inferred from evolutionary relationships among species. A taxonomy tree is also a branching tree based on traditional biological classification.

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 is 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. 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

This work was supported in part by Hiroshima City University Grant for Special Academic Research (General Studies).

K.Tamura and H.Kitakami are with Graduate School of Information Sciences, Hiroshima City University, 3-4-1, Ozuka-Higashi, Asa-Minami-Ku, Hiroshima 731-3194 Japan, corresponding e-mail: ktamura@hiroshima-cu.ac.jp, kitakai@hiroshima-cu.ac.jp

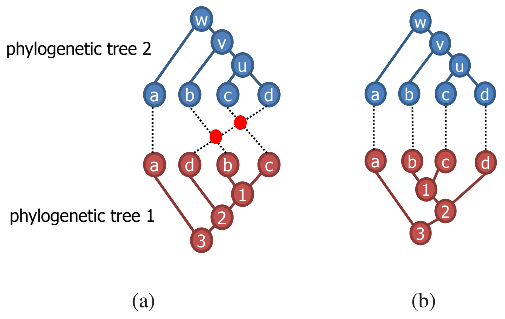


Fig. 1. Examples of reconciliation graphs ((a) shows a reconciliation graph that has two crossovers, and (b) shows a reconciliation graph that has no crossovers).

"d." The leaf nodes of phylogenetic tree 1 and those of phylogenetic tree 2 face each other.

It is difficult to compare two heterogeneous trees, if there are many crossed edges between leaf nodes in the reconciliation graph. 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, because the number of combinations increases exponentially as the number of leaf nodes increases. Therefore, there are some heuristics [5], [6], [7], [8] that can be used for reducing crossovers in a reconciliation graph. The reconciliation graph shown in Fig. 1(a) has two crossovers. If order of node "1" and node "d" are replaced, we can obtain a optimal reconciliation graph shown in Fig. 1(b), which has no crossovers.

In our previous study [8], we proposed distributed modified extremal optimization (DMEO), which is a hybrid of population-based modified extremal optimization (PMEO) [7] and the distributed genetic algorithm (DGA) [9], [10] using the island model [11]. Extremal optimization (EO) [12], [13], [14] is a general-purpose heuristic inspired by the Bak-Sneppen model [15] of self-organized criticality from the field of statistical physics. EO generates a neighbor individual, which is represented as a solution, randomly at an alternation of generations. On the other hand, modified extremal optimization (MEO) [16] generates multiple neighbor individuals and selects the best individual that has the best fitness value.

Since MEO generates multiple neighbor solutions, MEO can avoid falling into local optimal in regard to reducing crossovers in a reconciliation graph: however, MEO has a performance problem in mechanism of generating neighbor individuals. At the end of alternation of generations, MEO often becomes stuck in poor-evaluated areas or areas where evaluate plateau. Therefore, MEO has to avoid pitfalls and explore regions of the search space that would be left unexplored. In other word, MEO need to carefully explore the neighborhood of each individual as the search progresses. The experimental results of DMEO show that DMEO is sometimes poorly-converged, because some individual can not explore regions of the search space that would be left unexplored.

To address this problem, we propose a novel MEO called MEO with a tabu list (MEOTL) that involves the mechanism of tabu list in tabu search [17] and DMEO with tabu lists (DMEOTL). The main contributions of this study are as follows:

- To avoid pitfalls and explore regions of the search space that would be left unexplored, MEOTL is proposed. MEOTL utilizes the mechanism of tabu list in tabu search, which can avoid generating recently visited individuals as neighbor individuals at each alternation of generations.
- To improve the performance of DMEO for reducing crossovers in a reconciliation graph, we incorporate MEOTL in DMEO. In DMEOTL, a population is divided into two or more sub-populations called islands and each island evolves individually. Each individual has a tabu list, individuals located in islands evolve using MEOTL, in DMEOTL.
- To evaluate MEOTL and DMEOTL, we implemented MEOTL and DMEOTL for reducing crossovers in a reconciliation graph. We evaluated MEOTL and its performance outperforms MEO. Moreover, we evaluated DMEOTL using two actual data sets for experiments. Experimental results shows that DMEOTL outperforms DMEO.

