XML Indexing II

CPS 216
Advanced Database Systems

Announcements (April 6)

- Welcome back!
- Homework #3 due tonight

XML indexing overview (review)

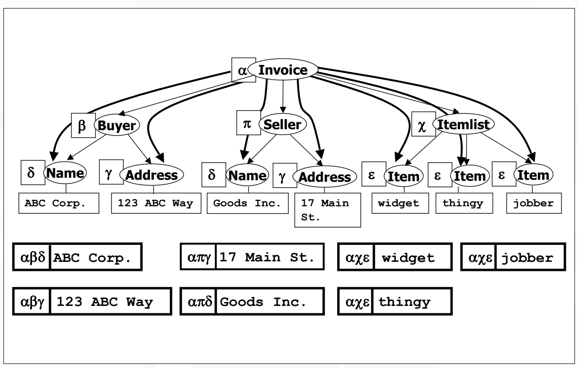
- It is a jungle out there
  - Different representation scheme lead to different indexes
  - Will we ever find the "One Tree" that rules them all?
- Building blocks: B^+-trees, inverted lists, tries, etc.
- Indexes for node/edge-based representations (graph)
- Indexes for interval-based representations (tree)
- ☞ Indexes for path-based representations (tree)
- ☞ Indexes for sequence-based representations (tree)
- ☞ Structural indexes (graph)

Index Fabric: a path-based index

Cooper et al. "A Fast Index for Semistructured Data." *VLDB* 2001

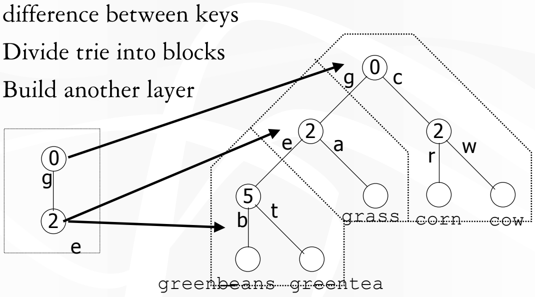
- Use a label-path encoding for XML
  - Each element is associated with a sequence of labels on the path from the root (e.g., `/Invoice/Buyer/Name/ABC Corp.`)
  - Encode the label path as a string (e.g., `/Invoice/Buyer/Name` $\rightarrow \alpha\beta\delta$)
- Index all label paths in a Patricia trie
  - And try to make the trie balanced and I/O-efficient

Example of label paths in Index Fabric



Balancing Patricia trie in Index Fabric

- Recall that Patricia trie indexes first point of difference between keys
- Divide trie into blocks
- Build another layer



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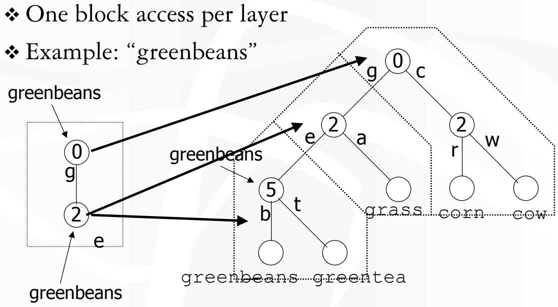
Searching Patricia trie in Index Fabric

- Start searching in the root layer
- One block access per layer
- Example: “greenbeans”



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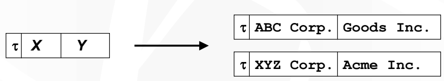
Refined paths in Index Fabric

- Queries supported by Index Fabric so far:
  - Label paths from the root (e.g., `/Invoice/Buyer/Name/`)
  - How about `//Buyer/Name`, or `//Buyer/Name|Address`?
- Refined paths: frequent queries
  - Just invent labels for these queries and index them in the same Patricia trie
  - Example: find invoices where *X* sold to *Y*



☞Extra refined paths → more space required

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ViST: a sequence-based index

Wang et al. “ViST: A Dynamic Index Method for Querying XML Data by Tree Structures.” *SIGMOD* 2003

