Tree Edit Distance with Variables. Measuring the Similarity between Mathematical Formulas

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May 12, 2021

Abstract

In this article, we propose tree edit distance with variables, which is an extension of the tree edit distance to handle trees with variables and has a potential application to measuring the similarity between mathematical formulas, especially, those appearing in mathematical models of biological systems. We analyze the computational complexities of several variants of this new model. In particular, we show that the problem is NP-complete for ordered trees. We also show for unordered trees that the problem of deciding whether or not the distance is 0 is graph isomorphism complete but can be solved in polynomial time if the maximum outdegree of input trees is bounded by a constant. This distance model is then extended for measuring the difference/similarity between two systems of differential equations, for which results of preliminary computational experiments using biological models are provided.

1 Introduction

In this article, we consider the problem of computing edit distance between trees with variables. This problem is motivated from studies on comparison of mathematical formulas/models [11, 13]. For example, consider two functions $f(x, y, z)$ and $g(x, y, z)$ defined by:

$$f(x, y, z) = (x + y) * z,$$

$$g(x, y, z) = (x + z) * y.$$ 

These two functions are essentially the same: the former one is identical to the latter one by replacing $y$ and $z$ with $z$ and $y$, respectively. In addition, consider a function $h(x, y, z)$ defined by:

$$h(x, y, z) = z * (x + y).$$

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This function is also essentially the same as \( f \) and \( g \) because multiplication satisfies the commutative law.

In order to examine the identify/similarity of mathematical expressions, \textit{tree edit distance} has been utilized because mathematical expressions can often be represented as rooted trees, where tree edit distance is a measure of dissimilarity between two rooted trees \cite{2, 5}. For example, functions \( f, g, \) and \( h \) can be respectively represented as \( T_1, T_2, \) and \( T_3 \) shown in Fig. 1. If we ignore variable names assigned to leaves, these trees are identical as unordered rooted trees.

![Tree representations of mathematical expressions.](image)

However, considering variable names is important, where variables are often referred to as species in biological models. For example, consider a function \( k \) defined by

\[
    k(x, y) = (x + y) \ast x.
\]

This function can be represented as a rooted tree \( T_4 \) in Fig. 1. Although (unordered) tree structures of \( T_1, \ldots, T_4 \) are identical, \( k \) is clearly different from \( f, g, \) and \( h \). Therefore, variable names assigned to leaves should be taken into account. In order to take variables names into account, unification with commutative and/or associative laws has been studied \cite{4, 8}. However, unification is used to decide a kind of identity between two expressions and thus does not give a similarity (or distance) measure.

Based on the above discussion, we introduce \textit{tree edit distance with variables} in this article. Before giving this new distance measure, we briefly review the standard \textit{tree edit distance}. Let \( T_1 \) and \( T_2 \) be two rooted trees in which each node has a label from an alphabet \( \Sigma \). We consider two cases: both \( T_1 \) and \( T_2 \) are ordered trees, and both \( T_1 \) and \( T_2 \) are unordered trees. This distinction can be taken into account only when we consider whether or not two trees are identical (i.e., isomorphic) after tree editing operations. The tree edit distance \( d_0(T_1, T_2) \) between \( T_1 \) and \( T_2 \) is defined as the cost of the minimum cost sequence of edit operations that transforms \( T_1 \) to \( T_2 \), where an operation is one of deletion of a node, insertion of a node, and change of the label of a node. Then, we define the tree edit distance between two trees with variables \( T_1 \) and \( T_2 \) by

\[
    \text{dist}(T_1, T_2) = \min_{\theta} \text{dist}_0(T_1\theta, T_2\theta),
\]

where \( \theta \) is a substitution (i.e., a set of assignments of constants to variables). See Section 2 for the precise definitions.

In this article, we analyze the computational complexities of several variants/subcases of the tree edit distance problem with variables. When discussing the complexity classes, we consider a decision version of the problem: whether or not \( \text{dist}(T_1, T_2) \leq d \) for given \( T_1, T_2, \) and a given non-negative real number \( d \). The results are summarized in Table 1 where ‘iso’ asks whether \( d(T_1, T_2) = 0 \), ‘BD’ means that the maximum outdegree (i.e., the maximum number of children) of both \( T_1 \) and \( T_2 \) is bounded by a constant. \( P, \) NPC, and GIC mean that the target problem is polynomial-time solvable, NP-complete, and Graph Isomorphism complete (i.e., as hard as the graph isomorphism problem under polynomial-time reduction), respectively. It is interesting to see that the complexity substantially changes according to introduction of variables.