The rest of the paper is organized as follows. In Section 2, the problem definition is presented. In Section 3, we explains EO and MEO. In Section 4, we proposed MEOTL. In Section 5, DMEOTL is presented. In Section 6, experimental results are presented, and Section 7 is the conclusion of the paper.

II. Problem Definition

Phylogenetic trees and taxonomic trees are referred to as ordered trees. 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 has a parent and multiple child nodes. Let $\mathcal{PT}(v)$ be the parent node of node v. If $\mathcal{PT}(v)$ is NULL, the node v is the root node. Let $\mathcal{CN}(v)$ be child nodes of node v. 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}.

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 $\mathcal{NC}(M)$ returns the number of crossovers:

$$\mathcal{NC}(CM) = \sum cm_{j,\beta} cm_{k,\alpha} [1 \le j < k \le n, \quad 1 \le \alpha < \beta \le n], \tag{1}$$

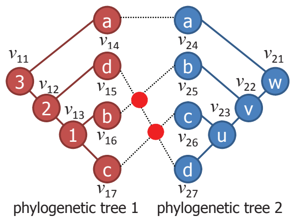


Fig. 2. Problem definition (OL_1 is given by $OL_1 = [v_{14}, v_{15}, v_{16}, v_{17}]$ and OL_2 is given by $OL_2 = [v_{24}, v_{25}, v_{26}, v_{27}]$).

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

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

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 $cm_{0,0}$ is 1 because $\mathcal{L}(v_{14})$ equals $\mathcal{L}(v_{24})$. Similarly, the $(1, 1)$th-element $cm_{1,1}$ is 0 because $\mathcal{L}(v_{15})$ does not equal $\mathcal{L}(v_{25})$. The following is the connection matrix of the reconcilication graph shown in the Fig. 2.

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

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

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

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. Modified Extremal Optimization

EO [12], [13], [14] 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. Many studies [12], [13], [14], [18], [19], [20], [21] have applied EO to combinatorial optimization problems such as the traveling salesman problem, graph partitioning problem, and image rasterization.

Algorithm 1 shows the details of processing steps of EO. In EO, an individual I consists of n components O_i ($1 \le i \le n$). Let λ_i be the fitness value of O_i. First, EO selects

Algorithm 1 EO

```
1:  Generate initial individual $I$ at random.
2:  $I_{best} \leftarrow I$
3:  $m \leftarrow 0$
4:  while $m < max\_of\_generations$ do
5:      Evaluate fitness value $\lambda_i$ of each component $O_i$.
6:      Select $O_{worst}$ with the worst fitness value.
7:      Change the state of $O_{worst}$ at random.
8:      if $\mathbf{F}(I) > \mathbf{F}(I_{best})$ /* The function which returns the fitness value of an individual is denoted as $\mathbf{F}$. */ then
9:          $I_{best} \leftarrow I$
10:     end if
11:     $m \leftarrow m + 1$
12: end while
```

Algorithm 2 MEO

```
1:  Generate initial individual $I$ at random.
2:  $I_{best} \leftarrow I$
3:  $m \leftarrow 0$
4:  while $m < max\_of\_generations$ do
5:      Evaluate fitness value $\lambda_i$ of each component $O_i$.
6:      $Candidates \leftarrow \phi$
7:      $n \leftarrow 0$
8:      while $n < num\_of\_candidates$ do
9:          Select $O_{selected}$ with roulette selection according to fitness values of components.
10:         Generate new individual $I'$ from $I$ by changing the state of $O_{selected}$.
11:         $Candidates \leftarrow Candidates \cup I'$
12:         $n \leftarrow n + 1$
13:     end while
14:     $I \leftarrow \mathbf{BEST}(Candidates)$
15:     if $\mathbf{F}(I) > \mathbf{F}(I_{best})$ then
16:         $I_{best} \leftarrow I$
17:     end if
18:     $m \leftarrow m + 1$
19: end while
```

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.

