Structural Join Algorithm for Sequential Regular Path Expressions

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XML queries employ regular path expressions to find structural patterns within XML documents. The operation of structural join is a crucial part of XML query processing. Existing approaches reduce complex join expressions to several binary structural joins. It implies generation of superfluous intermediate data. In this paper, we propose a new structural join algorithm, called sequence join algorithm, for sequential regular path expressions. It exploits information about position of the elements in the document to skip generation of the redundant intermediate lists. The algorithm performs merge of several input lists of nodes in one pass. Experimental results prove the algorithm is better than multiple binary join algorithm for queries of both small and large cardinality.

Keywords: XML document, regular path expression, structural join algorithm.

1. Introduction

Extensible Markup Language (XML) is now used as the *de facto* means to handle semistructured data over the Web [1]. Semistructured data arises when a data source does not impose a rigid structure and/or data is combined from several heterogeneous sources. The power of XML is in its ability to describe hierarchical structures and extend the dictionary of available data types.

XML documents are described in terms of *elements* [8]. The elements are enfolded by *tags*, which represent their type names. Each element is either treated as a container for some other elements or associated with an atomic value (such as text, multimedia content, etc.). Structural relationships among the elements are defined by nesting (containment) of the elements or by referencing.

A query over the XML data specifies *structural patterns* among the elements in the document. The result of such a query is intended to locate all occurrences of these patterns within the XML document or database. Such patterns are also known as *regular path expressions* (RPEs) and constitute the basis for the statements of XML query languages, for instance XQuery [11], Lorel [5], XML-QL [7], XPath [9], etc. For example, the XQuery path expression `//project/task/resource/name` specifies the retrieval of the names of all resources assigned to the tasks of the project.

The specified structural patterns are often complex themselves, but can be decomposed into a set of basic structural relationships between elements. Finding matches of the query against the database can then be considered as matching each of the basic structural relationships against the data and following merging of the sub-results. This process is performed by means of a *structural join operation* [2]. The operation essentially depends on finding ancestor-descendant and parent-child relationships among nodes of the semistructured database. The effective implementation of the structural join operation over ancestor-descendant (parent-child) pattern is the crucial part of XML query processing.

The recently proposed join algorithms take advantage of the element numbering to compute ancestor-descendant (parent-child) relationship. The element numbering allows uniquely identify the element *position* within the XML database. The position of the element can be described by 4-tuple (`DocID, StartPos, EndPos, Level`). `DocID` is the identifier of the XML document within the XML database; `StartPos`, `EndPos` are the text positions of the first and the last character of the element within the document respectively, and `Level` is the nesting depth of the element within the document [6]. The alternative representations of the element position preserve the `DocID` and `Level` components of the tuple, but differ in the way to define the start and end positions within the document. For example, there is another representation (`DocID, PrePos, PostPos, Level`), which uses the position numbers assigned to the element by pre-order (`PrePos`) and post-order (`PostPos`) traversals of the document tree accordingly. The other approaches are equivalent to the latter one and can be transformed by appropriate mapping.

The key idea underlying the implementation of the existing join algorithms is the decomposition of the original query path expression into a set of simple (binary) path expressions. Each binary expression produces an intermediate join result, which is used on the subsequent stage. For example, the path expression `//project/task/resource/name` can be decomposed to `project/task` and `resource/name`. Then the intermediate results are joined together. At each of the stages, the join algorithm uses element numbering to check the ancestor-descendant or parent-child relation between the nodes.

The XISS system [3] introduces three join algorithms: element-attribute (EA-join), element-element (EE-join), and Kleene-closure (KC-join). The element-attribute algorithm joins two intermediate results from subexpressions, which are a list of elements and a list of attributes. The element-element algorithm joins two lists of elements. The principal difference between these algorithms is that the latter one checks ancestor-descendant relationship between each pair of the input lists while the former one tests parent-child relationship. The Kleene-closure algorithms iteratively use element-element algorithm to compute closure of the expression. It repeatedly applies EE-join to the result from the previous stage of iteration. Both EA-join and EE-join algorithms have a loop over one input list nested into a loop over another list and, therefore, have time complexity $O(|E_1| \cdot |E_2|)$, which is quadratic in the size of the input lists. As KC-join depends upon EE-join, it also has quadratic time complexity.

