LCS-TRIM: Dynamic Programming Meets XML Indexing and Querying

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Main Idea

- Convert XML documents (tree structure) to sequences (linear structure)
- Do the subsequence matching.
- Do the structure refinement

Approach

- Data representation
- Matching
  - Subsequence matching
  - Structure matching
- Indexing
- Optimizations
  - Labeling Filtering
  - Dominant Match Processing

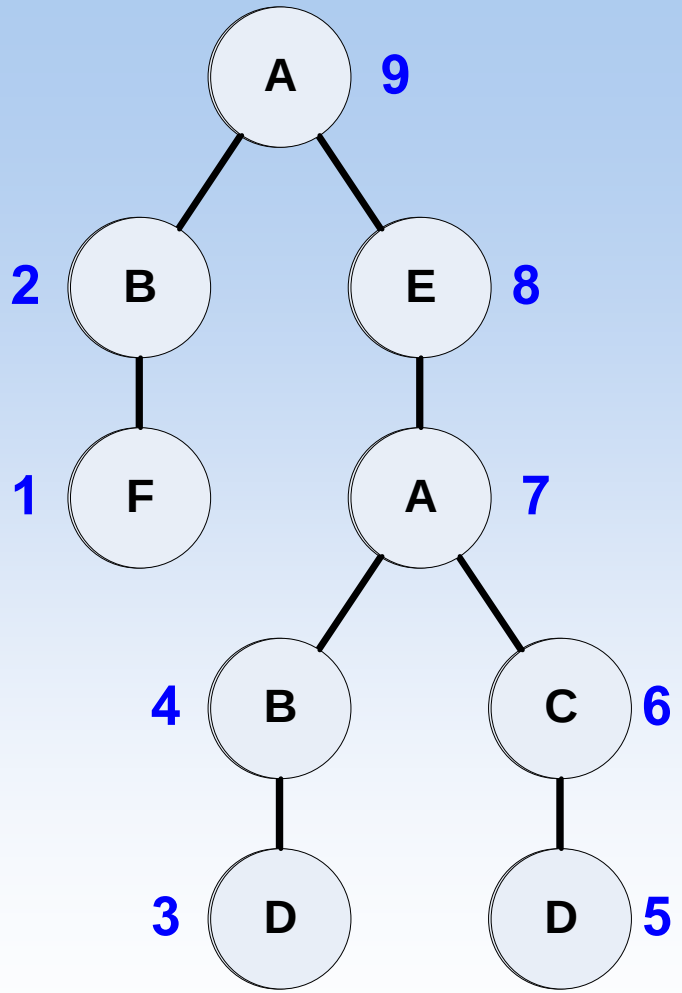
Data Representation

- Convert the XML documents (tree structure) into sequences (linear structure)
- Main idea:
  - Numbering the nodes
    - Post-order
  - In some order, record the number and/or the label of the nodes
    - Post-order, Pre-order

Prüfer Sequence

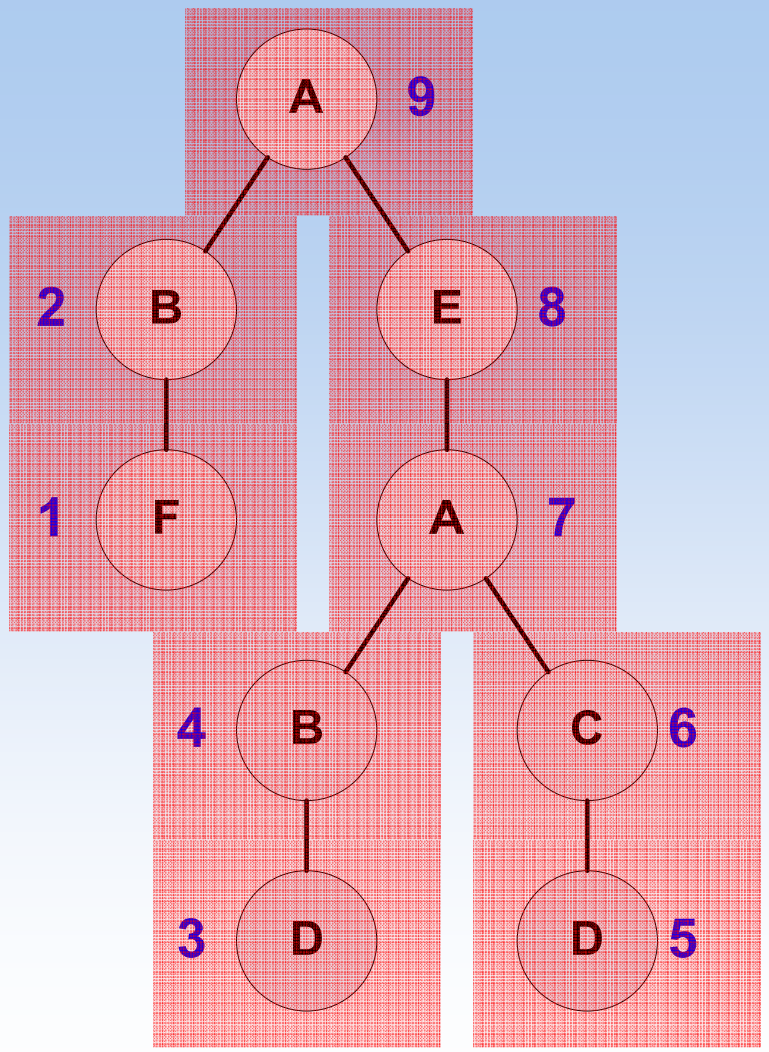
- Constructed by two sequences:
  - Numbered Prüfer Sequence (NPS)
  - Label Sequence LS
- How to convert?
  - Number the nodes by *post-order* traversal.
  - Delete the node with the smallest number:
    - To NPS, append the number of ***its parent***.
    - To LS, append the label of ***itself***.
  - PRIX uses both the number and label of the ***parent*** of the deleted-node.