MEO [16] generates multiple neighbor individuals as candidates for the next generation individual. The best neighbor individual in the candidates is selected as the next generation individual. Moreover, MEO uses roulette selection to select a component. The experimental results in [16] show that MEO outperforms EO. Moreover, MEO is good performance compared with the GA-based heuristic [5], [6]. Algorithm 2 shows the details of processing steps of MEO. MEO generates multiple neighbor individuals at each alternation of generations through the following steps (step 8 - step 13). First, MEO selects $O_{selected}$ with roulette selection (step 9). The selection rates of roulette selection are reciprocals of fitness values with components. Second, MEO generates new

Algorithm 3 MEOTL

```
1:  Generate initial individual $I$ at random.
2:  $I_{best} \leftarrow I$
3:  $m \leftarrow 0$
4:  $TL \leftarrow \phi$
5:  while $m < max\_of\_generations$ do
6:      Evaluate fitness value $\lambda_i$ of each component $O_i$.
7:      $Candidates \leftarrow \phi$
8:      $n \leftarrow 0$
9:      while $n < num\_of\_candidates$ do
10:         Select $O_{selected}$ with roulette selection according to fitness values of components.
11:         Generate new individual $I'$ from $I$ by changing the state of $O_{selected}$.
12:         if $\mathbf{IS\_INCLUDED}(I', TL)$ == false then
13:             $Candidates \leftarrow Candidates \cup I'$
14:             $n \leftarrow n + 1$
15:         end if
16:     end while
17:     $I \leftarrow \mathbf{BEST}(Candidates)$
18:     if $\mathbf{F}(I) > \mathbf{F}(I_{best})$ then
19:         $I_{best} \leftarrow I$
20:     end if
21:     $TL \leftarrow \mathbf{UPDATE\_TABU\_LIST}(I, TL)$
22:     $m \leftarrow m + 1$
23: end while
```

individual I' from I by changing the state of $O_{selected}$ (step 10). Third, the generated I' is stored into $Candidates$ (step 11). After generating multiple neighbor individuals, MEO selects the best individual from $Candidates$ (step 14).

IV. Modified Extremal Optimization with Tabu List

In this section, we propose a novel extremal optimization framework called modified extremal optimization with tabu lists (MEOTL), which is a hybrid of MEO and the tabu search mechanism. To avoid retracing the steps used, the tabu search records recent moves in one or more tabu lists. The original intent of the tabu list is not to prevent a previous move from being repeated, but rather to insure it is not reversed. MEO generates two or more neighbor individuals randomly. MEOTL can improve the efficiency of search through the use of the tabu search mechanism.

Algorithm 3 shows the details of processing steps of MEOTL. MEOTL generates multiple neighbor individuals at each alternation of generations through the following steps (step 9 - step 16) like MEO. First, MEOTL selects $O_{selected}$ with roulette selection (step 10). The selection rates of roulette selection are reciprocals of fitness values with components. Second, MEOTL generates new individual I' from I by changing the state of $O_{selected}$ (step 11). Third, if the generated I' is not in a tabu list TL, the generated I' is stored into $Candidates$ (step 12 - step 15). After generating multiple neighbor individuals, MEOTL selects the best individual from $Candidates$ (step 17). Finally, TL is updated (step 21).

V. Distributed Modified Extremal Optimization with Tabu Lists

This section explains DMEOTL for reducing crossovers in a reconciliation graph.

A. Definition of Individual and Component

In this study, a reconciliation graph is referred as to as an individual. A pair of leaf nodes with the same label name is defined as a component:

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

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.

B. Definition of Fitness

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

$$\lambda_i = \frac{\mathcal{NC}(CM) - \mathcal{NC}(CM, i)}{\mathcal{NC}(CM)}, \tag{4}$$

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

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 $\lambda_4 = 3/4$.

C. Algorithm

DMEOTL is based the population-based approach; thus the approach has a population. DMEOTL divides the entire population into two or more sub-populations, as islands. A sub-population is located in an island. The sub-population located in each island evolves individually. The island model has the migration migration mechanism that some individuals are transferred to 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.

DMEOTL for reducing crossovers in a reconciliation graph be composed of two main steps:(1) Evolution Step and (2) Migration Step (Algorithm 4). First of all, an initial population consisting of multiple individuals are generated at random. Then the initial population divided to p sub-populations (p is the number of sub-populations) (step 3). Moreover, for each sub-population, the initial tabu list set is created (step 4). Sub-population $SubP_i$ is located in an island $ILND_i$ (step 5). In the Evolution Step (step 7), the sub-populations in all the islands are made to evolve through m generations by using the function **P_MEOTL**$(SubP_i, STL_i, m)$ (m is migration interval). In Migration Step (step 8), 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 9 and step 10).