- Use a sequence-based encoding for XML
- Turn twig queries to subsequence matches
- Index sequences in a virtual trie using interval-based encoding

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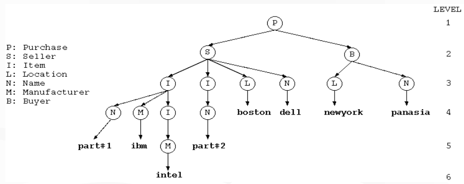
Sequence representation of XML



- A sequence of (*symbol*, *prefix*) pairs, in depth-first order:
  - (P, ε), (S, P), (I, PS), (N, PSI), (v_1, PSIN), (M, PSI), (v_2, PSIM), (I, PSI), (M, PSII), (v_3, PSIIM), (I, PS), (N, PSI), (v_4, PSIN), (L, PS), (v_5, PSL), (N, PS), (v_6, PSN), (B, P), (L, PB), (v_7, PBL), (N, PB), (v_8, PBN)
- ☞ What is the worst-case storage requirement?
- ☞ Would listing symbols in depth-first order be sufficient?

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Sequence representation of twigs

- Twigs can be represented sequences as well

	Path Expression	Structure-Encoded Sequence
Q_1:	$/Purchase/Seller/Item/Manufacturer$	$(P,\epsilon)(S,P)(I,PS)(M,PSI)$
Q_2:	$/Purchase/[Seller[Loc=v_5]]/Buyer[Loc=v_7]$	$(P,\epsilon)(S,P)(L,PS)(v_5,PSL)(B,P)(L,PB)(v_7,PBL)$
Q_3:	$/Purchase/*/[Loc=v_5]$	$(P,\epsilon)(L,P*)(v_5,P*L)$
Q_4:	$/Purchase//[Manufacturer=v_3]$	$(P,\epsilon)(M,P//)(v_3,P//M)$

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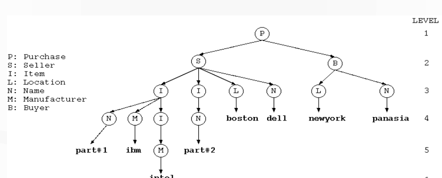
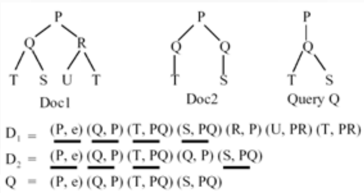
Matching twigs as sequences



- Data: (P, ε), (S, P), (I, PS), (N, PSI), (v_1, PSIN), (M, PSI), (v_2, PSIM), (I, PSI), (M, PSII), (v_3, PSIIM), (I, PS), (N, PSI), (v_4, PSIN), (L, PS), (v_5, PSL), (N, PS), (v_6, PSN), (B, P), (L, PB), (v_7, PBL), (N, PB), (v_8, PBN)
- Query (Boston seller New York buyer): (P, ε), (S, P), (L, PS), (v_5, PSL), (B, P), (L, PB), (v_7, PBL)
- ☞ Find a (non-contiguous) subsequence of data that matches the query

False alarms



- /P/Q[T]/S
  - Match sequences for /P/Q[T]/S and /P/[Q/T]/Q/S
  - Compute the difference between the answers
  - But what if a document exhibit both structures?

Indexing sequences with a trie

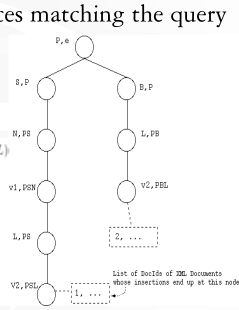
- Just insert sequences into a trie
- Search the trie for subsequences matching the query
  - Expensive because subsequences do not need to be contiguous