Example



- Post-order numbering

Construct the Sequences



Each entry in CPS is an edge.

CPS

NPS: 2 9 4 7 6 7 8 9 -

LS: F B D B D C A E A

Index: 1 2 3 4 5 6 7 8 9

PRIX

NPS: 2 9 4 7 6 7 8 9

LPS: B A B A C A E A

Each entry in PRIX is about the same node.

Approach

- Data representation
- Matching
  - Subsequence matching
  - Structure matching
- Indexing
- Optimizations
  - Labeling Filtering
  - Dominant Match Processing

Main Idea

- Theorem 3.1 Consider a tree T and a twig query Q with their label sequences LS_T *and* LS_Q, respectively. If Q is a subtree of T, then LS_Q is a subsequence of LS_T
- Subtree ➔ Subsequence
- Subsequence ➔ Subtree ?
- NOT sufficient! More conditions needed!
- First find subsequence, then check more conditions and then find the subtrees.

Subsequence Matching

- LCS: Longest Common Subsequence
- Using Dynamic Programming to solve LCS
- Use a matrix *R*, *R*[i,*j*] records the length of the LCS between $s_1[0..i\,]$ and $s_2[0..j\,]$.

$$R[i,\ j] = \begin{cases} 0 & i = 0,\ j = 0 \\ R[i-1,\ j-1]+1 & s_1[i] = s_2[\,j] \\ \max\left(R[i-1,\ j],\ R[i,\ j-1]\right) & s_1[i] \neq s_2[\,j] \end{cases}$$

Example of LCS

$$R[i,\ j] = \begin{cases} 0 & i = 0,\ j = 0 \\ R[i-1,\ j-1] + 1 & s_1[i] = s_2[j] \\ \max\left(R[i-1,\ j],\ R[i,\ j-1]\right) & s_1[i] \neq s_2[j] \end{cases}$$

	F	B	D	D	C	A	E	A
B	0	1	1	1	1	1	1	1
D	0	1	2	2	2	2	2	2
A	0	1	2	2	2	3	3	3
E	0	1	2	2	2	3	4	4
C	0	1	2	2	3	3	4	4

- Numbers in red are matches.

F	B	D	D	C	A	E	A	
	B	D			A	E		C

F	B	D	D	C	A	E	A	
	B		D		A	E		C

Subsequence Matching

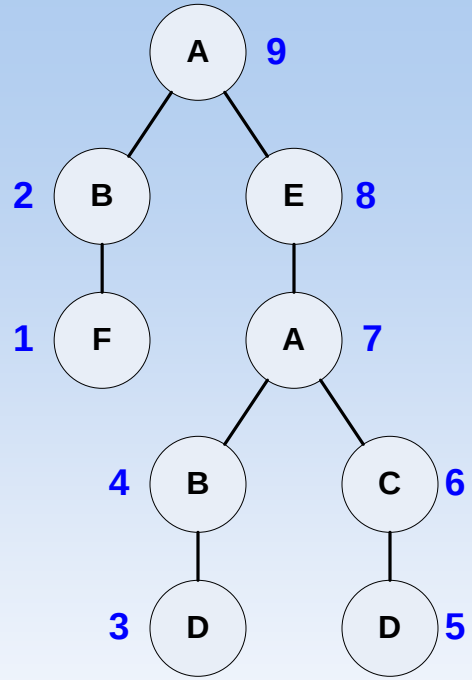
- Property 3.1 If a label sequence LS_Q is a subsequence of another label sequence LS_T, then LS_Q is the longest common subsequence (LCS) of LS_Q and LS_T.
- Each node in the query needs to match one in the document.
- The length of the LCS should be the same as the length of LS_Q

Subsequence Matching

- Two steps:
  - Construct the *R* matrix, check the length of LCS (whether LS_Q is a subsequence of LS_T)
  - Using backtrack to get all the matches
- Complexity
  - Time: $O(mn)$
  - Space: $O(mn)$

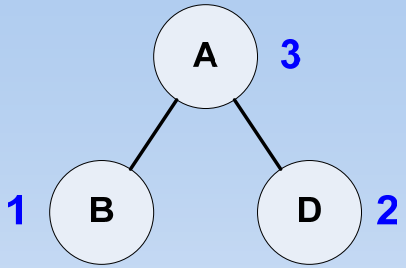
Example

Document



	1	2	3	4	5	6	7	8	9
NPS	2	9	4	7	6	7	8	9	-
LS	F	B	D	B	D	C	A	E	A

Query



	1	2	3
NPS	3	3	-
LS	B	D	A

R Matrix

		F	B	D	B	D	C	A	E	A
		1	2	3	4	5	6	7	8	9
B	1	0	1	1	1	1	1	1	1	1
D	2	0	1	2	2	2	2	2	2	2
A	3	0	1	2	2	2	2	3	3	3

Subsequence Matches:

M1(2, 3, 7) M2(2, 5, 7)
M3(4, 5, 7) M4(2, 3, 9)
M5(2, 5, 9) M6(4, 5, 9)

