Approximate Joins for Data-Centric XML

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Outline

1 Motivation

2 Windowed *pq*-Grams for Data-Centric XML
- Windowed *pq*-Grams
- Tree Sorting
- Forming Bases

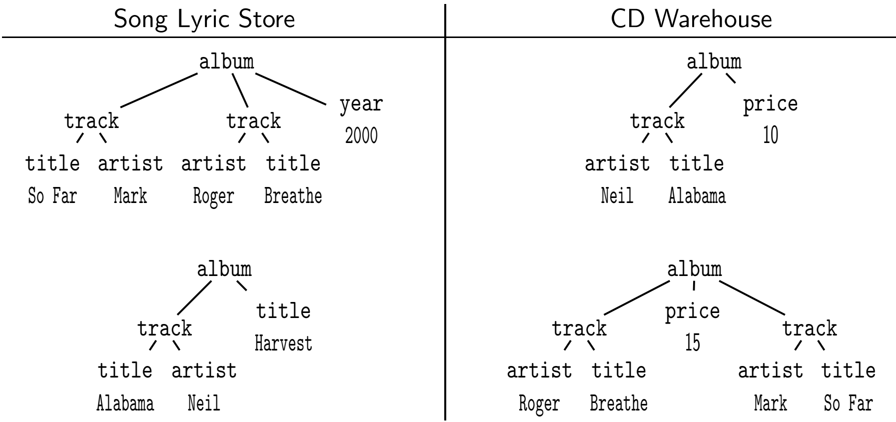
3 Efficient Approximate Joins with Windowed *pq*-Gram

4 Experiments

5 Related Work

6 Conclusion and Future Work

Approximate Join on Music CDs



- **Query:** Give me all album pairs that represent the same music CDs.

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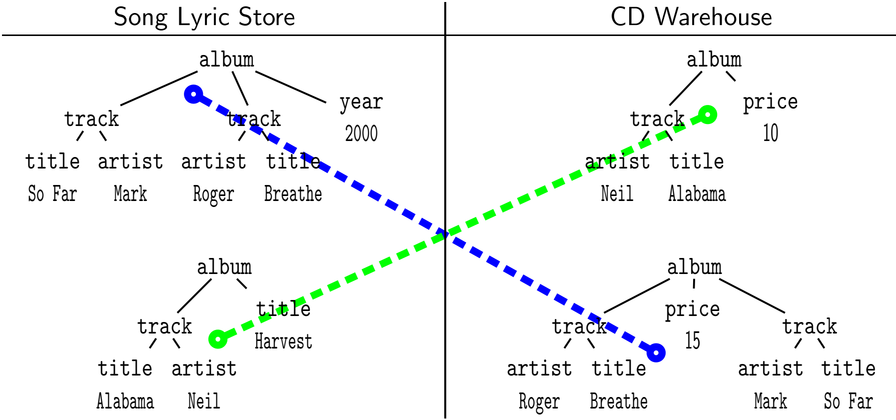

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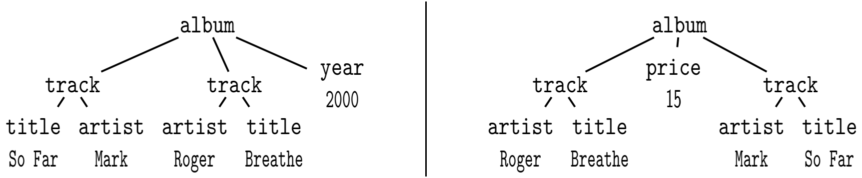

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  Minimum number of **node edit operations** (insert, delete, rename) that transforms one ordered tree into the other.

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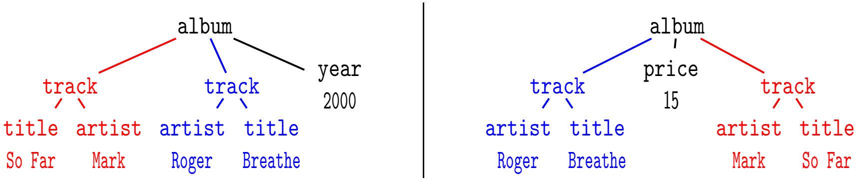
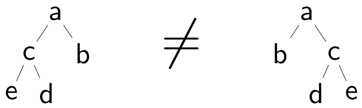


- **Standard solution $O(n^3)$:** tree edit distance
  Minimum number of **node edit operations** (insert, delete, rename) that transforms one ordered tree into the other.
- **Problem:** permuted subtrees are deleted/re-inserted node by node

Ordered vs. Unordered Trees

Ordered Trees
sibling order matters



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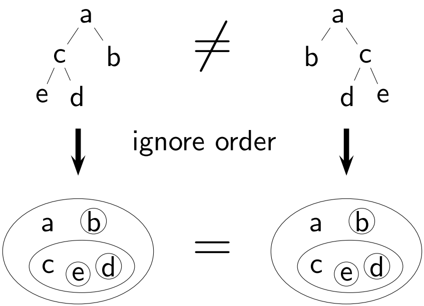

Unordered Trees
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sibling order ignored

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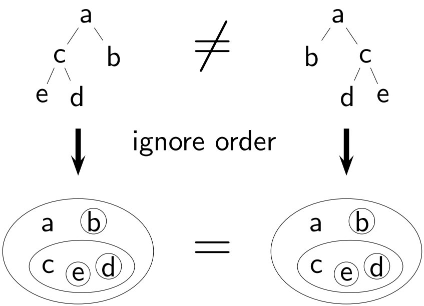

- **Edit distance** between unordered trees: **NP-complete**
  $\longrightarrow$ all sibling permutations must be considered!

