Indexing and Querying XML Data for Regular Path Expressions

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What's the big deal?

- Numbering scheme for elements and attributes
- **XISS**
  - Indexing and storing system for XML
- Query processing paradigm
  - Decompose regular path expressions
  - Path-join algorithms to process these expressions

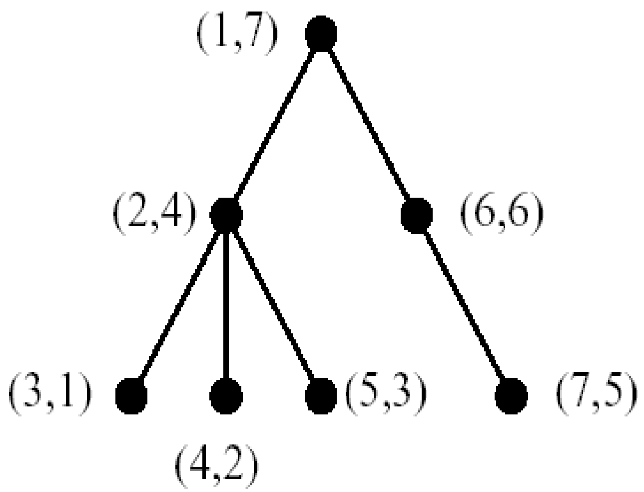
Storage for Retrieval

- Tree model for XML data
- Several XML query languages
  - Regular path expressions
- Approaches based on tree traversals are potentially expensive
- Optimal query plan
  - Value
    - Element names/values
    - Attribute names/values
  - Structure
    - Ancestor-descendant relationships

Numbering scheme

- *Extended preorder*
- Ancestor-descendant relationship between elements and attributes
- Support proposed join algorithms

Dietz's Numbering Scheme



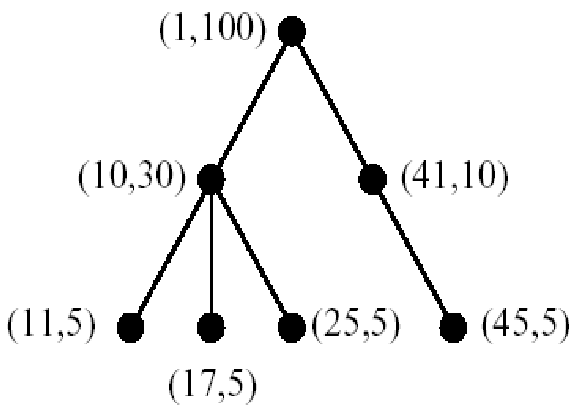
- First to use tree traversal order to determine the ancestor-descendant relationship between any pair of tree nodes
- Based on preorder and postorder

For two given nodes x and y of a tree T, x is an ancestor of y if and only if x occurs before y in the preorder traversal of T and after y in the post-order traversal

The Good and Bad

- The Good
  - Determine the ancestor-descendant relationship in constant time
- The Bad
  - Inflexible
  - Inserts/Deletes

The Extended Preorder Numbering Scheme



- Uses *extended preorder* and a *range of descendants*
- Each node has a pair of numbers
  - <order, size>
- For a tree node y and its parent x, *order(x) < order(y)* and *order(y) + size(y) <= order(x) + size(x)*
- The interval [*order(y), order(y)+size(y)*] is contained in the interval [order(x), order(x) + size(x)]
- For two sibling nodes x and y, if x is the predecessor of y in preorder traversal, order(x) + size(x) < order(y)
- For a tree node x, size(x) >= $\sum_y$size(y) for all y's that are a direct child of x

For two given nodes x and y of a tree T, x is an ancestor of y if and only if order(x) < order(y) <= order(x) + size(x).