Algorithm 4 DMEOTL

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

Algorithm 5 P_MEOTL(P, STL, m)

```
 1: for $i = 1$ to $m$ do
 2:    for all $I \in P$ do
 3:       Evaluate fitness value $\lambda_i$ 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:          $I' \leftarrow \mathbf{GNI}(I, O_{selected})$
 9:          if $\mathbf{IS\_INCLUDED}(I', STL[I])$ == false then
10:             $C \leftarrow C \cup \mathbf{GNI}(I, O_{selected})$
11:             $n \leftarrow n + 1$
12:          end if
13:       end while
14:       $I \leftarrow \mathbf{BEST}(C)$
15:    end for
16:    for all $I \in P$ do
17:       Select $O_{selected}$ by roulette selection. Copy the
          good structure of $O_{selected}$ to $I$.
18:    end for
19:    $STL[I] \leftarrow \mathbf{UPDATE\_TABU\_LIST}(P, STL[I])$
20: end for
```

D. Evolution Step

In the Evolution Step, each sub-population is in an island is made to evolve through m generations by using the function **P_MEOTL** (Algorithm 5). At each alternation of generations, first, for each individual, the state of the individuals in P is changed by using the MEOTL scheme. Second, for each individual, the individual copies a good sub-structure of another individual, which is selected by the

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

roulette selection.

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 I' by changing the state of component $O_{selected}$. Third, I' is stored in C (step 10), if I' is not in $STL[I]$, where $STL[I]$ is the tabu list of individual I. Finally, the best individual in C is selected and I is replaced by it (step 14). After evolving, for each individual, the individual copies a good sub-structure of another individual (for more details, refer to [7]) and STL is updated.

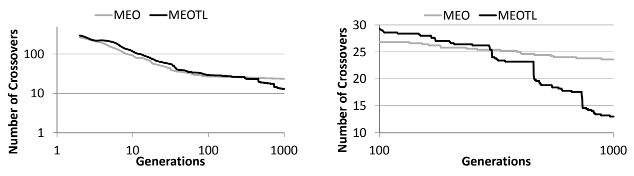
The state of $O_{selected}$ is changed by changing the order of child nodes in an intermediate node, which is an ancestor node of $O_{selected}$. The processing steps of **GNI** are as follows. First, T_1 or T_2 is selected randomly and $\mathcal{AS}(T_1, \mathcal{L}(O_{selected}))$ or $\mathcal{AS}(T_2,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

E. Migration Step

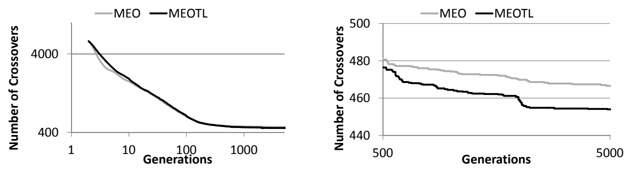
In the Migration Step, some individuals in each island are migrated to another island. The island model requires $number\ of\ sub-populations$, $migration\ rate$, $migration\ interval$, and $migration\ model$. The first three items are user-given parameters. The last item consists of two things: $selection\ method$ 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.

VI. EXPERIMENTAL RESULTS

We performed three experiments for evaluating the performance of DMEOTL. This section shows the experimental results.

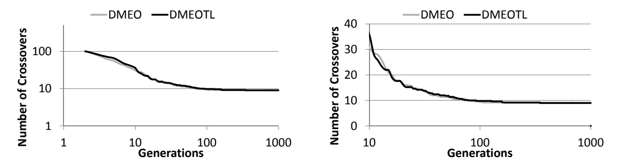


(a) $Housekeeping$ data set

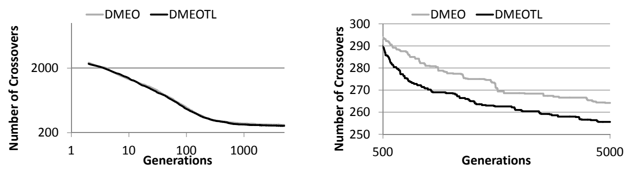


(b) $Moss$ data set

Fig. 3. Experiment 1 (This experiment compares MEOTL with MEO. (a) and (b) shows the number of crossovers of the best individual) .



