

Similarity Search

Traversal Strings and Constrained Edit Distance

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Outline

- 1 Search Space Reduction for the Tree Edit Distance
 - Similarity Join and Search Space Reduction
 - Lower Bound: Traversal Strings
 - Upper Bound: Constrained Edit Distance

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Definition: Similarity Join

Definition (Similarity Join)

Given two sets of trees, S_1 and S_2 , and a distance threshold τ , let $\delta_t(T_i, T_j)$ be a function that assesses the edit distance between two trees $T_i \in S_1$ and $T_j \in S_2$. The similarity join operation between two sets of trees reports in the output all pairs of trees $(T_i, T_j) \in S_1 \times S_2$ such that $\delta_t(T_i, T_j) \leq \tau$.

Similarity Join Algorithm with Upper and Lower Bounds

```
simJoin( $S_1, S_2$ )
```

```
for each  $T_i \in S_1$  do  
  for each  $T_j \in S_2$  do  
    if upperBound( $T_i, T_j$ )  $\leq \tau$  then  
      output( $T_i, T_j$ )  
    else if lowerBound( $T_i, T_j$ )  $> \tau$  then  
      /* do nothing */  
    else if  $\delta_t(T_i, T_j) \leq \tau$  then  
      output( $T_i, T_j$ )
```

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Preorder and Postorder Traversal Strings

- Each node label is a **single character** of an alphabet Σ .
- **Traversal Strings:**
 - $pre(T)$ is the string of T 's node labels in preorder
 - $post(T)$ is the string of T 's node labels in postorder

Lemma (Tree Inequality)

Let $pre(T_1)$ and $pre(T_2)$ be the preorder strings, and $post(T_1)$ and $post(T_2)$ be the postorder strings of two trees T_1 and T_2 , respectively. Then

$$pre(T_1) \neq pre(T_2) \text{ or } post(T_1) \neq post(T_2) \Rightarrow T_1 \neq T_2$$

Proof.

The inversion of the argument is obviously true:

$$T_1 = T_2 \Rightarrow pre(T_1) = pre(T_2) \text{ and } post(T_1) = post(T_2) \quad \square$$

Lower Bound

Theorem (Lower Bound)

If the trees are at tree edit distance k , then the string edit distance between their preorder and postorder traversals is at most k .

Proof.

Tree operations map to string operations (illustration on next slide):

- **Insertion** ($ins(v, p, k, m)$): Let $t_1 \dots t_f$ be the subtrees rooted in the children of p . Then the preorder traversal of the subtree rooted in p is

$$p \text{ pre}(t_1) \dots \text{pre}(t_{k-1}) \text{pre}(t_k) \dots \text{pre}(t_m) \text{pre}(t_{m+1}) \dots \text{pre}(t_f).$$

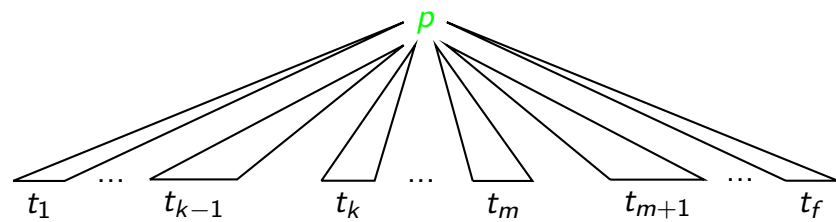
Inserting v moves the subtrees k to m :