The Good and the Bad

- The Good
  - More flexible
  - Tolerant of dynamic data updates
  - Order values of deleted nodes can be recycled
- The Bad
  - They don't tell us how they plan to recycle these order values

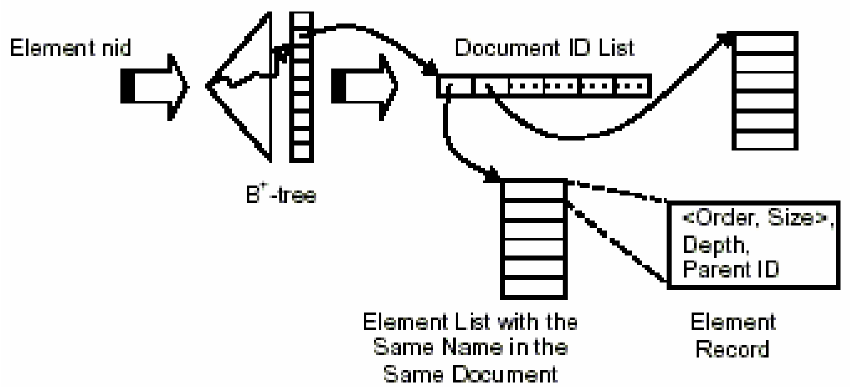
XISS

- **X**ML **I**ndexing and **S**torage **S**ystem
- Three major index structures
  - Element index
  - Attribute index
  - Structure index
- Two additional structures
  - Name index
  - Value table
- Data loader **(not discussed)**
- Query processor **(not discussed)**

XISS Components

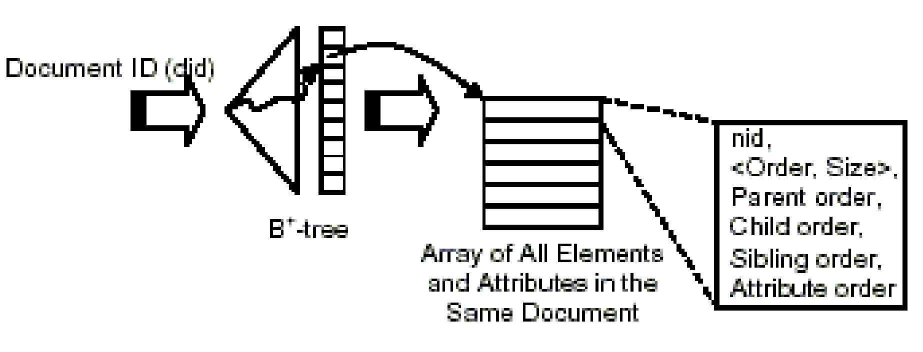
- Document id (did) for each XML document
- Name index
  - B+ tree
  - Name identifier (nid)
- Element, attribute, structure indices
  - B+ tree
  - Name identifiers (nid) as keys

Element and Attribute Indices



- Element index
  - Allows quick search for elements with the same name string
- Attribute index
  - Each record has a value identifier (vid)
    - Key into the value table

Structure Index



- Collection of linear arrays
  - Elements and attributes are sorted by the *order* value
  - Attributes are placed before their sibling elements

Supported operations

- For a given element name string, say figure, find a list of elements having the same name string (*i.e.* figure), grouped by documents which they belong to (element index)
- For a given attribute name string, say caption, find a list of attributes having the same name string (*i.e.*, caption), grouped by documents which they belong to (attribute index)
- For a given element, find its parent element and child elements (or attributes). For a given attribute, find its parent element (structure index)

Conventions and recommendations

- Conventional approaches
  - Top-down
    - Tree traversal cost
  - Bottom-up
    - Expensive if there are more ancestors and fewer descendants
  - Hybrid
    - Effectiveness not always guaranteed

Join Algorithms and Decomposing Path expressions

```
/chapter/ */figure[@caption="Tree Frogs"]
```

- Different basic subexpressions
  - a subexpression with a single element or a single attribute
  - a subexpression with an element and an attribute (*e.g.*, `figure[@caption = "Tree Frogs"]`) {EA Join}
  - a subexpression with two elements (*e.g.*, `chapter/figure` or `chapter/_*/figure`) {EE Join}
  - a subexpression that is a Kleene closure (+,*) of another subexpression {KC Join}
  - a subexpression that is a union of two other subexpressions
- Cons: No detail on decomposition strategies

Performance results

- EE Join algorithm outperforms the bottom-up method
  - Access patterns
  - Nature of data
- Bottom-up method outperformed the EA Join algorithm
  - Nature of data
- KC Join performance was not evaluated
- Query processing time increased almost linearly, as the size of the XML data increased

Open Issues

- A more formal analysis of the algorithms
- Explore optimal ways to decompose expressions
- Explore trade-off between disk access efficiency and storage utilization