We also extend the tree edit distance with variables for computing the distance between two systems of first-order differential equations. Then, we develop practical methods for computing
Table 1: Summary of Theoretical Results

|               | \(d_0(T_1, T_2)\) | iso       | iso-BD    | \(d(T_1, T_2)\) | \(d(T_1, T_2)\)-BD |
|---------------|---------------------|-----------|-----------|------------------|---------------------|
| ordered       | P [10]              | (Prop. 1) | P (Prop. 2) | NPC (Thm. 1)    | NPC (Thm. 1)        |
| unordered     | NPC [12]            | GIC       | P (Thm. 2) | NPC [12]        | NPC [12]            |

this new distance and its variant using integer linear programming (ILP). Furthermore, we conduct preliminary computational experiments on these methods using several mathematical models of biological systems obtained from the BioModels data repository (https://www.ebi.ac.uk/biomodels/).

2 Preliminaries

In this section, we review the precise definition of the tree edit distance and then formally define the tree edit distance with variables.

Let \(T_1\) and \(T_2\) be two rooted trees in which each node has a label from an alphabet \(\Sigma\). As mentioned in Section 1, we consider two cases: both \(T_1\) and \(T_2\) are ordered trees, and both \(T_1\) and \(T_2\) are unordered trees, and this distinction can be taken into account only when we consider whether or not two trees are identical after tree edit operations. We consider three kinds of edit operations (see also Fig. 2):

- **Deletion**: Delete a non-root node \(v\) in \(T\) with parent \(u\), making the children of \(v\) become children of \(u\). The children are inserted in the place of \(v\) into the set of the children of \(u\).
- **Insertion**: Inverse of delete. Insert a node \(v\) as a child of \(u\) in \(T\), making \(v\) the parent of some of the children of \(u\).
- **ChangeLabel**: Change the label of a node \(v\) in \(T\).

We assign a *cost* for each editing operation: \(\gamma(a, b)\) denotes the cost of changing a node with label \(a\) to label \(b\), \(\gamma(a, \epsilon)\) denotes the cost of deleting a node labeled with \(a\), \(\gamma(\epsilon, a)\) denotes the cost of inserting a node labeled with \(a\). We assume that \(\gamma(x, y)\) satisfies the conditions of distance metric: \(\gamma(x, x) = 0\), \(\gamma(x, y) = \gamma(y, x)\), \(\gamma(x, y) \geq 0\), and \(\gamma(x, z) \leq \gamma(x, y) + \gamma(y, z)\). Then, the *edit distance* between \(T_1\) and \(T_2\) is defined as the cost of the minimum cost sequence of edit operations that transforms \(T_1\) to \(T_2\) (precisely, transforms \(T_1\) to a tree identical to \(T_2\)). It is well-known that this distance satisfies the conditions of distance measure, in both ordered and unordered cases.

![Figure 2: Tree edit operations.](image-url)
Here we define tree edit distance with variables. Let $\Sigma$ be a set of constant symbols, where each constant is denoted by a lower-case letter (e.g., $a, b, c, x, y, z, a_1, a_2$). Let $\Lambda$ be a set of variables, where each variable is denoted by an upper-case letter (e.g., $X, Y, Z, X_1, X_2$). A substitution is a set of variable-constant pairs, $\theta = \{(X_1, x_1), (X_2, x_2), \ldots, (X_k, x_k)\}$, where $X_i \neq X_j$ holds for all $i \neq j$ but $x_i = x_j$ can hold for some $(i, j)$. For a rooted tree $T$ and a substitution $\theta$, $T\theta$ denotes the tree obtained by changing variables appeared in $T$ to constants according to $\theta$ (each $X_i$ is replaced with $x_i$).