Structure Matching

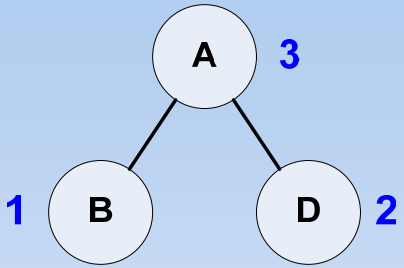
DEFINITION: 3.2. **Structure Agreement:** *Consider two sequentures, derived from two trees* T_1 *and* T_2, $S_1 = ((A_1, B_1) \ldots (A_m, B_m))$ *and* $S_2 = ((C_1, D_1) \ldots (C_m, D_m))$, *where* A_i*'s and* C_i*'s define the structure;* B_i*'s and* D_i*'s provide the labels. Both* S_1 *and* S_2 *are said to* **agree on structure at position i** *if and only if the following three conditions hold:*

i) $1 \leq i \leq m$,
ii) B_i *is equal to* D_i,
iii) If A_i *is the parent of* B_i *in* T_1 *then* C_i *is the parent of* D_i *or the nearest ancestor of* C_i *that is in* S_2 *must agree on structure with* S_1 *at position* A_i [1].

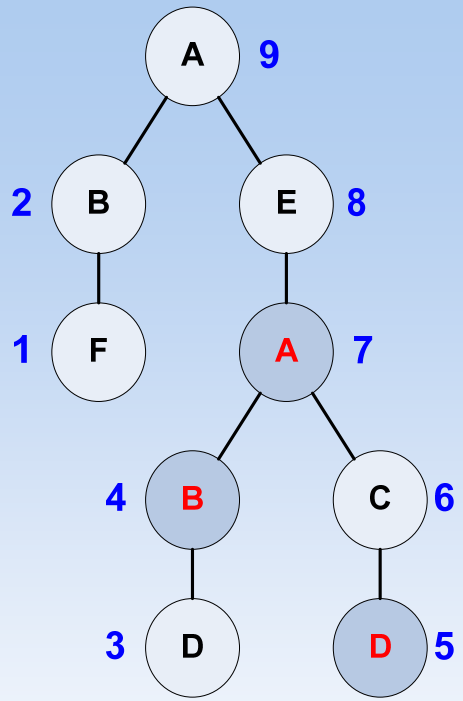
Structure Agreement

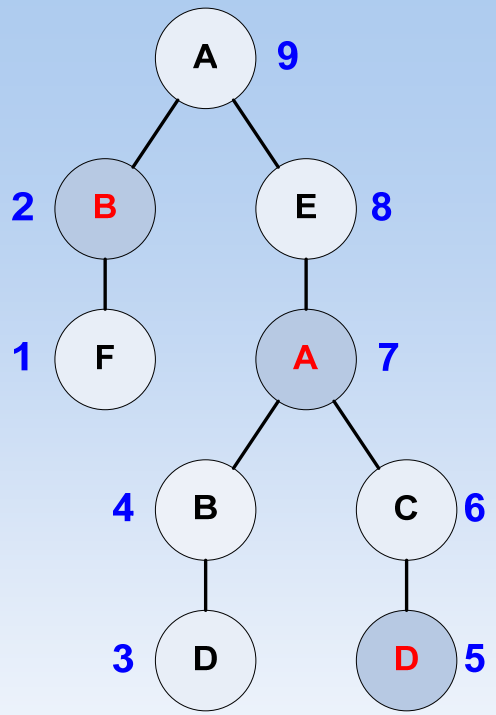
- To check two nodes (NPS_{Ti}, LS_{Ti}) and (NPS_{Qj}, LS_{Qj})
- NPS_{Ti} and NPS_{Qj} are their parents.
- Either the parents share the same label,
- or the *NEAREST* ancestor of NPS_{Qj} matches NPS_{Ti}.
- (Apply some *level-wise constraints* for wildcards “*”, etc).

Example



	1	2	3
NPS	3	3	-
LS	B	D	A





	1	2	3	4	5	6	7	8	9
NPS	2	9	4	7	6	7	8	9	-
LS	F	B	D	B	D	C	A	E	A

Order of the Matching

- For each pair of nodes in the document and the query, we want to check whether their parents matches each other.
- In the CPS, we can see that child always appears before its parent
- So, we need to match the nodes from the end of the sequence to the beginning

Algorithm

Algorithm 2 Subtree matching

Input: CPS(Q), CPS(T), SM=(i_1, .., i_m)
Output: *mapping*: positions at which Q matches to a subtree in T

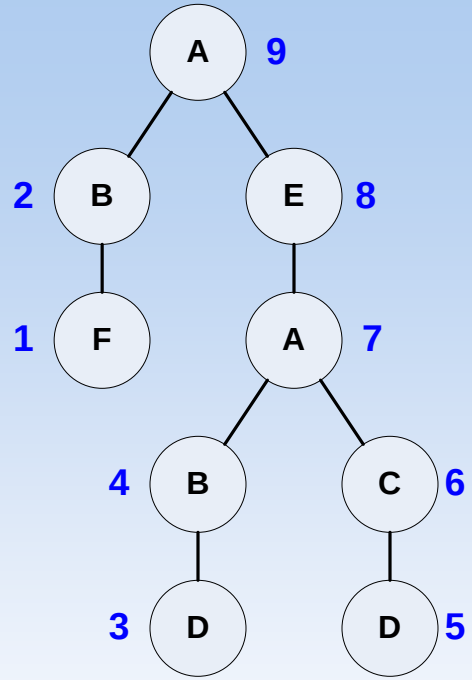
1: $mapping[m] \leftarrow i_m$
2: **for** $k = m - 1$ to 1 **do**
3: $p_q \leftarrow NPS_Q[k]$
4: $p_t \leftarrow NPS_T[i_k]$
5: **if** $mapping[p_q]$ is equal to p_t or is an ancestor of p_t in T **then**
6: $mapping[k] \leftarrow i_k$
7: **else**
8: Report that Q is *not* an embedded subtree of T
9: Report that Q is an embedded subtree of T