Structural join algorithms proposed by Al-Khalifa et al. [2] exploit the advantage of element numbering to decrease the time of processing. The tree-merge join algorithm is an extension of relational equality merge join performed on sorted inputs. It was adopted to deal with ancestor-descendant or parent-child tests. The time complexity of the tree-merge join is non-quadratic $O(|E_1| + |E_2|)$, but may include multiple passes over the same input set of descendant nodes. To avoid this problem, the second of the proposed algorithms, stack-tree join algorithm, utilises stack of nodes and has time complexity $O(|E_1| + |E_2|)/B)$, where B is the blocking factor.

The main drawback of the considered algorithms is their limitation to merge only two input lists per join. It means that for a sequential regular path expression there may be generated several intermediate results. For example, processing the path expression `//project/task/resource/name` results in two joins (`project/task`) and (`resource/name`). Then, yet another join is performed to merge intermediate results. This requires additional time to create and scan intermediate data: two intermediate tables will be created and scanned. This factor becomes even more important when processing big semistructured databases. Our approach allows to reduce intermediate processing by simultaneous merging of several inputs. For the given example, it will require only one join operation instead of three.

Bruno et al. have extended the structural join algorithm to avoid multiple binary joins and further merge of intermediate results [10]. The introduced twig join algorithm uses stacks to store elements of the paths successfully tested against a query. Although this is similar to our approach, we exploit numbering, not only for elimination of unnecessary ancestor-descendant checks within the current element subtree, but for fast skipping of entire subtrees.

The main goal of the paper is to introduce an effective structural join algorithm for sequential regular path expressions, which takes several sets of single-element subexpressions as an input. It exploits the element numbering and performs merging of all the input sets in one pass. We present experimental results performed by our prototype system over several real and synthetic datasets. They show that the proposed algorithm can process regular path expressions faster than other algorithms.

The rest of the paper is organised as follows. Section 2 presents background material (data model, query expressions, structural relationships and element numbering). In section 3 we develop the structural join algorithm for regular path expressions. Section 4 addresses experimental aspect and evaluates the proposed algorithm. Section 5 summarises results of the paper and discusses future work.

2. Background and Overview

The XML data can be modelled either as a tree or as a graph. The tree model reflects the logical structure of an XML document. Nodes of the tree correspond to the elements of the document. Nesting of the elements is reflected by the parent-child relationships among nodes. Some of the tree nodes have as their values references to other elements (usually in form of IDREF attributes). The graph model extends the tree by treating such reference nodes as arcs [5]. Although the graph model is more powerful than the tree, it challenges more problems, like cycle-references.

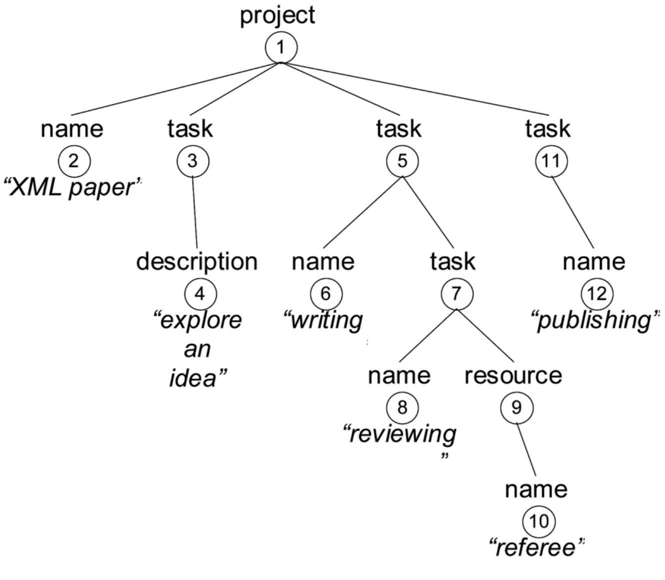
As this paper concentrates on handling ancestor-descendant relationship, we use a tree data model. The tree model can be used both to store and query semistructured data [2], [3]. Within the XML database, the order numbers of the tree node, along with its depth level and document number, are used to find the structural relationships between these nodes. This section describes the tree data model and introduces basic structural relationships used for querying XML documents. Then it explains the node position notion and its usage for finding structural relationships between the nodes.