Problem Definition

Find an **effective distance** for the approximate matching of hierarchical data represented as **unordered labeled trees** that is **efficient for approximate joins**.

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Naive approaches that fail:

- unordered tree edit distance: NP-complete
- allow subtree move: NP-hard
- compute minimum distance between all permutations: $O(n!)$
- sort by label and use ordered tree edit distance: error $O(n)$

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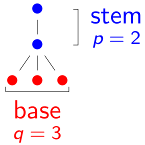
Our Solution: Windowed *pq*-Grams

- **Windowed pq-Gram:** small subtree with stem and base



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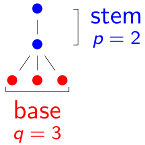

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- **Key Idea:** split unordered tree into set of windowed *pq*-grams that is
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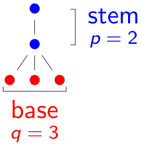

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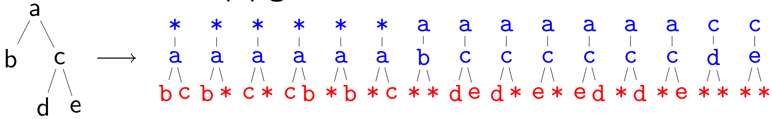
- **Intuition:** similar unordered trees have similar windowed *pq*-grams
- **Systematic computation** of windowed *pq*-grams
  1. **sort** the children of each node by their label (works OK for *pq*-grams)
  2. **simulate permutations** with a **window**
  3. **split** tree into windowed *pq*-grams

Implementation of Windowed *pq*-Grams

- **Set of windowed *pq*-grams:**



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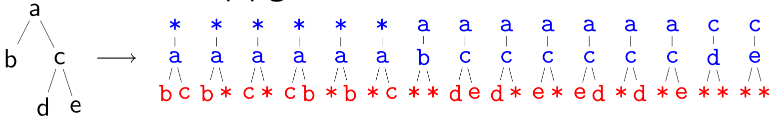
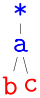


- **Hashing:** map *pq*-gram to integer:



$\xrightarrow{\textit{serialize}}$ (*, a, b, c) $\xrightarrow{\textit{(shorthand)}}$ *abc $\xrightarrow{\textit{hash}}$ 0973

label l	$h(l)$
*	0
a	9
b	7
c	3
...	...

Note: labels may be strings of arbitrary length!

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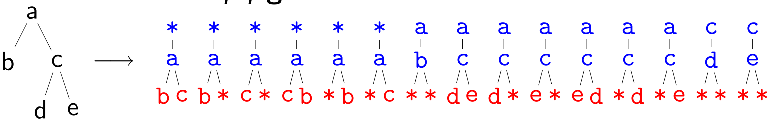

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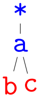

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- ***pq*-Gram index:** bag of hashed *pq*-grams

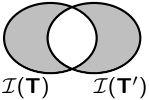
$$\mathcal{I}(\mathbf{T}) = \{0973, 0970, 0930, 0937, 0907, 0903, 9700, 9316, 9310, 9360, 9361, 9301, 9306, 3100, 3600\}$$

Tree is represented by a bag of integers!

The Windowed *pq*-Gram Distance

- The **windowed** *pq*-**gram distance** between two trees, **T** and **T**′:

$$\text{dist}^{pq}(\mathbf{T}, \mathbf{T}') = |\mathcal{I}(\mathbf{T}) \uplus \mathcal{I}(\mathbf{T}')| - 2|\mathcal{I}(\mathbf{T}) \cap \mathcal{I}(\mathbf{T}')|$$



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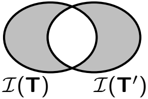
  - ✓ self-identity: $x = y \quad \Rightarrow \text{dist}^{pq}(x, y) = 0$



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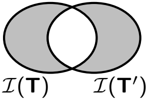

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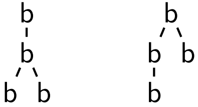

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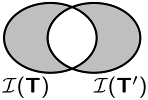

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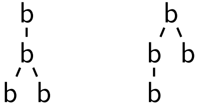

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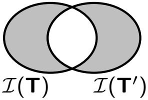

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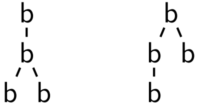

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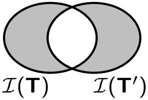

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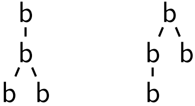

- **Runtime** for the distance computation is $O(n \log n)$.