Let $\text{dist}_0(T_1, T_2)$ be the standard tree edit distance between $T_1$ and $T_2$ (i.e., distance between trees without variables). We reasonably assume the following:

- Variable symbols appear only in leaves.
- The sets of variables appearing in $T_1$ and $T_2$ are disjoint.
- Distinct variables in the same tree must be substituted to distinct constants by $\theta$.
- Every variable appearing in $T_1$ (resp., $T_2$) is substituted to a constant symbol not appearing in $T_1$ or $T_2$ (because otherwise the cost of substituting a variable to a constant would be 0, which is not appropriate for measuring the distance between two mathematical expressions).

Then, we define the tree edit distance with variables as follows.

**Definition 1.** The tree edit distance with variables between $T_1$ and $T_2$ is

$$\text{dist}(T_1, T_2) = \min_{\theta} \text{dist}_0(T_1\theta, T_2\theta).$$

For example, consider trees $T_1$ and $T_2$ shown in Fig. 3 and the unit cost model (i.e., $\gamma(x, y) = 1$ for any $x \neq y$). Then, $\text{dist}(T_1, T_2) = 5$ (in both ordered and unordered cases) by $\theta = \{(X, x), (Y, y), (Z, z), (W, w), (U, x), (V, y)\}$ and the following sequence of editing operations: change the label of node ‘w’ to ‘x’, insert node ‘h’, change the label of node ‘b’ to ‘f’, delete node ‘c’, and change the label of node ‘z’ to ‘g’, where we identify nodes by their labels.

![Figure 3: Example of a tree pair. In this case, dist(T_1, T_2) = 5 under the unit cost model.](image)

As the basic property, the following is straightforward.

**Proposition 1.** For both ordered and unordered cases, tree edit distance with variables satisfies the conditions of distance measure.

### 3 Ordered Trees

In this section, all trees are ordered trees, which means that the children of each node are ordered from left to right and that this ordering must be preserved among isomorphic trees. For each tree

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For ordered trees, the tree edit distance problem with variables is NP-complete.

**Theorem 1.** For ordered trees, the tree edit distance problem with variables is NP-complete.

**Proof.** We construct an Euler string \( \text{str}(T_i) \) from each of a given tree \( T_i \) using depth first search. In constructing \( \text{str}(T_i) \), we assign a unique integer number from 1, 2, \( \cdots \) as the label of a variable node every when we first encounter the variable. Then, it is straightforward to see \( \text{dist}(T_1, T_2) = 0 \) if and only if \( \text{str}(T_1) = \text{str}(T_2) \).

**Proposition 2.** For ordered trees, whether or not \( \text{dist}(T_1, T_2) = 0 \) can be determined in polynomial time.

**Proof.** It is clear that the problem is in NP. Then, we show a polynomial-time reduction from the maximum clique problem (see also Fig. 4). The maximum clique problem is, given an undirected graph \( G(V, E) \) and an integer \( k \), to decide whether or not there exists a complete subgraph (clique) of size (\#vertices) \( k \) in \( G(V, E) \), where all vertices have the same label. It is well-known that the problem is NP-complete.

![Graph with maximum clique](image)

**Figure 4:** Reduction from maximum clique to ordered tree edit distance with variables, where only relevant labels are shown.

From a given \( k \), we construct \( T_1 \) as follows:

\[
V(T_1) = \{r_1\} \cup \{v_1, \ldots, v_k\} \cup \bigcup_{i \in \{1, \ldots, k\}} \{v_{i,1}, \ldots, v_{i,k}\},
\]

\[
E(T_1) = \bigcup_{i \in \{1, \ldots, k\}} \{(r_1, v_i)\} \cup \bigcup_{i \in \{1, \ldots, k\}} \{(v_i, v_{i,1}), \ldots, (v_i, v_{i,k})\},
\]

\[
\ell(r_1) = \ell(v_1) = \cdots = \ell(v_k) = a,
\]

\[
\ell(v_{i,j}) = \ell(v_{j,i}) = X_{i,j} \quad \text{for all } i < j,
\]

\[
\ell(v_{i,i}) = X_i \quad \text{for all } i,
\]

where \( X_{i,j} \neq X_{i',j'} \) for any \( i \neq i' \) or \( j \neq j' \).