2.1. Data Model

An XML database is a forest of trees corresponding to each document within the database. An XML document is a rooted, ordered, labelled tree. Each element of the document forms a *node* of the tree labelled with the element type (tag name) and value. The edges of the tree stand for parent-child (containment) relationship between the elements. All subelements nested within the element appear in the tree as the child nodes directly connected with the edges to a parent node. Attributes of the element are represented similarly to nested subelements and form additional nodes in the tree, emanating from their associated parent nodes.

```
<project>
   <name>XML paper</name>
   <task>
      <description>
         explore an idea
      </description>
   </task>
   <task
      name = 'writing'>
      <task
         name = 'reviewing'>
         <resource>
            <name>referee</name>
         </resource>
      </task>
   </task>
   <task
      name = 'publishing'>
   </task>
</project>
```

a)



b)

Fig. 1. Example XML data (a) and its corresponding tree (b).

An example of the XML data is shown in Figure 1(a) and its tree representation is shown in Figure 1(b).

The XML data tree has an implicit order of its nodes. The total order of all the nodes in the tree is obtained by a pre-order tree traversal (a depth-first, left-to-right traversal of the nodes). The nodes order of our example tree is shown in Figure 1(b) within the circles of corresponding nodes.

We exploit the order of the nodes in the data tree to compute position of the element in the database. A *position* of the element is a 4-tuple (`DocID, StartInt, EndInt, Level`). `DocID` is the identifier of the XML document within the XML database, `StartInt` is the tree order number of the node corresponding to the element, `EndPos` is the tree order number of the last descendant of the node, and `Level` is the nesting depth of the node within the tree. For the given example in Figure 2, the positions of the nodes are shown within rectangles. Consider, for instance, the node "resource". Its first position number stands for document identifier and equals to 1. The second and third position numbers represent the interval of the node [9,10]: order number of the node itself (9) and order number of the last descendant (10), node "name/"referee"". The last position number shows depth of the node within the tree and equals to 4. The position numbers of all other nodes are computed in the analogous way.

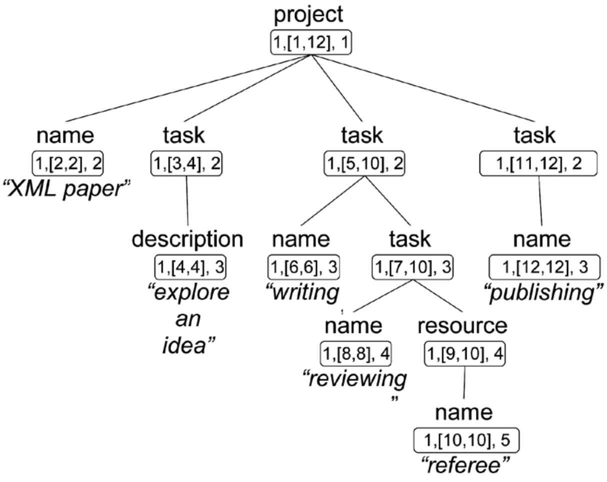


Fig. 2. Positions of the elements.

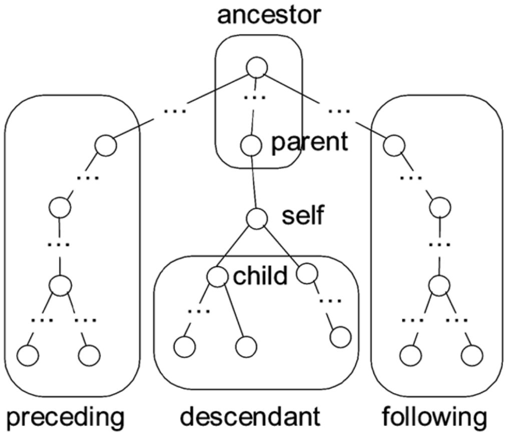
The position of the node is used to determine structural relationships between any two nodes of the tree.

2.2. Structural Relationships

Relationships between a node and the other nodes in the tree are not limited by implicit containment (parent-child) relationship and described by axes of the node [11]. An *axis* is a relation that parts the set of all the tree nodes into subsets with respect to the current node. The most commonly used axes of the node are summarised in Figure 3 (a).

axis name	**description**
ancestor	ancestors of the node
attribute	attributes of the node
child	children of the node
descendant	descendants of the node
following	all nodes after the node
parent	parent of the node
preceding	all nodes before the node
self	node itself

a)



b)

Fig. 3. Axes of the path-expressions.