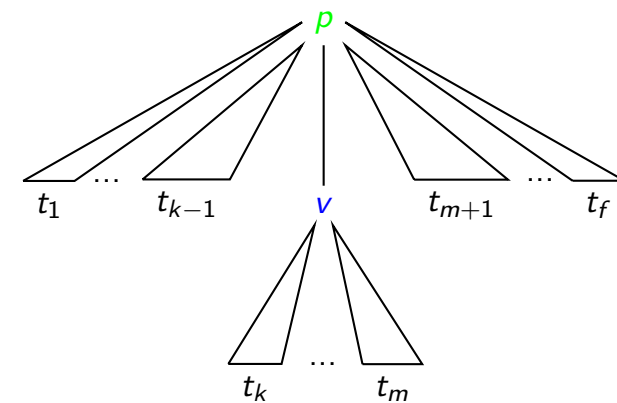
$$p \text{ pre}(t_1) \dots \text{pre}(t_{k-1}) v \text{ pre}(t_k) \dots \text{pre}(t_m) \text{pre}(t_{m+1}) \dots \text{pre}(t_f).$$

The string distance is 1. Analog rationale for postorder.

- **Deletion**: Inverse of insertion.
- **Rename**: With node rename a single string character is renamed. \square

Illustration for the Lower Bound Proof (Preorder)



$$\begin{array}{c} \text{ins}(v, p, k, m) \\ \rightleftharpoons \\ \text{del}(v) \end{array}$$


p $pre(t_1) \dots pre(t_{k-1})$
 $pre(t_k) \dots pre(t_m)$
 $pre(t_{m+1}) \dots pre(t_f)$

p $pre(t_1) \dots pre(t_{k-1})$
 v $pre(t_k) \dots pre(t_m)$
 $pre(t_{m+1}) \dots pre(t_f)$

Lower Bound

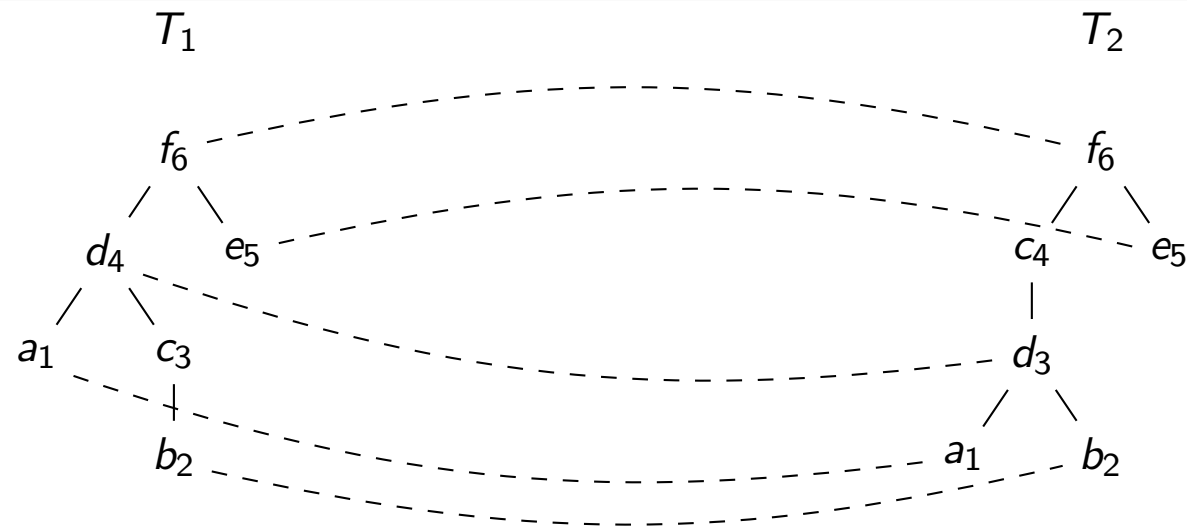
- From the **lower bound** theorem it follows that

$$\max(\delta_s(\text{pre}(T_1), \text{pre}(T_2)), \delta_s(\text{post}(T_1), \text{post}(T_2))) \leq \delta_t(T_1, T_2)$$

where δ_s and δ_t are the string and the tree edit distance, respectively.

