Similarity Search
The Binary Branch Distance

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Outline

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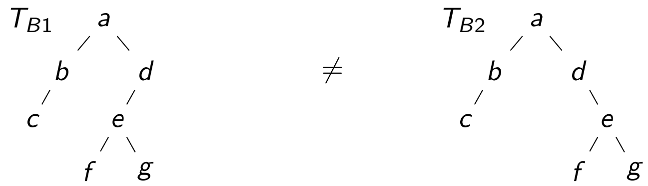
Binary Tree

- In a binary tree
  - each node has at most two children;
  - left child and right child are distinguished:
    a node can have a right child without having a left child;
- Notation: $\mathsf{T}_B = (N, E_l, E_r)$
  - T_B denotes a binary tree
  - N are the nodes of the binary tree
  - E_l and E_r are the edges to the left and right children, respectively
- Full binary tree:
  - binary tree
  - each node has exactly zero or two children.

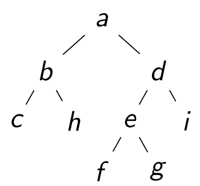
Example: Binary Tree

- Two different binary trees: $\mathrm{T}_B = (N, E_l, E_r)$

  $\mathrm{T}_{B1} = (\{a, b, c, d, e, f, g\}, \{(a, b), (b, c), (d, e), (e, f)\}, \{(a, d), (e, g)\})$
  $\mathrm{T}_{B2} = (\{a, b, c, d, e, f, g\}, \{(a, b), (b, c), (e, f)\}, \{(a, d), (d, e), (e, g)\})$



- A full binary tree:



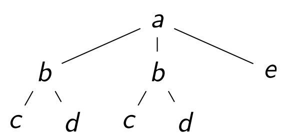
Binary Representation of a Tree

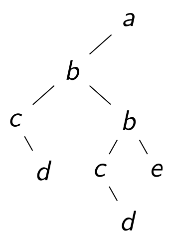
- Binary tree transformation:
  1. link all neighboring siblings in a tree with edges
  2. delete all parent-child edges except the edge to the first child
- Transformation maintains
  - label information
  - structure information
- Original tree can be reconstructed from the binary tree:
  - a left edge represents a parent-child relationships in the original tree
  - a right edge represents a right-sibling relationship in the original tree

Example: Binary Tree Transformation

- Represent tree T as a binary tree:

T $\rightarrow$ binary representation of T





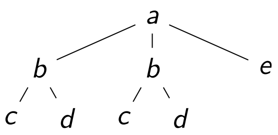
Normalized Binary Tree Representation

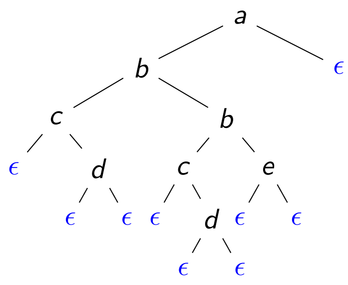
- We extend the binary tree with null nodes ϵ as follows:
  - a null node for each missing left child of a non-null node
  - a null node for each missing right child of a non-null node
- Note: Leaf nodes get two null-children.
- The resulting normalized binary representation
  - is a full binary tree
  - all non-null nodes have two children
  - all leaves are null nodes (and all null nodes are leaves)

Example: Normalized Binary Tree

- Transforming T to the normalized binary tree $B(\mathrm{T})$:

T $\rightarrow$ B(T)





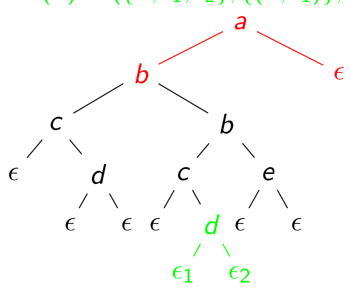
Outline

Binary Branch

- A binary branch $BiB(\mathrm{v})$ is
  - a subtree of the normalized binary tree $B(\mathrm{T})$
  - consisting of a non-null node v and its two children
- Example:

$BiB(a) = (\{a, b, \epsilon\}, \{(a, b)\}, \{(a, \epsilon)\})$

$BiB(d) = (\{d, \epsilon_1, \epsilon_2\}, \{(d, \epsilon_1)\}, \{(d, \epsilon_2)\})$ [1]

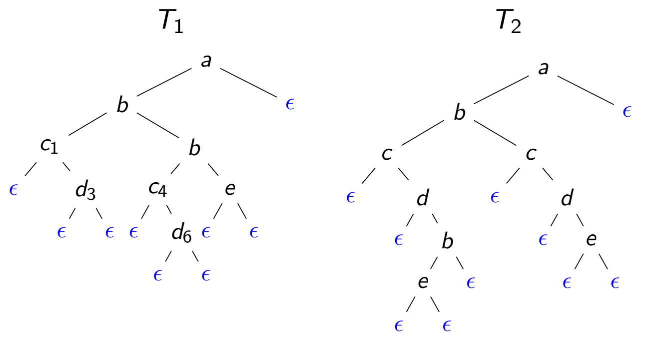


[1] Although the two null nodes have identical labels (ϵ), they are different nodes. We emphasize this by showing their IDs in subscript.