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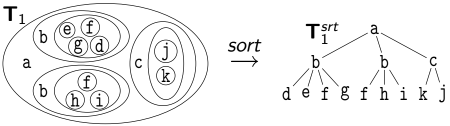

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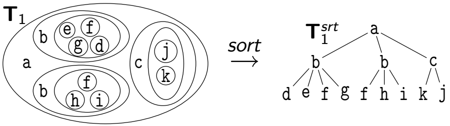

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✓ **Windowed *pq*-Grams**: tree sorting works OK

✘ Edit Distance: Tree Sorting Does Not Work

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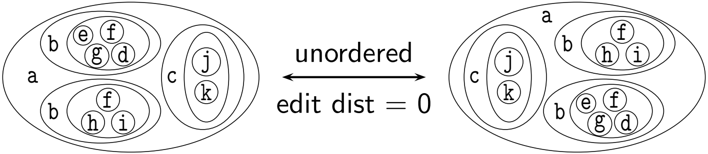

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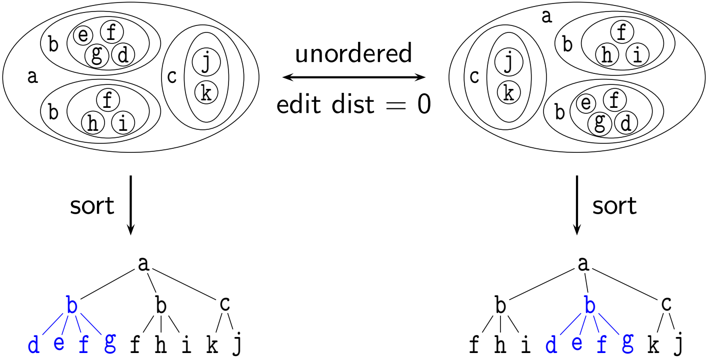

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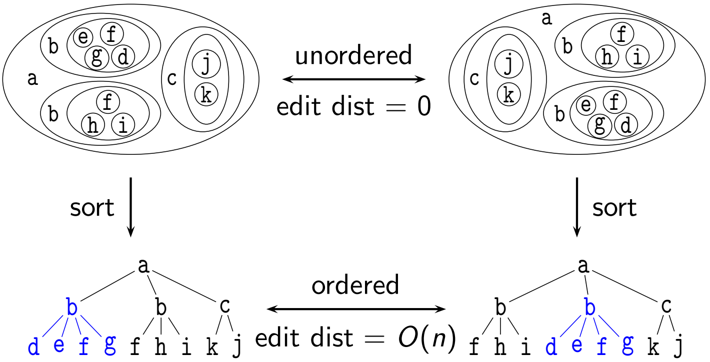
1. **Non-unique sorting**: edit distance $O(n)$ for identical trees



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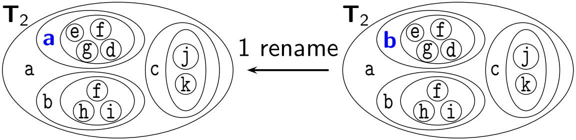

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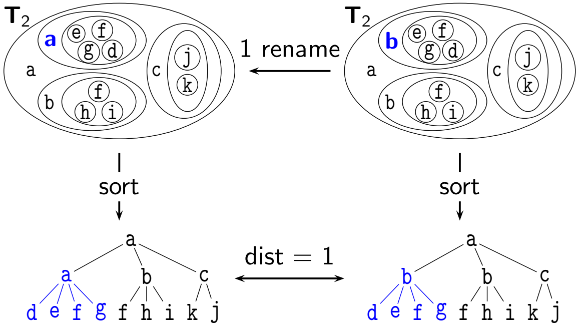

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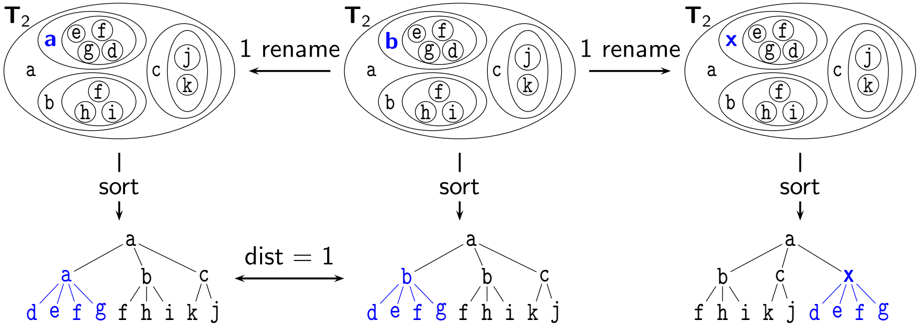

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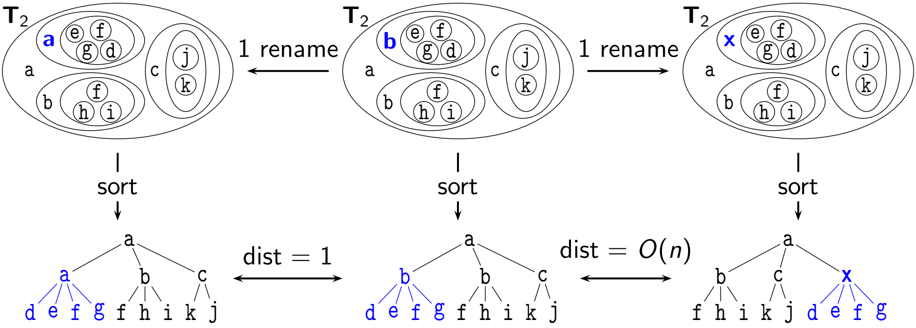
2. **Node renaming**: edit distance depends on node label

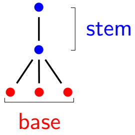


✓ Windowed *pq*-Grams: Tree Sorting Works OK

Theorem (Local Effect of Node Reordering)

If k children of a node are reordered, i.e., their subtrees are moved, only $O(k)$ windowed pq-grams change.