The ancestor, descendant, following, preceding, and self axes partition document nodes into non-overlapped subsets, as it is shown in Figure 3 (b). The child axis is the subset of the descendant axis and the parent axis is the subset of the ancestor axis.

A *regular path expression* or *location path* of a target node B from source node A (hereafter referred to as path) is a *sequence* of nodes in the tree, from the node A to the node B. Relationships between intermediate nodes in the path are described by axes. A location path is called *absolute path* if its source node is the root of the tree, otherwise it is called *relative path*.

Regular path expressions are an essential component of semistructured data query languages (e.g. XQuery [11]), which utilise variety of structural relationships between the nodes.

2.3. Handling Structural Relationships by Means of Position

Position is an important characteristic of elements within XML documents and it is intensely used for indexing and querying semistructured data.

The *position* of the node n_i is denoted as $(D_i,\ [S_i,\ E_i],\ L_i)$, where D_i is the identifier of the XML document within the XML database; S_i is the tree order number of the node n_i, E_i is the tree order number of the last descendant of the node n_i, and L_i is the nesting depth of the node n_i within the tree. The pair of the node order S_i and order of its last descendant E_i constitutes an interval of descendant order numbers $[S_i, E_i]$. Hereafter, we will refer to the interval $[S_i, E_i]$ as the *node interval*.

Ancestor-descendant relationship. Given a tree node n_i and its position $(D_i,\ [S_i,\ E_i],\ L_i)$ and a tree node n_j and its position $(D_j,\ [S_j,\ E_j],\ L_j)$, the node n_i is an ancestor of the node n_j (and node n_j is a descendant of the node n_i) iff:

a) $D_i = D_j$, i.e. both nodes belong to the same document;

b) $[S_i,\ E_i] \subset [S_j,\ E_j]$, the node interval of the ancestor includes the interval of the descendant, i.e. $S_i < S_j$ and $E_i > E_j$.

Parent-child relationship. Given a tree node n_i and its position $(D_i,\ [S_i,\ E_i], L_i)$ and a tree node n_j and its position $(D_j,\ [S_j,\ E_j],\ L_j)$, the node n_i is a parent of the node n_j (and node n_j is a child of the node n_i) iff:

a) $D_i = D_j$, i.e. both nodes belong to the same document;

b) $[S_i,\ E_i] \subset [S_j,\ E_j]$, the node interval of the ancestor includes the interval of the descendant, i.e. $S_i < S_j$ and $E_i > E_j$;

c) $L_i = L_j - 1$, the descendant is nested immediately within the ancestor node.

For instance, consider the nodes "project" and "resource" in Figure 2. Their document ID numbers coincide and equal to 1. The node interval of "project" includes the interval of the "resource", [1,12] ⊂ [9,10], so the "project" is the ancestor of the "resource". The difference between their levels exceeds 1, so they are not bounded by parent-child relationship.

relation	**Document**	**Node interval**	**Level**
ancestor	$D_i = D_j$	$[S_i,\ E_i] \subset [S_j,\ E_j]$	$L_i < L_j$
attribute	$D_i = D_j$	$[S_i,\ E_i] \supset [S_j,\ E_j]$	$L_i = L_j + 1$
child	$D_i = D_j$	$[S_i,\ E_i] \supset [S_j,\ E_j]$	$L_i = L_j + 1$
descendant	$D_i = D_j$	$[S_i,\ E_i] \supset [S_j,\ E_j]$	$L_i > L_j$
following	$D_i = D_j$	$[S_i,\ E_i] > [S_j,\ E_j]$	
parent	$D_i = D_j$	$[S_i,\ E_i] \subset [S_j,\ E_j]$	$L_i = L_j - 1$
preceding	$D_i = D_j$	$[S_i,\ E_i] < [S_j,\ E_j]$	
self	$D_i = D_j$	$[S_i,\ E_i] = [S_j,\ E_j]$	$L_i = L_j$

Table 1. Summary of position constraints to represent structural relationships.

The other structural relationships between any two nodes can be verified by analogy. They are summarised in Table 1.