Binary Branches of Trees and Datasets

- Binary branches can be serialized as strings:
  - $BiB(\mathrm{v}) = (\{\mathrm{v}, \mathrm{a}, \mathrm{b}\}, \{(\mathrm{v}, \mathrm{a})\}, \{(\mathrm{v}, \mathrm{b})\}) \rightarrow \lambda(\mathrm{v}) \circ \lambda(\mathrm{a}) \circ \lambda(\mathrm{b})$
  - we can sort these strings ($\epsilon > \lambda(\mathrm{v})$ for all non-null nodes v)
- Binary branch sets:
  - $BiB(\mathrm{T})$ is the set of all binary branches of $B(\mathrm{T})$
  - $BiB(S) = \bigcup_{\mathrm{T} \in S} BiB(\mathrm{T})$ is the set of all binary branches of dataset S
  - $BiB_{sort}(S)$ is the vector of sorted serialized strings of $BiB(S)$
- Note:
  - nodes are unique in the tree, thus binary branches are unique
  - labels are *not* unique, thus the serialized binary branches are *not* unique

Example: Binary Branches of Trees and Datasets

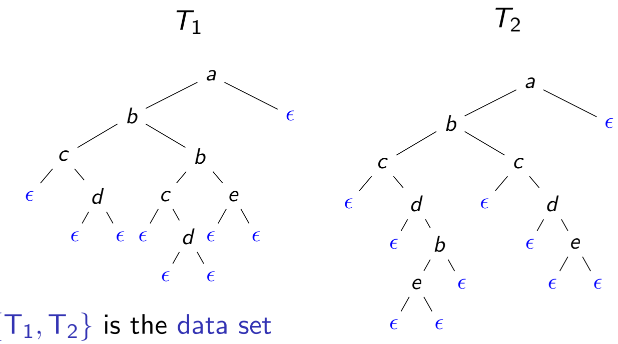


- $BiB(c_1) \neq BiB(c_4)$:
  - $BiB(c_1) = (\{c_1, \epsilon_2, d_3\}, \{(c_1, \epsilon_2)\}, \{(c_1, d_3)\})$
  - $BiB(c_4) = (\{c_4, \epsilon_5, d_6\}, \{(c_4, \epsilon_5)\}, \{(c_4, d_6)\})$
- Serialization of both, $BiB(c_1)$ and $BiB(c_2)$, is identical: $'c\epsilon d'$
- Sorted vector of serialized strings of $BiB(S)$, where $S = \{\mathrm{T}_1, \mathrm{T}_2\}$:
  $BiB_{sort}(S) = (ab\epsilon, bcb, bcc, bce, be\epsilon, c\epsilon d, d\epsilon b, d\epsilon e, d\epsilon\epsilon, e\epsilon\epsilon)$

Binary Branch Vector

- The binary branch vector $BBV(\mathrm{T})$
  - is a representation of the binary branch set $BiB(\mathrm{T})$
- Construction of the binary branch vector $BBV(\mathrm{T})$:
  - compute $BiB_{sort}(S)$ (*serialize* and sort $BiB(S)$)
  - b_i is the i-th serialized binary branch in sort order ($b_i = BiB_{sort}(S)[i]$)
  - $BBV(\mathrm{T})[i]$ is the number of binary branches in $B(\mathrm{T})$ that serialize to b_i
- Note: $BBV(\mathrm{T})[i]$ is zero if b_i does not appear in $BiB(\mathrm{T})$

Example: Binary Branch Vectors



- $S = \{\mathrm{T}_1, \mathrm{T}_2\}$ is the data set
- $BiB_{sort}(S)$ is the vector of sorted serialized strings of $BiB(S)$
- $BBV(\mathrm{T}_i)$ is the binary branch vector of T_i
- the vector of serialized strings and the binary branch vectors are:

$BiB_{sort}(S)$	$ab\epsilon$	bcb	bcc	bce	$be\epsilon$	$c\epsilon d$	$d\epsilon b$	$d\epsilon e$	$d\epsilon\epsilon$	$e\epsilon\epsilon$
$BBV(\mathrm{T}_1)$	1	1	0	1	0	2	0	0	2	1
$BBV(\mathrm{T}_2)$	1	0	1	0	1	2	1	1	0	2