For each pair of nodes…

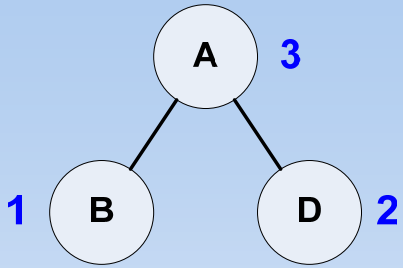
- We have P_q: the parent of the node in Q
- P_t: the parent of the node in T
- mapping[P_q] the node in T that is already matched with P_q in Q
- P_t must be the same or the NEAREST ancestor of mapping[P_q]
- NEAREST: search each ancestor of P_t bottom up, until the first already mapped node, it should be the same as mapping[P_q]

Example

Document



Query



	1	2	3
NPS	3	3	-
LS	B	D	A

	1	2	3	4	5	6	7	8	9
NPS	2	9	4	7	6	7	8	9	-
LS	F	B	D	B	D	C	A	E	A

R Matrix

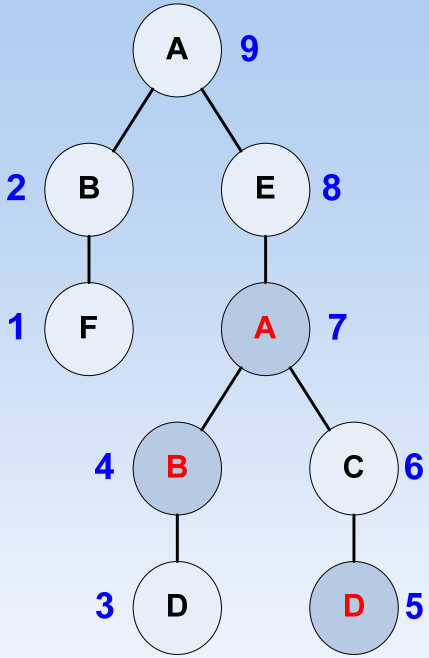
		F	B	D	B	D	C	A	E	A
		1	2	3	4	5	6	7	8	9
B	1	0	1	1	1	1	1	1	1	1
D	2	0	1	2	2	2	2	2	2	2
A	3	0	1	2	2	2	2	3	3	3

Subsequence Matches:

M1(2, 3, 7) M2(2, 5, 7)
M3(4, 5, 7) M4(2, 3, 9)
M5(2, 5, 9) M6(4, 5, 9)

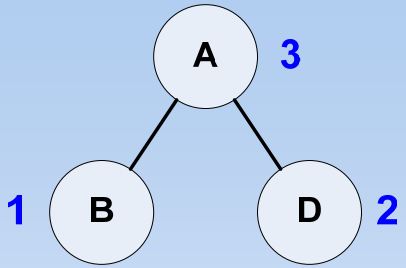
Example

Document



	1	2	3	4	5	6	7	8	9
NPS	2	9	4	7	6	7	8	9	-
LS	F	B	D	B	D	C	A	E	A

Query



	1	2	3
NPS	3	3	-
LS	B	D	A

M3(4, 5, 7)

	1	2	3
mp	4	5	7

Q2 matches T5?

$P_q = 3$

$P_t = 6$

mp[3] = 7 ≠ 6

In T, 7 is the parent of 6.

Match!

Q1 matches T4?

$P_q = 3$

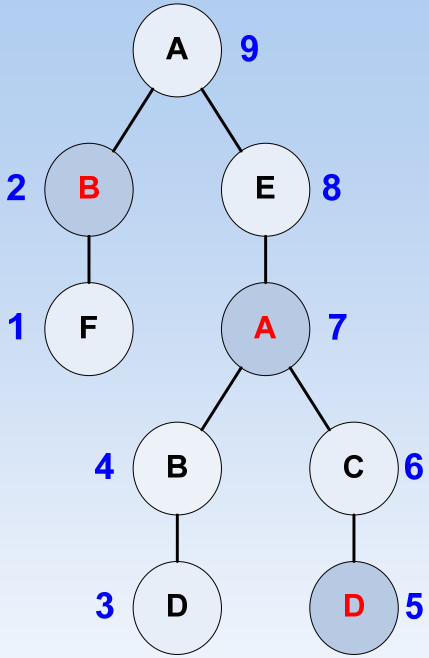
$P_t = 7$

mp[3] = 7

Match!

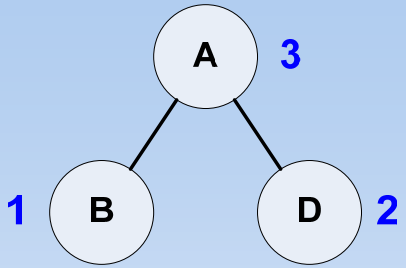
Example

Document



	1	2	3	4	5	6	7	8	9
NPS	2	9	4	7	6	7	8	9	-
LS	F	B	D	B	D	C	A	E	A

Query



	1	2	3
NPS	3	3	-
LS	B	D	A

M2(2, 5, 7)

	1	2	3
mp	X	5	7

Q2 matches T5?

$P_q = 3$

$P_t = 6$

mp[3] = 7 ≠ 6

In T, 7 is the parent of 6.

Match!

Q1 matches T2?