- **Proof (idea)**:
  - *pq*-grams consist of a stem and a base
  - stems are invariant to the sibling order
  - bases: only the $O(k)$ *pq*-grams with the reordered nodes in the bases change



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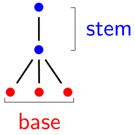

✓ **Non-unique sortings** are equivalent: distance is 0 for identical trees

✓ **Node renaming** is independent of the node label

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How To Form Bases?

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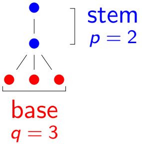

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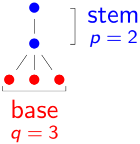
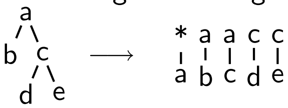


- **Stems**: ignore sibling order



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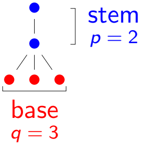

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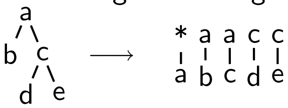

- **Bases:** do not ignore sibling order!

Requirements for Bases

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  - detection of node moves
  - robustness to different sortings
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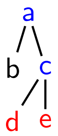
- **Our solution**:
  - **windows**: simulate all permutations within a window
  - **wrapping**: wrap windows that extend beyond the right border
  - **dummies**: extend small sibling sets with dummy nodes

Solution: Windowed *pq*-Gram Bases

Algorithm 1: **Form bases** from a sorted sibling sequence

- **Example**: stem, sorted sibling sequence, window $w = 3$



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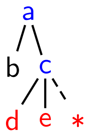
Algorithm 2: **Form bases** from a sorted sibling sequence

---

1 if *sibling sequence* < *window* then extend with dummy nodes;

- **Example**: stem, sorted sibling sequence, window $w = 3$



Solution: Windowed *pq*-Gram Bases

Algorithm 3: **Form bases** from a sorted sibling sequence

1 if *sibling sequence* < *window* then extend with dummy nodes;
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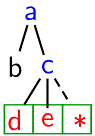

Solution: Windowed *pq*-Gram Bases

Algorithm 4: **Form bases** from a sorted sibling sequence

```
if sibling sequence < window then extend with dummy nodes;
initialize window: start with leftmost node;
repeat
    form bases in window: all q-permutations that contain start node;

until processed all window positions
```

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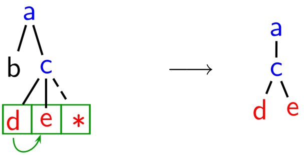


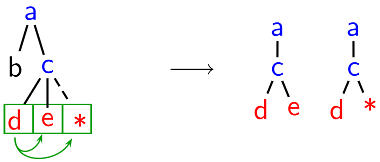
Solution: Windowed *pq*-Gram Bases

Algorithm 5: **Form bases** from a sorted sibling sequence

```
if sibling sequence < window then extend with dummy nodes;
initialize window: start with leftmost node;
repeat
    form bases in window: all q-permutations that contain start node;

until processed all window positions
```

- **Example**: stem, sorted sibling sequence, window $w = 3$



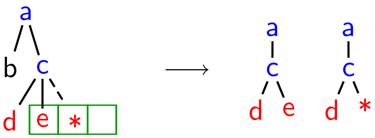
Solution: Windowed *pq*-Gram Bases

Algorithm 6: **Form bases** from a sorted sibling sequence

if *sibling sequence* < *window* then extend with dummy nodes;
initialize window: start with leftmost node;
repeat
    form bases in window: all *q*-permutations that contain start node;
    shift window to the right by one node;

until *processed all window positions*

- **Example**: stem, sorted sibling sequence, window $w = 3$

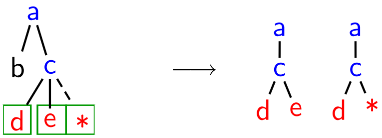


Solution: Windowed *pq*-Gram Bases

Algorithm 7: Form bases from a sorted sibling sequence

```
if sibling sequence < window then extend with dummy nodes;
initialize window: start with leftmost node;
repeat
    form bases in window: all q-permutations that contain start node;
    shift window to the right by one node;
    if window extends the right border then wrap window;
until processed all window positions
```

- **Example**: stem, sorted sibling sequence, window $w = 3$



Solution: Windowed *pq*-Gram Bases

Algorithm 8: **Form bases** from a sorted sibling sequence

```
if sibling sequence < window then extend with dummy nodes;
initialize window: start with leftmost node;
repeat
    form bases in window: all q-permutations that contain start node;
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    if window extends the right border then wrap window;
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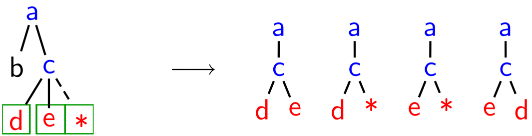
```