Outline

Binary Branch Distance [YKT05]

Definition (Binary Branch Distance)

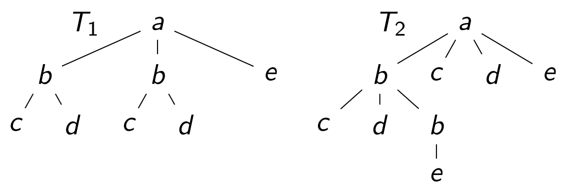
Let $BBV(\mathrm{T}) = (b_1, \ldots, b_k)$ and $BBV(\mathrm{T}') = (b'_1, \ldots, b'_k)$ be binary branch vectors of trees T and T′, respectively. The binary branch distance of T and T′ is

$$\delta_B(\mathrm{T}, \mathrm{T}') = \sum_{i=1}^{k} |b_i - b'_i|.$$

- Intuition: We count the binary branches that do not match between the two trees.

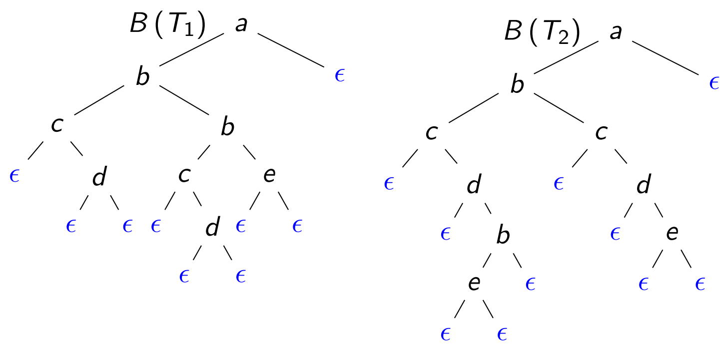
Example: Binary Branch Distance

- We compute the binary branch distance between T_1 and T_2:



Example: Binary Branch Distance

- The normalized binary tree representations are:



Example: Binary Branch Distance

- The binary branch vectors of T_1 and T_2 are:

$BiB_{sort}(S)$	$ab\epsilon$	bcb	bcc	bce	$be\epsilon$	$c\epsilon d$	$d\epsilon b$	$d\epsilon e$	$d\epsilon\epsilon$	$e\epsilon\epsilon$
$BBV(\mathrm{T}_1)$	1	1	0	1	0	2	0	0	2	1
$BBV(\mathrm{T}_2)$	1	0	1	0	1	2	1	1	0	2

- The binary branch distance is

$$\begin{aligned}\delta_B(\mathrm{T}_1, \mathrm{T}_2) &= \textstyle\sum_{i=1}^{10} |b_{1,i} - b_{2,i}| \\ &= |1-1| + |1-0| + |0-1| + |1-0| + |0-1| + \\ &\quad |2-2| + |0-1| + |0-1| + |2-0| + |1-2| \\ &= 9,\end{aligned}$$

where $b_{1,i}$ and $b_{2,i}$ are the i-th dimension of the vectors $BBV(\mathrm{T}_1)$ and $BBV(\mathrm{T}_2)$, respectively.

Lower Bound Theorem

Theorem (Lower Bound)

Let T *and* T′ *be two trees. If the tree edit distance between* T *and* T′ *is* $\delta_t(\mathrm{T}, \mathrm{T}')$, *then the binary branch distance between them satisfies*

$$\delta_B(\mathrm{T}, \mathrm{T}') \leq 5 \times \delta_t(\mathrm{T}, \mathrm{T}').$$

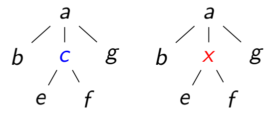
Proof (Sketch — Full Proof in [YKT05]).

- Each node v appears in at most two binary branches.
- *Rename*: Renaming a node causes at most two binary branches in each tree to mismatch. The sum is 4.
- Similar rational for *insert* and its complementary operation *delete* (at most 5 binary branches mismatch).