$P_q = 3$

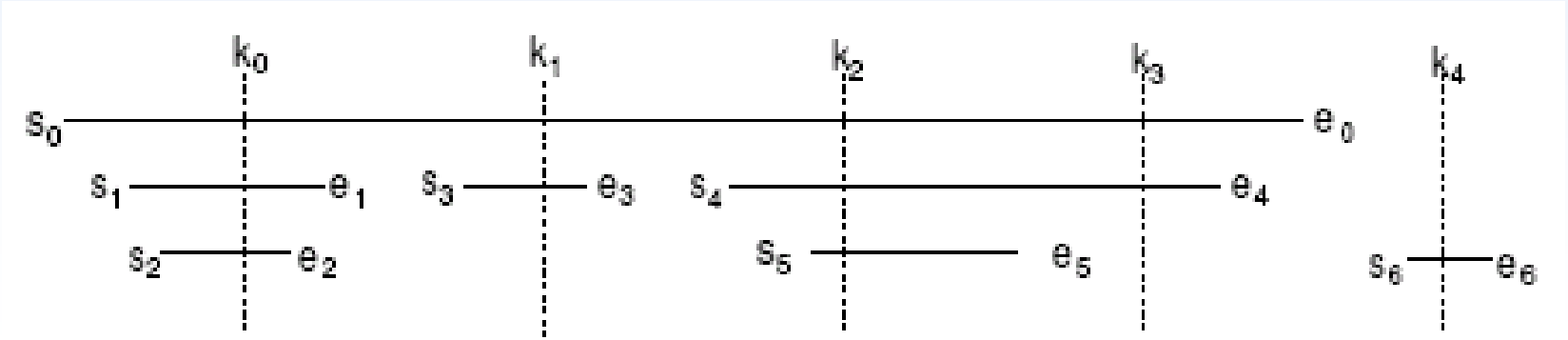
$P_t = 9$

mp[3] = 7

not the parent of 9!

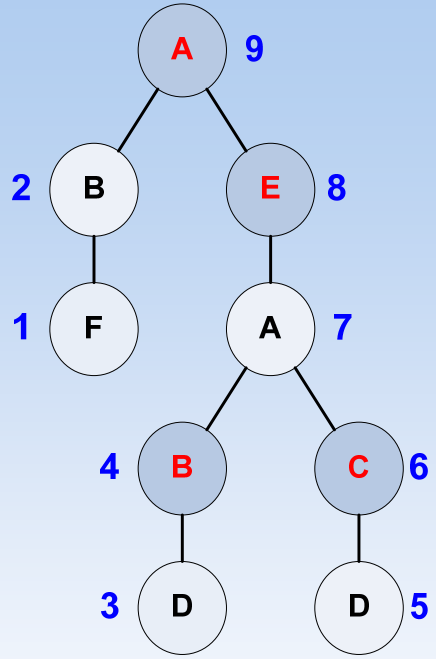
Nearest

- NEAREST: search each ancestor of P_t bottom up, until the first already mapped node, it should be the same as mp[P_q]
- Search for the ancestors one by one, we need O(depth of the tree), which is $O(n)$.
- The node scope representation DOES NOT work!

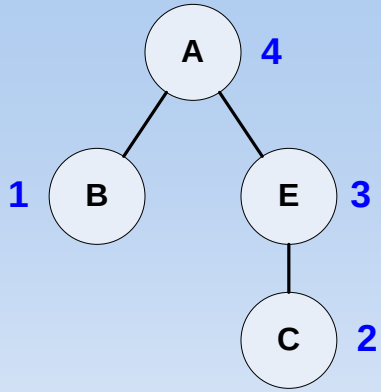


Example

Document



Query



	1	2	3	4
NPS	4	3	4	-
LS	B	C	E	A

	1	2	3	4	5	6	7	8	9
NPS	2	9	4	7	6	7	8	9	-
LS	F	B	D	B	D	C	A	E	A

M (4, 6, 8, 9)

	1	2	3	4
mp	X	6	8	9

Q1 matches T4?

$P_q = 4$

$P_t = 7$

mp[4] = 9

From Pt, the first ancestor that already matched is E(8), which is not A(9)!

Approach

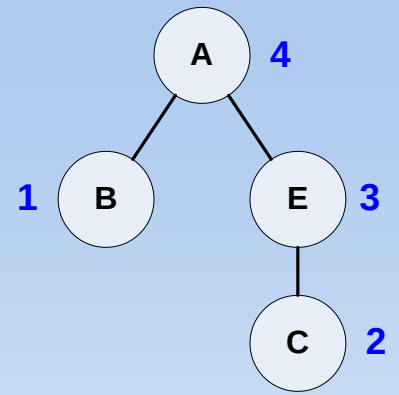
- Data representation
- Matching
  - Subsequence matching
  - Structure matching
- Indexing
- Optimizations
  - Labeling Filtering
  - Dominant Match Processing

Indexing

- For each label, collect the documents where it occurs.
- Only index infrequent labels (indexing frequent labels takes much space but not very helpful)
- α-infrequent: appears in less then a fraction of α trees in the database.
- For a query, find the label which occurs in lest documents, only search among those documents.

Example

- Totally 10,000 documents
- α=50%
- A occurs in 6,000 documents, so not indexed.
- B occurs in 4,000 documents;
- C occurs in 3,000
- E occurs in 3,500
- Use the list of C to do the match.



Approach

- Data representation
- Matching
  - Subsequence matching
  - Structure matching
- Indexing
- Optimizations
  - Labeling Filtering
  - Dominant Match Processing

Label Filtering

- The dynamic programming asks for $O(mn)$ in both time and space.
- Eliminate the irrelevant labels (labels not in the query) from the document.