- The **string edit distance** can be computed **faster**:
 - string edit distance runtime: $O(n^2)$
 - tree edit distance runtime: $O(n^3)$
- **Similarity join**: match all trees with $\delta_t(T_1, T_2) \leq \tau$
 - if $\max(\delta_s(\text{pre}(T_1), \text{pre}(T_2)), \delta_s(\text{post}(T_1), \text{post}(T_2))) > \tau$
then $\delta_t(T_1, T_2) > \tau$
 - thus we do not have to compute the expensive tree edit distance

Example: Traversal String Lower Bound


 $pre(T_1) = fdacbe$
 $pre(T_2) = fcdabe$
 $post(T_1) = abcdef$
 $post(T_2) = abcdef$

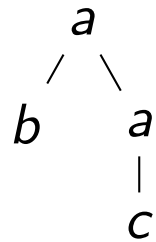
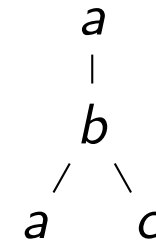
$$\delta_s(pre(T_1), pre(T_2)) = 2$$

$$\delta_s(post(T_1), post(T_2)) = 2$$

$$\delta_t(T_1, T_2) = 2$$

Example: Traversal String Lower Bound

- The string distances of **preorder** and **postorder** may be different.
- The **string distances** and the **tree distance** may be different.

 T_1

 $pre(T_1) = abac$
 $post(T_1) = bcaa$
 T_2

 $pre(T_2) = abac$
 $post(T_2) = acba$
 $\delta_s(pre(T_1), pre(T_2)) = 0$
 $\delta_s(post(T_1), post(T_2)) = 2$
 $\delta_t(T_1, T_2) = 3$

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Edit Mapping

- Recall the definition of the edit mapping:

Definition (Edit Mapping)

An **edit mapping** M between T_1 and T_2 is a set of node pairs that satisfy the following conditions:

- (1) $(a, b) \in M \Rightarrow a \in N(T_1), b \in N(T_2)$
- (2) for any two pairs (a, b) and (x, y) of M :
 - (i) $a = x \Leftrightarrow b = y$ (one-to-one condition)
 - (ii) a is to the left of $x^1 \Leftrightarrow b$ is to the left of y (order condition)
 - (iii) a is an ancestor of $x \Leftrightarrow b$ is an ancestor of y (ancestor condition)
- (3) Optional: $a = \text{root}(T_1)$ and $b = \text{root}(T_1) \Rightarrow (a, b) \in M$ (forbid deleting the root node)

¹i.e., a precedes x in both preorder and postorder

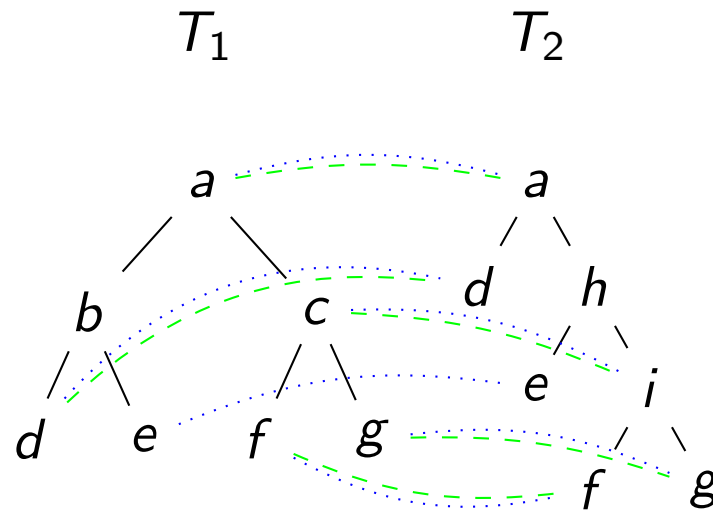
Constrained Edit Distance

- We compute a **special case** of the edit distance to get a faster algorithm.
- $lca(a, b)$ is the **lowest common ancestor** of a and b .
- **Additional requirement** on the mapping M :
 - (4) for any pairs (a_1, b_1) , (a_2, b_2) , (x, y) of M :

$$\begin{aligned} lca(a_1, a_2) \text{ is a proper ancestor of } x \\ \Leftrightarrow \\ lca(b_1, b_2) \text{ is a proper ancestor of } y. \end{aligned}$$