- **Example**: stem, sorted sibling sequence, window $w = 3$

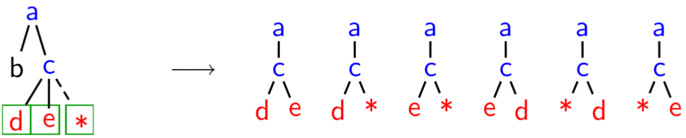


Solution: Windowed *pq*-Gram Bases

Algorithm 9: Form bases from a sorted sibling sequence

```
if sibling sequence < window then extend with dummy nodes;
initialize window: start with leftmost node;
repeat
    form bases in window: all q-permutations that contain start node;
    shift window to the right by one node;
    if window extends the right border then wrap window;
until processed all window positions
```

- **Example**: stem, sorted sibling sequence, window $w = 3$



Solution: Windowed *pq*-Gram Bases

Algorithm 10: Form bases from a sorted sibling sequence

```
if sibling sequence < window then extend with dummy nodes;
initialize window: start with leftmost node;
repeat
    form bases in window: all q-permutations that contain start node;
    shift window to the right by one node;
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until processed all window positions
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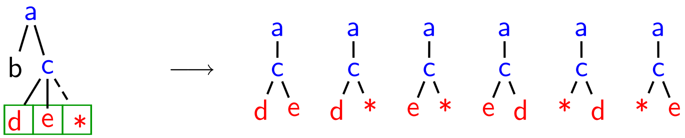
- **Example**: stem, sorted sibling sequence, window $w = 3$



Optimal Windowed *pq*-Grams

Theorem (Optimal Windowed *pq*-Grams)

For trees with fanout f, windowed pq-grams with base size $q = 2$ and window size $w = \frac{f+1}{2}$ have the following properties:

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3. **Balanced node weight:**

   Each non-root node appears in exactly $2w - 2$ bases.

Illustration: Detection of Node Moves

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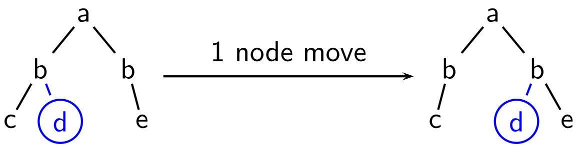

Goal: bases must change

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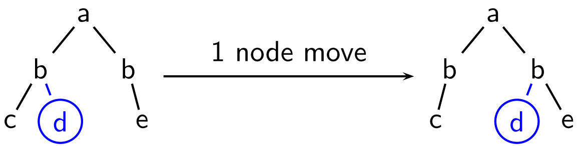

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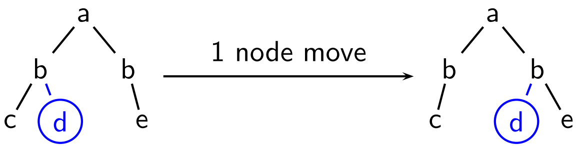

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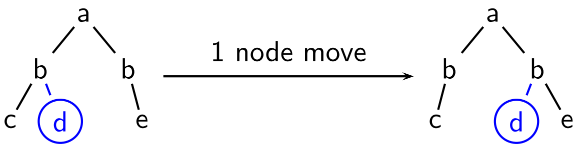

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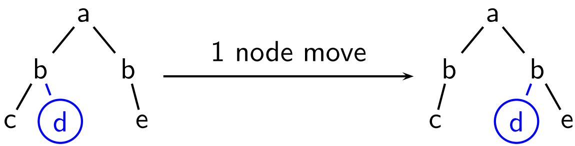

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Windowed *pq*-grams detect node moves.

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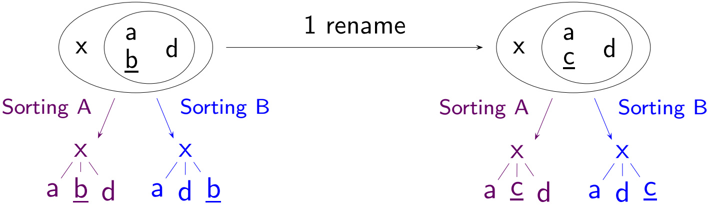

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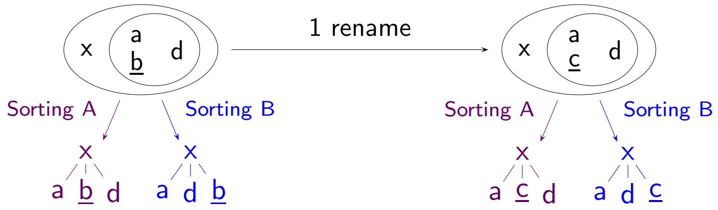

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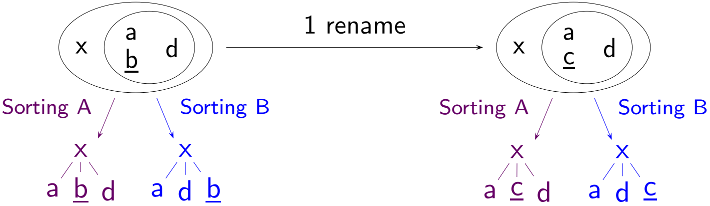

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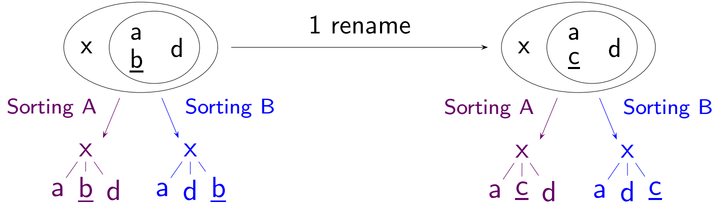

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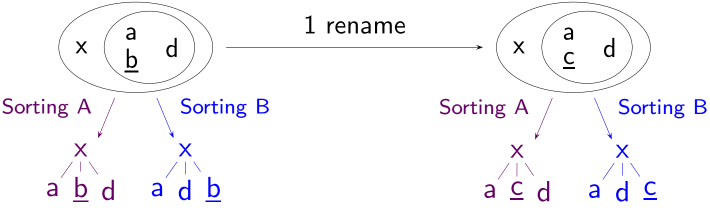

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Windowed *pq*-grams: Robust to different sortings.

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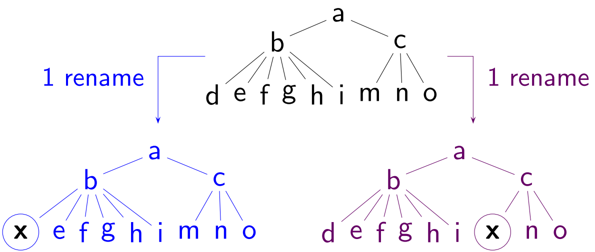