		F	B	D	B	D	C	A	E	A
		1	2	3	4	5	6	7	8	9
B	1	0	1	1	1	1	1	1	1	1
D	2	0	1	2	2	2	2	2	2	2
A	3	0	1	2	2	2	2	3	3	3

Query: BDA
Tree: FBDBDCAEA

Ignore the label F, C, E from the tree, because they are not in the query.

O(3*9) -> O(3*6)

Dominant Match

- Dominant match:
  - $LS_T[\,i\,]=LS_Q[\,j\,]$
  - $R\,[\,i, j\,]=i$
- Consider only dominant matches, ignore other cells.

		A	B	D	B	D	C	A	E	A
		1	2	3	4	5	6	7	8	9
B	1	0	1	1	1	1	1	1	1	1
D	2	0	1	2	2	2	2	2	2	2
A	3	1	1	2	2	2	2	3	3	3

Numbers in red are dominant matches.

Notice that R[3, 1] is only a match, but not dominant. It cannot appears in any result.

Put All Together

- For each query Q:
  - Using indexing to get a short list of candidate documents.
  - For each document T:
    - Using Label Filtering
    - Construct *R* matrix
    - Check the length of the LCS
    - Back track:
      - Find each dominant match
      - do the structure match at the same time

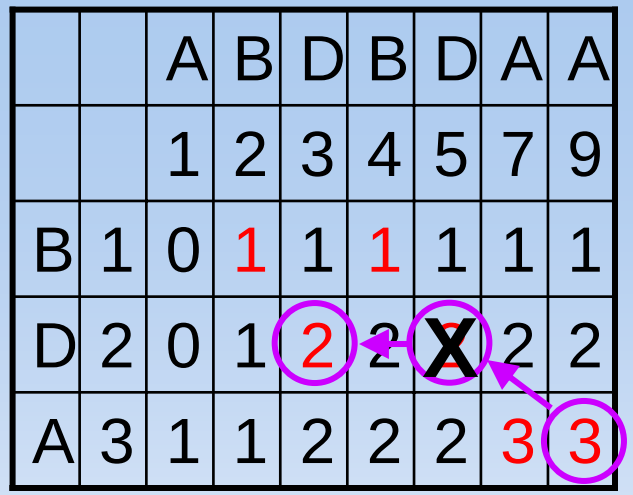
Algorithm 3 The unified subtree matching algorithm

Input: A database tree T and a twig query Q
labelFilter (T, Q) {T contains the filtered sequence}
$R \leftarrow$ *computeLcsMatrix* (T, Q)
if $R[m, n] != m$ **then**
  Report that Q is not a subtree of T
$SM \leftarrow null$
processLCS (m, n, m)

Function:
processLCS ($Qind$, $Tind$, $matchLen$)
1: **if** $matchLen = 0$ **then**
2: Report SM as the twig match
3: **for** $i = Tind$ to 1 **do**
4: **if** $R[Qind][i]$ is dominant & $R[Qind][Tind] = matchLen$ **then**
5: **if** isInAgreement(CPS(Q), SM, $Qind$) **then**
6: $SM[Qind] \leftarrow CPS_T[Tind]$
7: *processLCS* ($Qind$-1, $Tind$-1, $matchLen$-1)

Early prune

- Subsequence matches:
  - M1(2, 3, 7) M2(2, 5, 7)
  - M3(4, 5, 7) M4(2, 3, 9)
  - M5(2, 5, 9) M6(4, 5, 9)

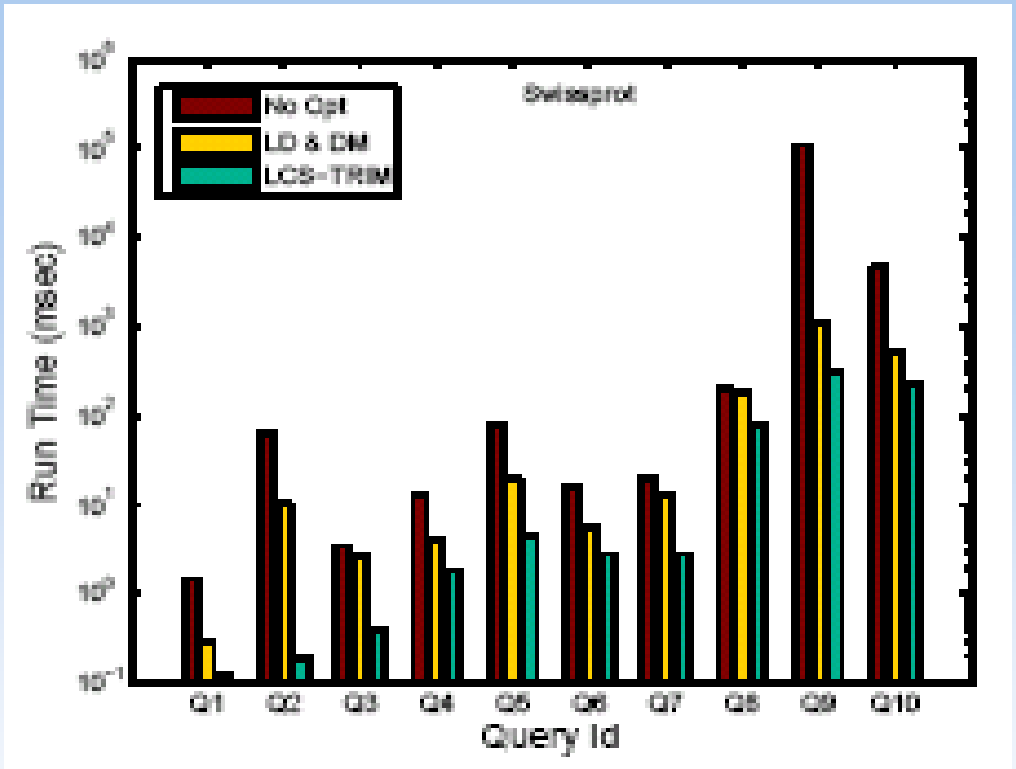


- In the backtrack, say A9 is a match but D5 is not a match, we won't continue to process B4 or B2. Prune M5 and M6 early! Instead, check D3.