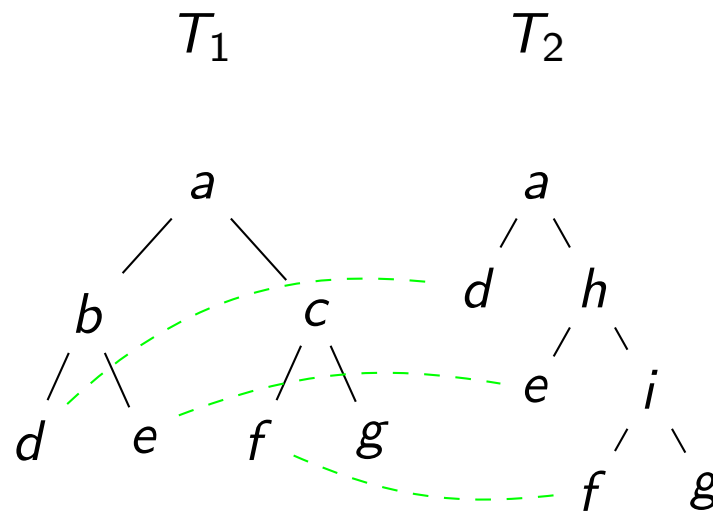
- **Intuition:** Distinct subtrees of T_1 are mapped to distinct subtrees of T_2 .

Example: Constrained Edit Distance



- **Constrained** edit distance (dashed lines): $\delta_c(T_1, T_2) = 5$
 - constrained mapping $M_c = \{(a, a), (d, d), (c, i), (f, f), (g, g)\}$
 - edit sequence: $ren(c, i), del(b), del(e), ins(h), ins(e)$
- **Unconstrained** edit distance (dotted lines): $\delta_t(T_1, T_2) = 3$
 - mapping $M_t = \{(a, a), (d, d), (e, e), (c, i), (f, f), (g, g)\}$
 - edit sequence: $ren(c, i), del(b), ins(h)$

Example: Constrained Edit Distance



- (e, e) violates the 4th condition of the constrained mapping:
 - $lca(e, f)$ in T_1 is a
 - a is a proper ancestor of d in T_1
 - assume $(e, e), (f, f), (d, d) \in M_c$
 - $lca(e, f)$ in T_2 is h
 - h is **not a proper ancestor** of d in T_2

Complexity of the Constrained Edit Distance

Theorem (Complexity of the Constrained Edit Distance)

Let T_1 and T_2 be two trees with $|T_1|$ and $|T_2|$ nodes, respectively. There is an algorithm that computes the constrained edit distance between T_1 and T_2 with runtime

$$O(|T_1||T_2|).$$

Proof.

See [Zha95, GJK⁺02]. □

Constrained Edit Distance: Upper Bound

Theorem (Upper Bound)

Let T_1 and T_2 be two trees, let $\delta_t(T_1, T_2)$ be the unconstrained and $\delta_c(T_1, T_2)$ be the constrained tree edit distance, respectively. Then

$$\delta_t(T_1, T_2) \leq \delta_c(T_1, T_2)$$

Proof.

See [GJK⁺02]. □

Use of the Upper Bound

- The **constrained edit distance** can be computed **faster**:
 - constrained edit distance runtime: $O(n^2)$
 - unconstrained edit distance runtime: $O(n^3)$
- **Similarity join**: match all trees with $\delta_t(T_1, T_2) \leq \tau$
 - if $\delta_c(T_1, T_2) \leq \tau$ then also $\delta_t(T_1, T_2) \leq \tau$.
 - thus we do not have to compute the expensive tree edit distance



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Approximate XML joins.

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