\(^1\)We mainly use ‘nodes’ for trees and ‘vertices’ for graphs.
From a given $G(V, E)$ with $V = \{w_1, \ldots, w_n\}$, we construct $T_2$ as follows:

$$V(T_2) = \{r_2\} \cup \{u_1, \ldots, u_n\} \cup \left( \bigcup_{i \in \{1, \ldots, n\}} \{u_i, 1, \ldots, u_i, n\} \right),$$

$$E(T_2) = \left( \bigcup_{i \in \{1, \ldots, n\}} \{(r_2, u_i)\} \right) \cup \left( \bigcup_{i \in \{1, \ldots, n\}} \{(u_i, u_{i, 1}), \ldots, (u_i, u_{i, n})\} \right),$$

$$\ell(r_2) = \ell(u_1) = \cdots = \ell(u_n) = a,$$

$$\ell(u_{i, j}) = \ell(u_{j, i}) = Y_{i, j} \text{ for all } \{w_i, w_j\} \in E \text{ with } i < j,$$

$$\ell(u_{i, j}) = b_{i, j} \text{ for other nodes}.$$

where $Y_{i, j} \neq Y_{i', j'}$ holds for any $i \neq i'$ or $j \neq j'$, and all $b_{i, j}$s are distinct constants.

Here, we note that $n_1 = 1 + k + k^2$ and $n_2 = 1 + n + n^2$. Then, it is straightforward to see that $G(V, E)$ has a clique of size $k$ if and only if $\text{dist}(T_1, T_2) \leq n_2 - n_1$ (under the unit cost model).

For the bounded case, it is enough to encode each non-leaf node as in Fig. 5 where the details are omitted.

![Figure 5: Encoding of non-leaf node.](image)

### 4 Unordered Trees

In this section, all trees are unordered rooted trees. The graph isomorphism problem is, given two undirected graphs $G_1(V_1, E_1)$ and $G_2(V_2, E_2)$, to decide whether or not there exists a bijection $\phi$ from $V_1$ to $V_2$ such that $\{u, v\} \in E_1$ if and only if $\{\phi(u), \phi(v)\} \in E_2$. It is unclear that graph isomorphism is in P or NP-complete (many researchers believe that it lies between P and NP-complete). However, it is known that graph isomorphism can be solved in polynomial time if the maximum degree of input graphs is bounded by a constant.

**Theorem 2.** For unordered trees, the problem of deciding $\text{dist}(T_1, T_2) = 0$ is graph isomorphism complete. Furthermore, the problem can be solved in polynomial time if the maximum outdegree of $T_1$ and $T_2$ is bounded by a constant.

**Proof.** First, we show that graph isomorphism is reduced to the problem in polynomial time. For each of $G_1$ and $G_2$, we construct trees as for $T_2$ in the proof of Theorem. Then, it is straightforward to see that $G_1$ and $G_2$ are isomorphic if and only if $\text{dist}(T_1, T_2) = 0$.

Next, we show that the problem is reduced to graph isomorphism in polynomial time (see also Fig. 6). Here, we consider without loss of generality (w.l.o.g.) graph isomorphism over labeled graphs (because it is known that labeled cases can be reduced to unlabeled cases in polynomial
time). We show how to construct \( G_1(V_1, E_2) \) from \( T_1 \), where an identical construction can be used for \( T_2 \). We construct \( G_1(V_1, E_1) \) by adding vertices and edges to \( T_1 \) as follows. For each variable \( X \), we create a new vertex \( v_X \) with constant label ‘a’, connect \( v_X \) to all leaves in \( T_1 \) having label \( X \), and change the labels of these leaves to ‘b’, where ‘a’ and ‘b’ are constant symbols not appearing \( T_1 \) or \( T_2 \) (we use the same ‘a’ and ‘b’ for all variables in \( T_1 \) and \( T_2 \)). Then, it is straightforward to see that \( G_1 \) and \( G_2 \) are isomorphic if and only if \( \text{dist}(T_1, T_2) = 0 \).