$Doc_1 : (P,\epsilon)(S,P)(N,PS)(v_1,PSN)(L,PS)(v_2,PSL)$

$Doc_2 : (P,\epsilon)(B,P)(L,PB)(v_2,PBL)$

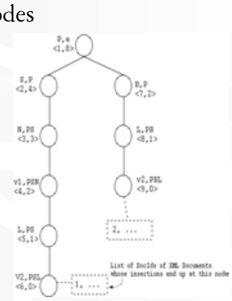
$Q_1 : (P,\epsilon)(B,P)(L,PB)(v_2,PBL)$

$Q_2 : (P,\epsilon)(L,P*)(v_2,P*L)$



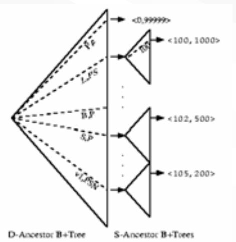
"Virtual trie" idea

- Use (*left*, *size*) to encode trie nodes
  - *size* = *right* – *left*
  - Supports efficient "skipping"
- Index in a regular B^+-tree
- No need to store the trie itself



ViST structures

- D-Ancestor B^+-tree indexes trie nodes by (*symbol*, *prefix*)
  - Facilitates prefix matching (checking for ancestor-descendent relationships in documents)
- Leaf nodes point to S-Ancestor B^+-trees, which further index nodes by (*left*, *size*)
  - Facilitates skipping in the trie (checking for ancestor-descendent relationships in the trie)
- Subsequence matching → repeated index lookups



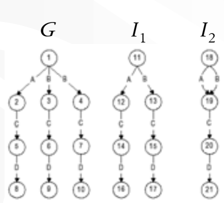
Lore's DataGuide: a structural index

Goldman & Widom. "DataGuides: Enabling Query Formulation and Optimization in Semistructured Databases." *VLDB*, 1997

- Given an XML data graph G, a DataGuide is an index graph I with the following properties
  - Every label path in G also occurs in I
    - Complete coverage
  - Every label path in I also occurs in G
    - Accurate coverage
  - Every label path in I (starting from a particular object) is unique (i.e., I is a DFA)
    - Efficient search: a label path of length n traverses n edges and ends at one node
  - Each index node in I points to its extent: a set of data nodes in G
    - Label path query on G → label path query on I

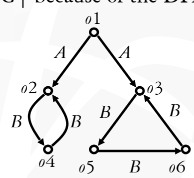
Strong DataGuide

- Let p, p' be two label path expressions and G a graph; define $p \equiv_G p'$ if $p(G) = p'(G)$
  - That is, p and p' are indistinguishable on G
- I is a strong DataGuide for a database G if the equivalence relations $\equiv_I$ and $\equiv_G$ are the same
- Example
  - I_1 is strong; I_2 is not
  - A.C(G) = { 5 }, B.C(G) = { 6, 7 }
    - Not equal
  - A.C(I_2) = { 20 }, B.C(I_2) = { 20 }
    - Equal



Size of DataGuides

- If G is a tree, then $|I| \leq |G|$
  - Linear construction time
- In the worst case, the size of a strong DataGuide may be exponential in $|G|$ because of the DFA requirement



☞ Relax the DFA requirement?

NFA-based structural indexes

- Defined using an equivalence relation (based on the graph structure)
  - Each index node v corresponds to an equivalence class of data nodes in G (denoted *v.extent*)
  - There is a edge from u to v in I iff there exists a edge from a node in *u.extent* to a node in *v.extent*

☞ $|I| \leq |G|$ by definition because extents do not overlap; however, the structure is no longer a DFA

1-index

Milo & Suciu, "Index Structures for Path Expressions." *ICDT*, 1997

- "Perfect" equivalence relation: two data nodes are equivalent iff they are not distinguishable by label path expressions
  - That is, the sets of label path expressions that can reach them are the same
  - Too expensive to compute in practice
- 1-index uses a less perfect equivalent relation, bisimilarity, which is easier to compute
  - If two nodes are bisimilar, then they are not distinguishable by label path expressions
  - The converse is not necessary true
  - ☞ May result in larger indexes