(a) $Housekeeping$ data set



(b) $Moss$ data set

Fig. 4. Experiment 2 (This experiment compares DMEOTL with DMEO. (a) and (b) shows the number of crossovers of the best individual) .

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 MEOTL with MEO. Experiment 2 measured the number of crossovers of the best individual at each generation to compare DMEOTL with DMEO. In Experiment 3, we measured the number of crossovers of the best individual at different time instants.

B. Experiment 1

In Experiment 1, we measured the number of crossovers of the best individual in each generation. In MEO and MEOTL, $num\_of\_candidates$ was set to 50. The maximum number of generations of the $Housekeeping$ data set and the $Moss$ data set were set to 1000 and 5000 respectively. In MEOTL, the length of a tabu list is set to 10. Figure3(a) and Figure3(b)

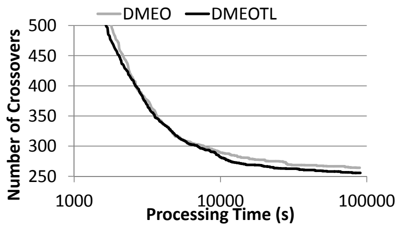


Fig. 5. Experiment 3 ($Moss$ data set).

show the number of crossovers (vertical axis: the number of crossovers, horizontal axis: generations). The number of crossovers is the average of five trials.

Fig. 3(a) shows that the number of crossovers of MEOTL is less than that of MEO at the end of alternation of generations. MEO fell into a cycle of local optimal solutions; however MEOTL could get away from local optimal solutions. Fig. 3(b) shows the results of the $Moss$ data set. The number of crossovers of MEOTL is less than that of MEO after 100-th generations. Experiment 1 shows that MEOTL outperforms MEO.

C. Experiment 2

In Experiment 2, we measured the number of crossovers of the best individual in each generation. In DMEO and DMEOTL, the number of individuals in the population was set to 50. The user parameters $num\_of\_candidates$, $migration\_interval(m)$, $number\ of\ sub\text{-}populations(p)$, and $migration\ rate$ were set to be 50, 10, 5 and 0.1, respectively. In DMEOTL, the length of a tabu list is set to 10. The number of individuals in a sub-population is 10. The number of crossovers was the average of five trials. Fig. 4(b) shows that the number of crossovers of DMEOTL is less than that of DMEO when we used the $Moss$ data set. The number of crossovers of DMEOTL is less than that of DMEO after 100-th generations. Experiment 2 shows that DMEOTL outperforms DMEO.

D. Experiment 3

In Experiment 3, we measured the number of crossovers of the best individual at different time instants. The computation time of DMEOTL is longer than that in the case of DMEO because the former includes the matching generated individuals to individuals in tabu lists. Therefore, it is necessary to compare the number of crossovers for the same computation time. Fig. 5 shows the number of crossovers at different time instants (vertical axis: the number of crossovers, horizontal axis: processing time), when the $Moss$ data set is used. At the end of the processing, DMEOTL have fewer crossovers than DMEO. This result indicates DMEOTL performs better with fewer crossovers than DMEO.

VII. Conclusion

In this paper, we propose a novel bio-inspired heuristic called distributed modified extremal optimization with tabu lists (DMEOTL). This heuristic is a hybrid of distributed modified extremal optimization (DMEO) and the tabu search mechanism. 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, DMEOTL can maintain diversity at the end of alternation of generations. Moreover, each individual has a tabu list, individuals located in islands evolve using MEOTL, in DMEOTL. Therefore, DMEOTL has to avoid pitfalls and explore regions of the search space that would be left unexplored. We have evaluated DMEOTL by using actual data sets. Experimental results show that DMEOTL is better performance compared with DMEO. In the future work, we will develop extended DMEOTL for making it applicable to other combination optimization problems.