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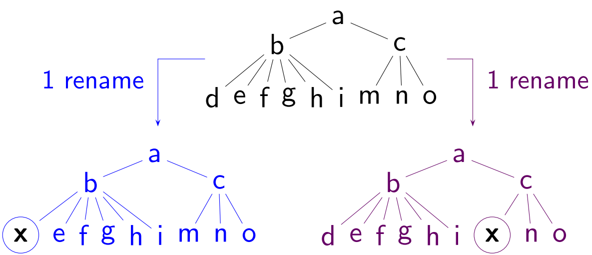

Goal:	Same number of bases change for both renames.	
Permutations:	60/137 bases change	6/137 bases change

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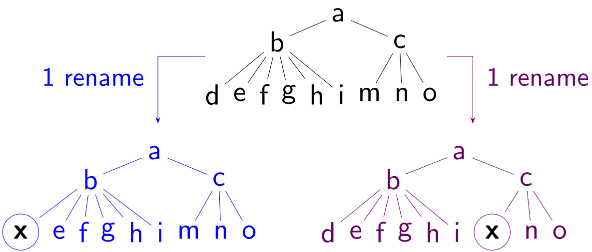

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Illustration: Balancing the Node Weight

- **Permutations**: all permutations of size q form a base
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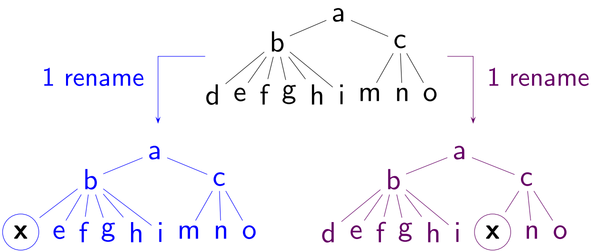

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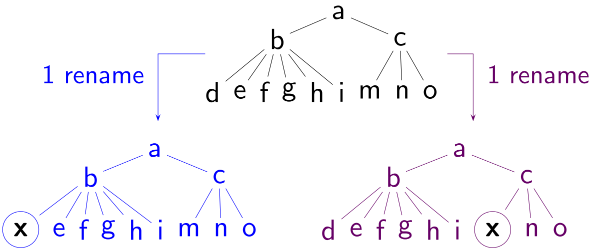

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Windowed *pq*-grams: Node weight is independent of sibling number.

Outline

1. Motivation

2. Windowed *pq*-Grams for Data-Centric XML
   - Windowed *pq*-Grams
   - Tree Sorting
   - Forming Bases

3. Efficient Approximate Joins with Windowed *pq*-Gram

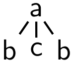
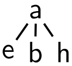
4. Experiments

5. Related Work

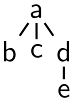
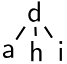
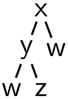
6. Conclusion and Future Work

Approximate Join

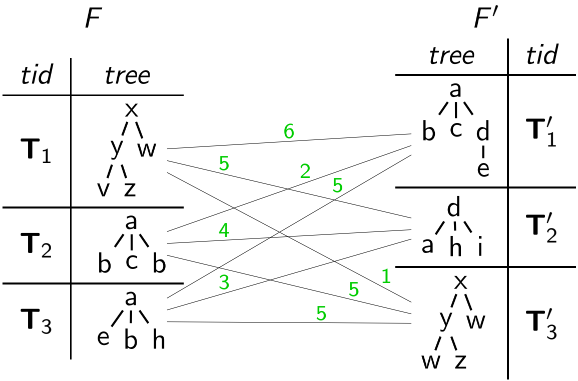
F

tid	*tree*
$\mathbf{T}_1$	
$\mathbf{T}_2$	
$\mathbf{T}_3$	

F'

tree	*tid*
	$\mathbf{T}'_1$
	$\mathbf{T}'_2$
	$\mathbf{T}'_3$

Approximate Join



- **Simple approach:** distance join
  1. compute distance between all pairs of trees

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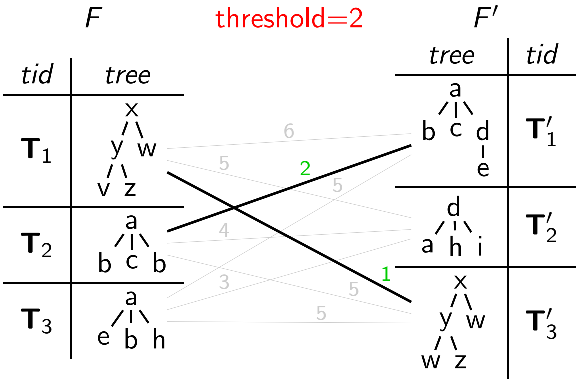

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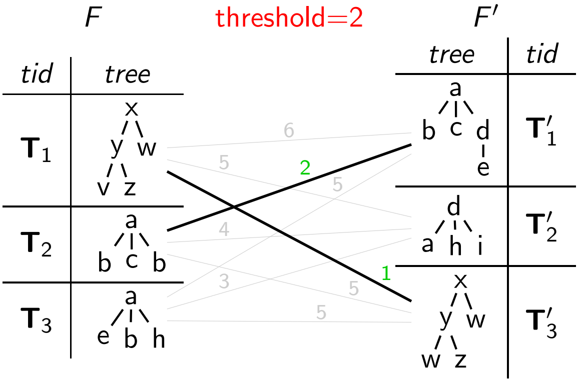

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- Very **expensive**: N^2 distance computations!

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- **Distance join:** expensive
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- **Solution:** reduce **distance join to equality join** on *pq*-grams

Reducing a Distance Join to an Equality Join

- **Distance join** between trees: N^2 intersections between integer bags

$\{1,7\}_a$	$\{1,7\}_d$
$\{1,0\}_b$	$\{5,5\}_e$
$\{4,6\}_c$	$\{0,8\}_f$

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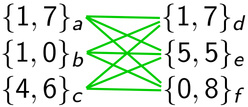

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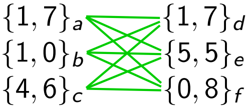

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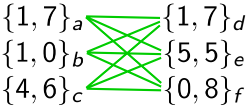

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- **Optimized** *pq***-gram join**: empty intersections are never computed!
  1. union

     $\{1_a, 7_a, 1_b, 0_b, 4_c, 6_c\}$ $\quad$ $\{1_d, 7_d, 5_e, 5_e, 0_f, 8_f\}$