Results

- With/without optimization
- Compare with PRIX
- Compare with TwigStack

With/without optimization



- No Opt
- Label Filtering & Dominant Match
- LCS-TRIM (back tract and structure match together)

Compare with PRIX

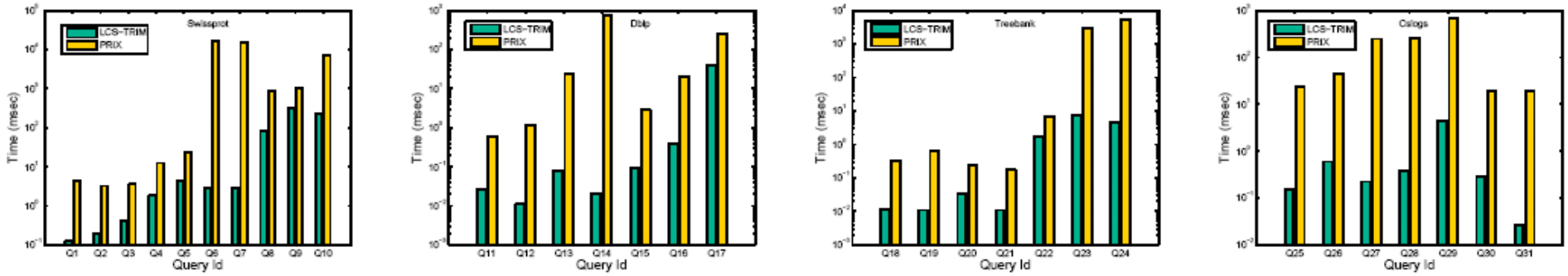


Figure 4: Performance comparison with PRIX on different data sets

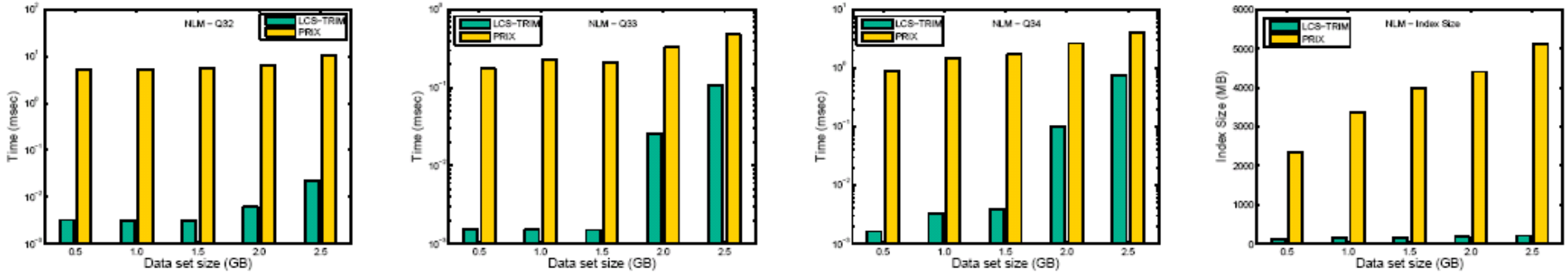
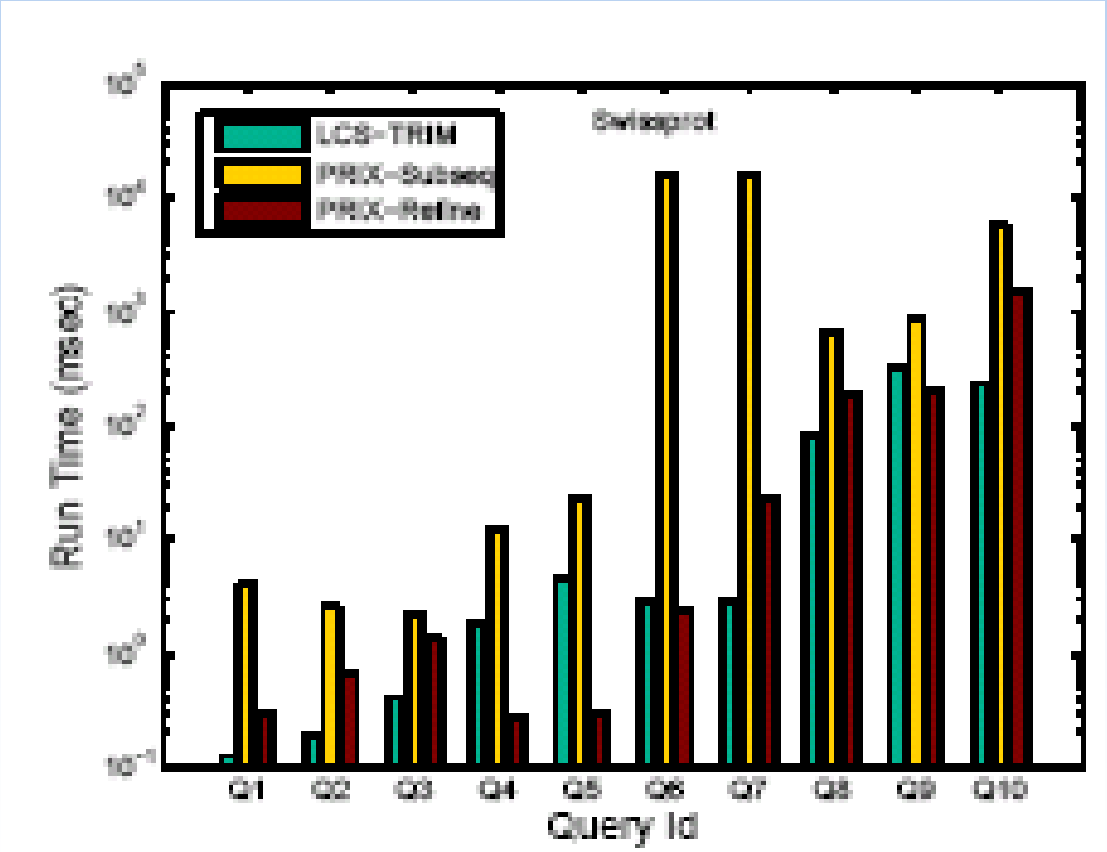