Finally, we show the last claim. We modify the reduction shown above (see also \( G'_1 \) in Fig. 4). In order to reduce the degree of each of new vertices, we make a copy of \( T_1 \) for each variable \( X \). Then, we keep leaves labeled with \( X \) and the nodes in the copy each of which has multiple children whose descendants contain leaves labeled with \( X \) (some child can be such a leaf), and delete all other nodes in the copy. Then, the maximum degree of the resulting graphs is bounded by the maximum degree (not outdegree) of the input trees. It is not difficult to see that \( G'_1 \) and \( G'_2 \) are isomorphic if and only if \( \text{dist}(T_1, T_2) = 0 \).

\[
\begin{align*}
\theta_1 &= \{(X, u), (Y, v), (U, u), (V, v), (W, w)\}, \\
\theta_2 &= \{(X, v), (Y, u), (U, u), (V, v), (W, w)\}, \\
\theta_3 &= \{(X, u), (Y, w), (U, u), (V, v), (W, w)\}, \\
\theta_4 &= \{(X, w), (Y, u), (U, u), (V, v), (W, w)\}, \\
\theta_5 &= \{(X, v), (Y, w), (U, u), (V, v), (W, w)\}, \\
\theta_6 &= \{(X, w), (Y, v), (U, u), (V, v), (W, w)\}, 
\end{align*}
\]

Figure 6: Transformation from tree \( T_1 \) to graph \( G_1 \) of unbounded degree and graph \( G'_1 \) of bounded degree.

Let \( m_1 \) and \( m_2 \) be the number of distinct variables appearing in \( T_1 \) and \( T_2 \), respectively, where we assume w.l.o.g. \( m_1 \leq m_2 \). Then, we have the following.

**Proposition 3.** \( \text{dist}(T_1, T_2) \) can be computed in \( O(m_1^{m_1} \cdot 1.26^{n_1+n_2}) \) time.

**Proof.** Recall \( \text{dist}(T_1, T_2) = \min_\theta \text{dist}_0(T_1 \theta, T_2 \theta) \). Therefore, the problem can be solved by computing \( \text{dist}_0(T_1 \theta, T_2 \theta) \) for all essentially different \( \theta \), where “essentially different” \( \theta_1 \) and \( \theta_2 \) mean that \( \theta_1 \) and \( \theta_2 \) give distinct correspondences between variables in \( T_1 \) and those in \( T_2 \). The number of essentially different \( \theta \) is clearly bounded by \( m_2^{m_1} \). Since the tree edit distance between two unordered trees can be computed in \( O(1.26^{n_1+n_2}) \) time [3], the proposition holds. \( \square \)

For example, consider \( T_1 \) and \( T_2 \) in Fig. 7. In this case, the following are essentially different substitutions:

\[
\begin{align*}
\theta_1 &= \{(X, u), (Y, v), (U, u), (V, v), (W, w)\}, \\
\theta_2 &= \{(X, v), (Y, u), (U, u), (V, v), (W, w)\}, \\
\theta_3 &= \{(X, u), (Y, w), (U, u), (V, v), (W, w)\}, \\
\theta_4 &= \{(X, w), (Y, u), (U, u), (V, v), (W, w)\}, \\
\theta_5 &= \{(X, v), (Y, w), (U, u), (V, v), (W, w)\}, \\
\theta_6 &= \{(X, w), (Y, v), (U, u), (V, v), (W, w)\}, 
\end{align*}
\]

7
where the number of substitutions is less than \( m_2^{m_1} = 3^2 = 9 \). Then, the minimum is attained for \( \theta_3 \) or \( \theta_5 \), and we have

\[
dist(T_1, T_2) = dist_0(T_1 \theta_3, T_2 \theta_3) = dist_0(T_1 \theta_5, T_2 \theta_5) = 2
\]

under the unit cost model with the following sequence of editing operations: inserting node ‘d’ and then changing the label of the leftmost node ‘Y’.

\[
\begin{align*}
T_1 & \quad T_2 \\
\text{b} & \quad \text{b} \\
\text{X} & \quad \text{b} \\
\text{Y} & \quad \text{Y} \\
\text{C} & \quad \text{V} \\
\end{align*}
\]

\[
\begin{align*}
\text{d} & \quad \text{d} \\
\text{A} & \quad \text{W} \\
\text{C} & \quad \text{W} \\
\end{align*}
\]