Reducing a Distance Join to an Equality Join

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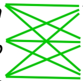
$\{1,0\}_b$  $\{5,5\}_e$
$\{4,6\}_c$ $\{0,8\}_f$

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- **Optimized *pq*-gram join**: empty intersections are never computed!

1. union

   $\{1_a, 7_a, 1_b, 0_b, 4_c, 6_c\}$ $\qquad$ $\{1_d, 7_d, 5_e, 5_e, 0_f, 8_f\}$

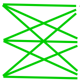
2. sort

0_b	0_f
1_a	1_d
1_b	5_e
4_c	5_e
6_c	7_d
7_a	8_f

Reducing a Distance Join to an Equality Join

- **Distance join** between trees: N^2 intersections between integer bags

$\{1,7\}_a$ $\{1,7\}_d$
$\{1,0\}_b$ $\{5,5\}_e$
$\{4,6\}_c$ $\{0,8\}_f$



$\|a \cap d\| = 2$	$\|a \cap e\| = 0$	$\|a \cap f\| = 0$
$\|b \cap d\| = 1$	$\|b \cap e\| = 0$	$\|b \cap f\| = 1$
$\|c \cap d\| = 0$	$\|c \cap e\| = 0$	$\|c \cap f\| = 0$

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     $\{1_a, 7_a, 1_b, 0_b, 4_c, 6_c\}$ $\{1_d, 7_d, 5_e, 5_e, 0_f, 8_f\}$
  2. sort
  3. merge-join

0_b	0_f
1_a	1_d
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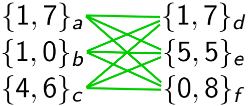

$|a \cap d| = 2 \quad |a \cap e| = 0 \quad |a \cap f| = 0$

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1_a	1_d
1_b	5_e
4_c	5_e
6_c	7_d
7_a	8_f

$|b \cap f|$

Reducing a Distance Join to an Equality Join

- **Distance join** between trees: N^2 intersections between integer bags

$\{1,7\}_a \quad \{1,7\}_d$

$\{1,0\}_b \quad \{5,5\}_e$

$\{4,6\}_c \quad \{0,8\}_f$

$\lvert a \cap d\rvert = 2$	$\lvert a \cap e\rvert = 0$	$\lvert a \cap f\rvert = 0$
$\lvert b \cap d\rvert = 1$	$\lvert b \cap e\rvert = 0$	$\lvert b \cap f\rvert = 1$
$\lvert c \cap d\rvert = 0$	$\lvert c \cap e\rvert = 0$	$\lvert c \cap f\rvert = 0$

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1. union

   $\{1_a, 7_a, 1_b, 0_b, 4_c, 6_c\}$ $\quad$ $\{1_d, 7_d, 5_e, 5_e, 0_f, 8_f\}$

2. sort
3. merge-join

   0_b — 0_f
   1_a — 1_d
   1_b $\quad$ 5_e
   4_c $\quad$ 5_e
   6_c $\quad$ 7_d
   7_a $\quad$ 8_f

$\lvert b \cap f\rvert$ |

$\lvert a \cap d\rvert$ |

Reducing a Distance Join to an Equality Join

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  3. merge-join
     0_b 0_f
     1_a 1_d
     1_b 5_e
     4_c 5_e
     6_c 7_d
     7_a 8_f

     $|b \cap f|$
     $|a \cap d|$
     $|b \cap d|$

Reducing a Distance Join to an Equality Join

- **Distance join** between trees: N^2 intersections between integer bags

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1_a — 1_d
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4_c 5_e
6_c 7_d
7_a 8_f

$|b \cap f|$ I
$|a \cap d|$ II
$|b \cap d|$ I

Outline

1 Motivation

2 Windowed *pq*-Grams for Data-Centric XML
- Windowed *pq*-Grams
- Tree Sorting
- Forming Bases