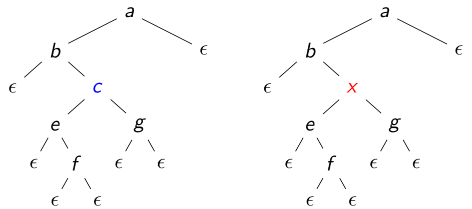
□

Proof Sketch: Illustration for Rename

- transform T_1 to T_2: $ren(c, x)$



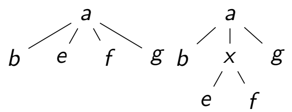
- binary trees $B(\mathrm{T}_1)$ and $B(\mathrm{T}_2)$



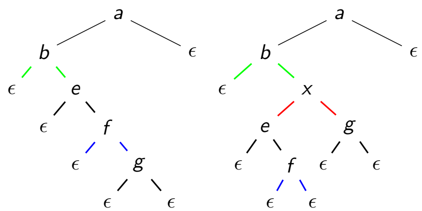
- Two binary branches ($b\epsilon c$, ceg) exist only in $B(\mathrm{T}_1)$
- Two binary branches ($b\epsilon x$, xeg) exist only in $B(\mathrm{T}_2)$
- $\delta_t(\mathrm{T}_1, \mathrm{T}_2) = 1$ (1 rename)
- $\delta_B(\mathrm{T}_1, \mathrm{T}_2) = 4$ (4 binary branches different)

Proof Sketch: Illustration for Insert

- transform T_1 to T_2: $ins(x, a, 2, 2)$



- binary trees $B(\mathrm{T}_1)$ and $B(\mathrm{T}_2)$



- Two binary branches ($b\epsilon e$, $f\epsilon g$) exist only in $B(\mathrm{T}_1)$
- Tree binary branches ($b\epsilon x$, $f\epsilon\epsilon$, xeg) exist only in $B(\mathrm{T}_2)$
- $\delta_t(\mathrm{T}_1, \mathrm{T}_2) = 1$ (1 insertion)
- $\delta_B(\mathrm{T}_1, \mathrm{T}_2) = 5$ (5 binary branches different)

Proof Sketch

- In general it can be shown that
  - Rename changes *at most* 4 binary branches
  - Insert changes *at most* 5 binary branches
  - Delete changes *at most* 5 binary branches
- Each edit operation changes at most 5 binary branches, thus

$$\delta_B(\mathrm{T}, \mathrm{T}') \leq 5 \times \delta_t(\mathrm{T}, \mathrm{T}').$$

Outline

Complexity: Binary Branch Distance

- Compute the distance between two trees of size $O(n)$: $(S = \{T_1, T_2\},\ n = \max\{|T_1|, |T_2|\})$
- Construction of the binary branch vectors $BBV(T_1)$ and $BBV(T_2)$:
  1. $BiB(S)$ – compute the binary branches of T_1 and T_2: $O(n)$ time and space (traverse T_1 and T_2)
  2. $BiB_{sort}(S)$ – sort *serialized* binary branches of $BiB(S)$: $O(n \log n)$ time and $O(n)$ space
  3. construct $BBV(T_1)$ and $BBV(T_2)$:
     a. traverse all binary branches: $O(n)$ time and space
     b. for each binary branch find position i in $BiB_{sort}(S)$: $O(n \log n)$ time (binary search in $BiB_{sort}(S)$ for n binary branches)
     c. $BBV(T)[i]$ is incremented: $O(1)$
- Computing the distance:
  - the two binary branch vectors are of size $O(n)$
  - computing the distance has time complexity $O(n)$ (subtracting two binary branch vectors)
- The overall complexity is $O(n \log n)$ time and $O(n)$ space.

Improving the Time Complexity with a Hash Function

- Note: Improvement using a hash function:
  - we assume a hash function that maps the $O(n)$ binary branches to $O(n)$ buckets without collision
  - we do *not* sort $BiB(S)$
  - position i in the vector $BBV(T)$ is computed using the hash function
  - $O(n)$ time (instead of $O(n \log n)$) and $O(n)$ space
- In the following we assume the sort algorithm with $O(n \log n)$ runtime.

Complexity for Similarity Joins

- Join two sets with N trees each (tree size: n):
- Compute Binary Branch Vectors (BBVs): $O(Nn \log(Nn))$ time, $O(N^2 n)$ space
  - BBVs are of size $O(Nn)$
  - time: sort $O(Nn)$ binary branches / $O(Nn)$ binary searches in BBVs
  - space: $O(N)$ BBVs must be stored
- Compute Distances: $O(N^3 n)$ time
  - computing the distance between two trees has $O(Nn)$ time complexity (subtracting two binary branch vectors)
  - $O(N^2)$ distance computations required
- Overal Complexity: $O(N^3 n + Nn \log n)^\dagger$ time and $O(N^2 n)$ space

$^\dagger O(N^3 n + Nn \log(Nn)) = O(N^3 n + Nn \log N + Nn \log n) = O(N^3 n + Nn \log n)$

Rui Yang, Panos Kalnis, and Anthony K. H. Tung.
Similarity evaluation on tree-structured data.
In *Proceedings of the ACM SIGMOD International Conference on Management of Data*, pages 754–765, Baltimore, Maryland, USA, June 2005. ACM Press.