Figure 7: Example for Proposition 3

5 Comparison of Systems of Differential Equations

In this section, we consider the problem of measuring the distance between systems of differential equations. We assume here that two systems of differential equations are given by

\[
\begin{align*}
\frac{dX_1}{dt} &= f_1(X_1, \ldots, X_{m_1}), \\
\frac{dX_2}{dt} &= f_2(X_1, \ldots, X_{m_1}), \\
& \quad \ldots \\
\frac{dX_{m_1}}{dt} &= f_{m_1}(X_1, \ldots, X_{m_1}), \\
\end{align*}
\]

and

\[
\begin{align*}
\frac{dY_1}{dt} &= g_1(Y_1, \ldots, Y_{m_2}), \\
\frac{dY_2}{dt} &= g_2(Y_1, \ldots, Y_{m_2}), \\
& \quad \ldots \\
\frac{dY_{m_2}}{dt} &= g_{m_2}(Y_1, \ldots, Y_{m_2}), \\
\end{align*}
\]

where some variables in some functions can be irrelevant. In this article, these systems are referred to as elementary systems, and denoted by \( S_X \) and \( S_Y \), respectively. As in the previous section, we assume that each function is represented as a tree, \( T_i^1 \) for \( f_i \) and \( T_j^2 \) for \( g_j \), where each tree is regarded as an unordered tree. For simplicity, we assume that all variables appearing in the right hand side appear in the left hand side, although this restriction can be removed. We assume w.l.o.g. that \( m_1 \leq m_2 \). Let \( n_1 = \sum_{i=1}^{m_1} |V(T_i^1)| \) and \( n_2 = \sum_{i=1}^{m_2} |V(T_i^2)| \).

As in the algorithm given in the proof of Proposition 3 we consider all essentially different substitutions \( \theta \) over variables \( X_1, \ldots, X_{m_1} \) and \( Y_1, \ldots, Y_{m_2} \).

Let \( \hat{\theta} \) be the one-to-one mapping from \( \{1, \ldots, m_1\} \) to \( \{1, \ldots, m_2\} \) obtained from \( \theta \) by the following rule:
• $X_i$ and $Y_j$ are substituted by the same constant by $\theta$ if and only if $i$ is mapped to $j$ by $\hat{\theta}$ (i.e., $\hat{\theta}(i) = j$).

Let $I = \{j | \hat{\theta}(i) = j\}$ for some $i$ and $O = \{1, \ldots, m_2\} \setminus I$. Note that we can assume that $\hat{\theta}(i)$ is defined for all $i = 1, \ldots, m_1$ (otherwise, the distance would be larger). Let $\text{dist}_0(\epsilon, T) = \text{dist}_0(T, \epsilon)$ be the cost of deleting all nodes in $T$ (i.e., deleting the whole $T$).

**Definition 2.** The edit distance between two elementary systems $S_X$ and $S_Y$ is

$$\text{Dist}(S_X, S_Y) = \min_{\theta} \left[ \sum_{i=1}^{m_1} \text{dist}_0(T_i^1, T_{\hat{\theta}(i)}^2) + \sum_{j \in O} \text{dist}_0(\epsilon, T_j^2) \right].$$

**Proposition 4.** $\text{Dist}(S_X, S_Y)$ can be computed in $O(m_2^{m_1} \cdot 1.26^{n_1+n_2})$ time.

**Proof.** We compute $\text{Dist}(S_X, S_Y)$ as in the algorithm given in the proof of Proposition 3. We examine all essentially different $\theta$ and compute $\sum_{i=1}^{m_1} \text{dist}_0(T_i^1, T_{\hat{\theta}(i)}^2)$ for each $\theta$. Since the computation time needed to compute this sum is bounded by

$$\sum_{i=1}^{m_1} O(1.26^{V(T_i^1)|V(T_{\hat{\theta}(i)}^2)|}) \leq O(1.26^{n_1+n_2}),$$

the proposition holds. $\square$

For example, consider trees given in Fig. 8. Then, the minimum is attained for $\theta = \{(X_1, y_3), (X_2, y_2), (Y_1, y_1), (Y_2, y_2)\}$, where $\hat{\theta}(1) = 3$ and $\hat{\theta}(2) = 2$, and we have

$$\text{Dist}(S_X, S_Y) = \text{dist}_0(T_1^1 \theta, T_2^2 \theta) + \text{dist}_0(T_2^1 \theta, T_2^2 \theta) + \text{dist}_0(\epsilon, T_1^2 \theta) = \text{dist}_0(\epsilon, T_1^2 \theta) = 3.$$  