3 Efficient Approximate Joins with Windowed *pq*-Gram

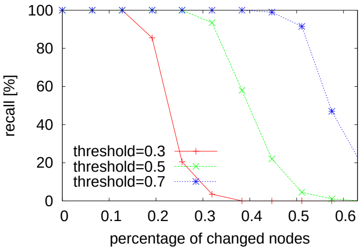
4 Experiments

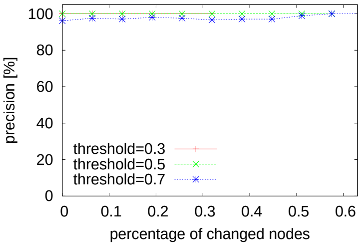
5 Related Work

6 Conclusion and Future Work

Effectiveness of the Windowed *pq*-Gram Join

Effectiveness of the Windowed *pq*-Gram Join



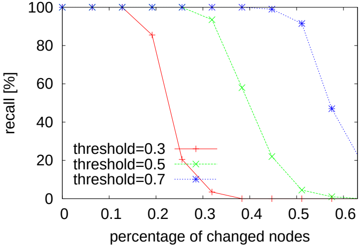


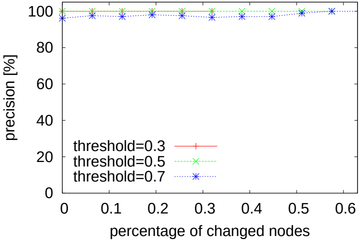
Experiment: match **DBLP** articles

- add noise to articles
  (missing elements and spelling mistakes)
- approximate join between original and noisy data
- measure precision and recall for different thresholds

Windowed *pq*-grams are effective for data-centric XML

Effectiveness of the Windowed *pq*-Gram Join





Experiment: match **DBLP** articles

- add noise to articles (missing elements and spelling mistakes)
- approximate join between original and noisy data
- measure precision and recall for different thresholds

Datasets:

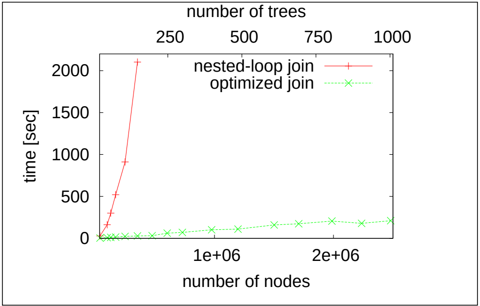
- **DBLP:** articles depth 1.9, 15 nodes (max 1494 nodes)
- **SwissProt:** protein descriptions depth 3.5, 104 nodes (max 2640 nodes)
- **Treebank:** tagged English sentences depth 6.9 (max depth 30), 43 nodes

Windowed *pq*-grams are effective for data-centric XML

Efficiency of the Optimized *pq*-Gram Join

Efficiency of the Optimized *pq*-Gram Join

Optimized *pq*-gram join: very efficient



- compute nested-loop join between trees
- compute optimized *pq*-gram join between trees
- measure wallclock time

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Distances between Unordered Trees

Edit Distances between Unordered Trees

- [Zhang et al., 1992]: proof for NP-completeness
- [Kailing et al., 2004]: lower bound for a restricted edit distance
- [Chawathe and Garcia-Molina, 1997]: $O(n^3)$ heuristics
- Our solution: $O(n \log n)$ approximation

Approximate Join

- [Gravano et al., 2001]: efficient approximate join **for strings**

Conclusion and Future Work

Windowed *pq*-grams for unordered trees:

- $O(n \log n)$ approximation of NP-complete edit distance
- **Key problem:** all permutations must be considered
- **Our approach:** sort trees and simulate permutations with window
- **Sorting:** works for *pq*-grams, but not for edit distance
- **Window technique** guarantees core properties
  - detection of node moves
  - robustness to different sortings
  - balanced node weight
- **Efficient approximate join**: reduces distance join to equality join

Conclusion and Future Work

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- **Efficient approximate join**: reduces distance join to equality join

Future work:

- incremental updates of the windowed *pq*-gram index
- include approximate string matching into XML distance

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