Figure 5: Performance and Index size comparison on NLM data set

PRIX

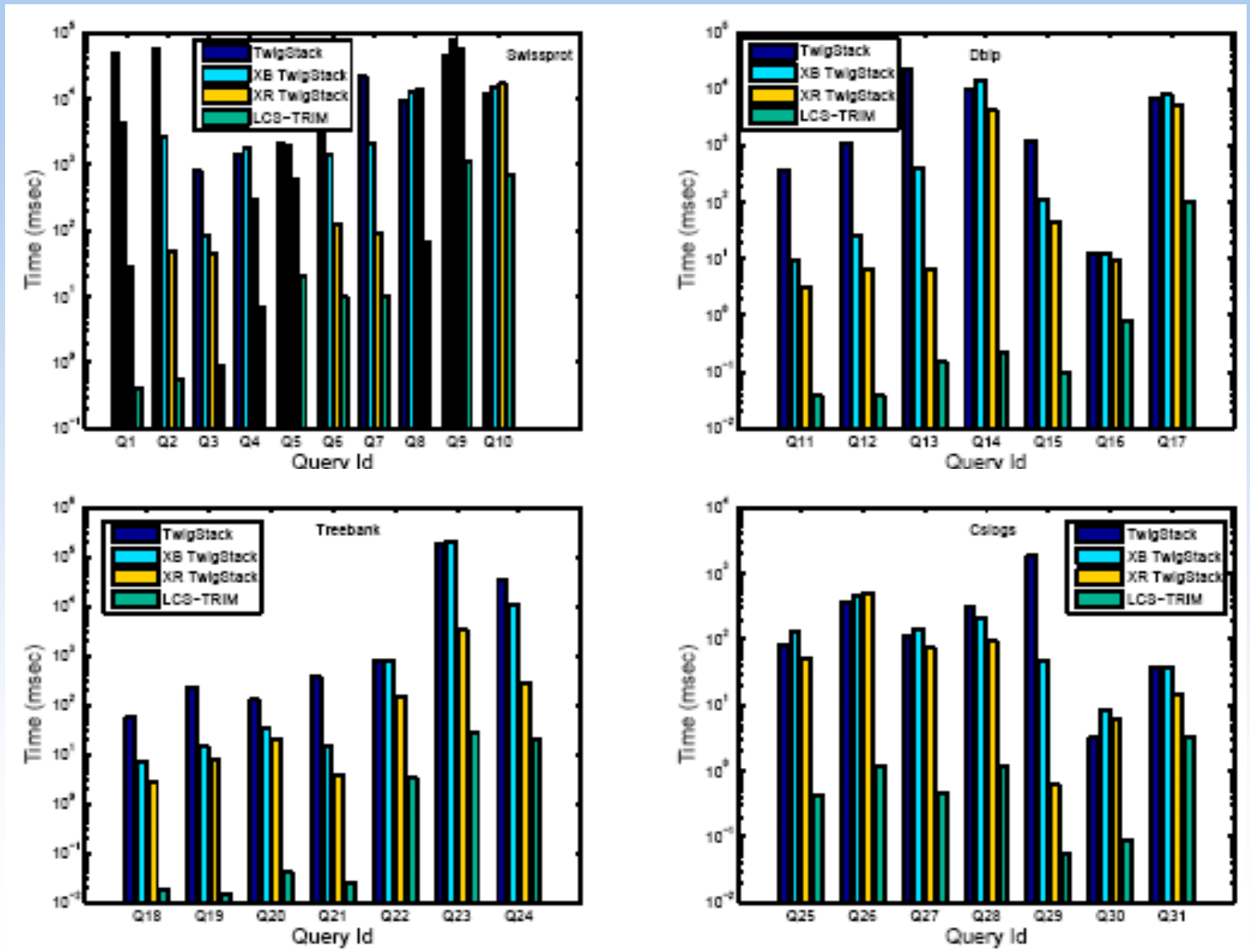
- PRIX: subsequence matching + structure refinements (3 phases)



Why?

- PRIX uses B+tree, virtual trie and node scope to do the subsequence match. LCS-TRIM uses dynamic programming.
- PRIX takes all the subsequences (false positive intermediate results) to do the structure refinements. LCS-TRIM prunes them very early.

Compare with TwigStack



Conclusion

- Novel sequence based representations
- Using dynamic programming of LCS
- Using inverted tree index
- Using several optimizations
- Prune out false candidate matches early
- Magnitude speedup over PRIX and TwigStack

Thank you!

Questions?