![Figure 8: Example for Proposition 4](image)

The factor of $m_2^{m_1}$ in the above proposition may be too large in practice. Therefore, it is worthy to give another definition of the distance. Let $\pi$ be a one-to-one mapping from $\{1, \ldots, m_1\}$ to $\{1, \ldots, m_2\}$, and let $O_\pi = \{1, \ldots, m_2\} \setminus \{j | \pi(i) = j\}$ for some $i$. Then, we define the pseudo edit distance between two elementary systems as below.

**Definition 3.** The pseudo edit distance between two elementary systems $S_X$ and $S_Y$ is

$$\text{Pdist}(S_X, S_Y) = \min_{\pi} \left[ \sum_{i=1}^{m_1} \text{dist}(T_i^1, T_{\pi(i)}^2) + \sum_{j \in O_\pi} \text{dist}_0(\epsilon, T_j^2) \right].$$
Proposition 5. \(P_{\text{dist}}(S_X, S_Y) \leq \text{Dist}(S_X, S_Y)\) holds for any \((S_X, S_Y)\), and \(P_{\text{dist}}(S_X, S_Y)\) can be computed in \(O(\text{poly}(m_1, m_2)1.26^{m_1+m_2})\) time.

Proof. First note that, different from Definition 2 substitutions for \(T^1_i\) and \(T^2_{\pi(i)}\) can be selected independently for all pairs in Definition \(\mathbf{5}\). Therefore, \(P_{\text{dist}}(S_X, S_Y) \leq \text{Dist}(S_X, S_Y)\) holds.

Next we show that computation of \(P_{\text{dist}}(S_X, S_Y)\) can be reduced to the minimum weight perfect matching for a bipartite graph. From given \(S_X\) and \(S_Y\), we construct a weighted bipartite graph \(G(U, V; E)\) such that \(U = \{u_1, \ldots, u_{m_2}\}, V = \{v_1, \ldots, v_{m_2}\}, E = U \times V\), and
\[
w(u_i, v_j) = \begin{cases} \text{dist}(T^1_i, T^2_j) & \text{if } i \leq m_1, \\ \text{dist}_0(\epsilon, T^2_j) & \text{otherwise.} \end{cases}
\]

Then, it is straightforward to see that \(G(U, V; E)\) has a perfect matching and the weight of the minimum weight perfect matching is equal to \(P_{\text{dist}}(S_X, S_Y)\). Since it is well-known that the minimum weight perfect matching can be computed in polynomial time (e.g., by Hungarian algorithm), the proposition holds.

\[\square\]

6 Computational Experiments

We conducted preliminary computational experiments to examine the possibility of the practical applicability of the proposed approach. We focused on the unordered tree cases because many operators (e.g., ‘+’, ‘×’) satisfy the commutative law. Accordingly, we computed \(\text{Dist}(S_X, S_Y)\) and \(P_{\text{dist}}(S_X, S_Y)\) using several systems of differential equations and normal equations obtained from the BioModels data repository (https://www.ebi.ac.uk/biomodels/). Equations whose left hand side parts contained variables that did not appear in the right hand side of any equation were ignored.

Here we notice that the algorithms given in Propositions 4 and 5 use an \(O(1.26^{m_1+m_2})\) time algorithm \(\mathbf{8}\) to compute the edit distance between unordered trees without variables. However, this algorithm is not practical. Thus, we employed an integer linear programming (ILP)-based approach proposed by Kondo et al. \(\mathbf{9}\) in place of \(\mathbf{9}\), where we used the unit cost model for the simplicity. Since the same constant symbols may be used for different meanings in different systems, all constants are treated as different ones in two input models. For the ease of implementation, we also employed a simple ILP-based method to compute the minimum weight perfect matching. All computations were done on a Linux server with Xeon(R) CPU E5-2620 CPU × 2 and 132GB memory, using IBM(R) ILOG(R) CPLEX(R) Interactive Optimizer 12.7.1.0 as an ILP solver.