References

[1] M. Goodman, J. Czelusniak, G. Moore, A. Romero-Herrera, and G. Matsuda, "Fitting the gene lineage into its species lineage, a parsimony strategy illustrated bycladograms constructed from globin sequences," *Systematic Zoology*, vol. 28, pp. 132–163, 1979.

[2] R. Page, "Maps between trees and cladistic analysis of historical associations among genes, organisms, and areas," *Systematic Biology*, vol. 43, pp. 58–77, 1994.

[3] R. D. M. Page and M. A. Charleston, "Reconciled trees and incongruent gene and species trees," *Discrete Mathametics and Theoretical Computer Science*, vol. 37, pp. 57–70, 1997.

[4] R. D. M. Page, "Genetree: comparing gene and species phylogenies using reconciled trees," *Bioinformatics*, vol. 14, no. 9, pp. 819–820, 1998.

[5] H. Kitakami and M. Nishimoto, "Constraint satisfaction for reconciling heterogeneous tree databases," in *Proceedings of DEXA 2000*, 2000, pp. 624–633.

[6] H. Kitakami and Y. Mori, "Reducing crossovers in reconciliation graphs using the coupling cluster exchange method with a genetic algorithm," *Active Mining, IOS press*, vol. 79, pp. 163–174, 2002.

[7] N. Hara, K. Tamura, and H. Kitakami, "Modified eo-based evolutionary algorithm for reducing crossovers of reconciliation graph," in *Proceedings of NaBIC 2010*, 2010, pp. 169–176.

[8] K. Tamura, H. Kitakami, and A. Nakada, "Distributed modified extremal optimization for reducing crossovers in reconciliation graph," in *Lecture Notes in Engineering and Computer Science: Proceedings of The International MultiConference of Engineers and Computer Scientists 2013, 13-15 March, 2013, Hong Kong*, pp. 1–6.

[9] R. Tanese, "Distributed genetic algorithms," in *Proceedings of the 3rd International Conference on Genetic Algorithms*, 1989, pp. 434–439.

[10] T. C. Belding, "The distributed genetic algorithm revisited," in *Proceedings of the 6th International Conference on Genetic Algorithms*, 1995, pp. 114–121.

[11] W. D. Whitley, S. B. Rana, and R. B. Heckendorn, "Island model genetic algorithms and linearly separable problems," in *Selected Papers from AISB Workshop on Evolutionary Computing*, 1997, pp. 109–125.

[12] S. Boettcher and A. G. Percus, "Extremal optimization: Methods derived from co-evolution," in *Proceedings of GECCO 1999*, 1999, pp. 825–832.

[13] S. Boettcher and A. Percus, "Nature's way of optimizing," *Artificial Intelligence*, vol. 119, no. 1-2, pp. 275–286, 2000.

[14] S. Boettcher, "Extremal optimization: heuristics via coevolutionary avalanches," *Computing in Science and Engineering*, vol. 2, no. 6, pp. 75–82, 2000.

[15] P. Bak, C. Tang, and K. Wiesenfeld, "Self-organized criticality. an explanation of 1/f noise," *Physical Review Letters*, vol. 59, pp. 381–384, 1987.

[16] K. Tamura, Y. Mori, and H. Kitakami, "Reducing crossovers in reconciliation graphs with extremal optimization (in japanese)," *Transactions of Information Processing Society of Japan*, vol. 49, no. 4(TOM 20), pp. 105–116, 2008.

[17] F. Glover and M. Laguna, *Tabu Search.* Norwell, MA, USA: Kluwer Academic Publishers, 1997.

[18] S. Meshoul and M. Batouche, "Robust point correspondence for image registration using optimization with extremal dynamics," in *Proceedings of DAGM-Symposium 2002*, 2002, pp. 330–337.

[19] S. Boettcher and A. G. Percus, "Extremal optimization at the phase transition of the 3-coloring problem," *Physical Review E*, vol. 69, 066703, 2004.

[20] T. Zhou, W.-J. Bai, L.-J. Cheng, and B.-H. Wang, "Continuous extremal optimization for lennard-jones clusters," *Physical Review E*, vol. 72, 016702, 2005.

[21] J. Duch and A. Arenas, "Community detection in complex networks using extremal optimization," *Physical Review E*, vol. 72, 027104, 2005.