The results are summarized in Table 2. The number inside parentheses denotes the number of variables, and "Time Over" means that computation did not finish within 20 minutes. CPU time denotes the total user CPU time, where CPLEX is parallelized to efficiently work on multi-core CPUs. It is seen that \(P_{\text{dist}}(S_X, S_Y)\) could be computed in reasonable CPU time even for systems with more than 10 variables, whereas \(\text{Dist}(S_X, S_Y)\) could be computed only for systems with 3 \(\sim\) 5 variables. It is reasonable from the high exponential factor given in Proposition 4. It is to be noted that \(P_{\text{dist}}(S_X, S_Y)\) could not be computed within the time limit for the pair of BIOMD0000000330 and BIOMD0000000331 although each system contains only 5 variables. It is reasonable because large equations are included in both models. It is also seen that \(P_{\text{dist}}(S_X, S_Y) \leq \text{Dist}(S_X, S_Y)\) holds for all pairs \((S_X, S_Y)\) for which \(\text{Dist}(S_X, S_Y)\) could be computed within the time limit. This result is reasonable from Prop. 5. The results of these preliminary computational experiments suggest that the ILP-based method for computing \(P_{\text{dist}}(S_X, S_Y)\) may be useful to comparing moderate size biological systems not containing large-scale differential equations.
Table 2: Results on Computational Experiments

| SX                  | SY                  | Pdist(SX, SY) | Dist | CPU time | Time Over |
|---------------------|---------------------|---------------|------|----------|-----------|
| BIOMD0000000274 (3)| BIOMD0000000680 (4)| 36.6 sec.     | 50.0 |          |           |
| BIOMD0000000679 (4)| BIOMD0000000252 (4)| 46.0 sec.     | 40.0 |          |           |
| BIOMD0000000274 (3)| BIOMD0000000330 (5)| 11 min. 29 sec.| 115.0|          |           |
| BIOMD0000000274 (3)| BIOMD0000000298 (11)| 8 min. 37 sec. | 246.0|          |           |
| BIOMD0000000252 (4)| BIOMD0000000377 (14)| 17.2 sec.     | 118.0|          |           |
| BIOMD0000000298 (11)| BIOMD0000000377 (14)| 10 min. 48 sec.| 253.0|          |           |
| BIOMD0000000330 (5)| BIOMD0000000331 (5)| Time Over     | N/A  |          |           |
| BIOMD0000000330 (5)| BIOMD0000000331 (5)| Time Over     | N/A  |          |           |
| BIOMD0000000330 (5)| BIOMD0000000331 (5)| Time Over     | N/A  |          |           |
| BIOMD0000000330 (5)| BIOMD0000000331 (5)| Time Over     | N/A  |          |           |

7 Concluding Remarks

In this article, we proposed tree edit distance with variables, motivated from needs for comparison of non-linear biological systems. We analyzed the computational complexities of several variants/subcases of the problem, and found that the complexity substantially changes according to introduction of variables. We also extended the tree edit distance problem with variables for computing the distance between two systems of first-order differential equations. Furthermore, we developed exponential-time algorithms for the distance problems for unordered trees and systems. However, the exponential factors are too high. Therefore, much efficient exponential-time algorithms, parameterized algorithms, and/or approximation algorithms should be developed.

From a practical viewpoint, some improvements should be made. We employed the ILP-based method given in [9] for computation of the unordered tree edit distance. However, it is not necessarily the fastest one. Indeed, the same research group developed an improve ILP-based method [7]. Therefore, such an improved method should be considered. In the computation of substitutions, we employed a kind of exhaustive search. However, this part could be improved by employing ILP or some other technique(s). Therefore, the use of such techniques should also be considered. Another important future work would be to assess the usefulness of the proposed distances in measuring biological systems. To this end, we need to conduct computational experiments using much more data from the BioModels data repository, which again requires developments of more practical methods.

Acknowledgment

We are also grateful to the members of Sato lab at ATR and Karydo TherapeutiX, Inc. for advice and discussion throughout the course of this work. This work was supported in part by JSPS KAKENHI Grant Numbers JP18H04113 (T.A.), JP17H06003 (N.N.), JP19H05422 (N.N.), JST ERATO Grant Number JPMJER1303(T.N.S), Nakatani Foundation(T.N.S) and AMED under Grant Number JP21he2102002 (T.N.S).

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