In Figure 2, the node "description" precedes the node "resource" as they have the same document number and the interval of the "description" occurs before the interval of the "resource", [4,4] < [9,10].

The operational cost to check any of the structural relationship includes document ID, node interval, and level comparison. The costs are equal for any type of relationship, but the ancestor-descendant and parent-child are the ones mostly used.

3. Algorithm

In this section, we develop new structural join algorithm, in order to efficiently process regular path expression queries. It exploits the concept of node position to merge several input lists in one pass. As it processes several binary structural relationships that form a sequence, we call it *sequence join* algorithm.

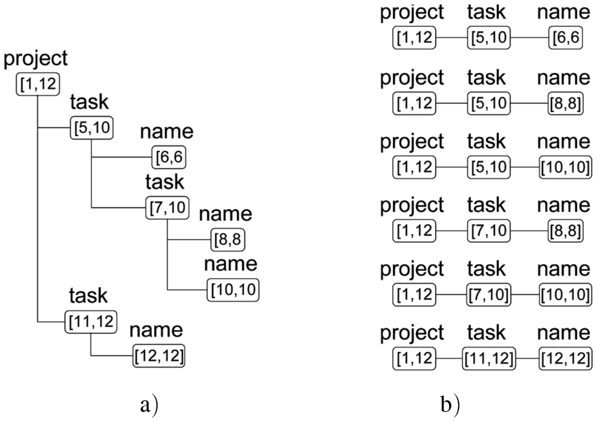
At the outset, we consider two ways of result representation (a tree-like form and tuples) and show the algorithm in action on a detailed example. Then we present algorithm itself and conclude with analytical estimation of its performance.

3.1. Representation of the Results

The results of the XML query can be represented either as a tree or as a list of tuples. Consider the following query example `//project//task//name` performed over the data shown in Figure 2. The query retrieves the names of the elements assigned to all tasks within the project (including names of the tasks themselves). The tree and the tuples of the result are shown in Figure 4 a) and b) respectively.

These two forms are equivalent and can be transformed from one to another. The tree representation can be obtained from the tuples by eliminating duplicates of the nodes.

The tree view is more compact and suitable for the data that originally has tree-like structure. Nevertheless, it may fit in applications that need results in a table-like form. In such a case, tuple representation is more appropriate. Final decision on which of the two forms is preferable should be made for each particular case.



a) b)

Fig. 4. Forms of query results: tree and tuple.

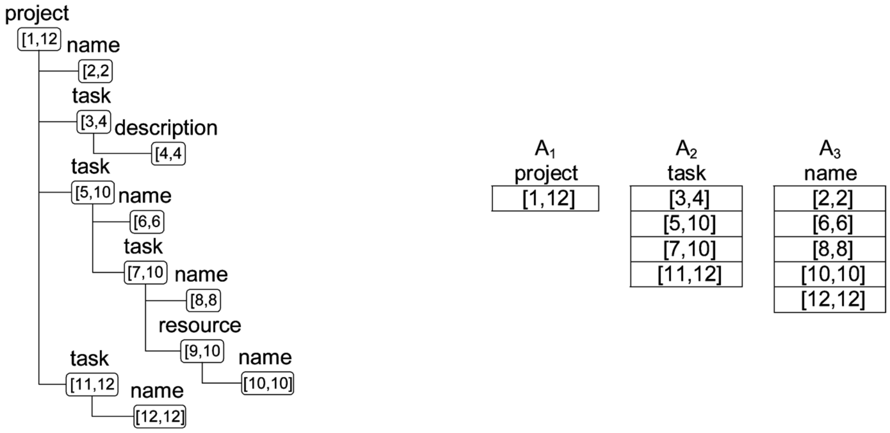
Hereafter, we use tree representation of the results, adding, if necessary, some comments on the tuple form.

3.2. Example

For the purpose of clarity, we demonstrate the algorithm on an example, before introducing it more formally.

Consider the query expression `//project//task//name` applied to the data in Figure 2. The simplified data tree is presented in Figure 5 a). The `document number` and `level` components of the node position are omitted. The `document number` is equal for all the nodes of the example and `level` is not important as no parent-child relationship is tested through the query processing. The input lists of the example are shown in Figure 5 b). The list A_1 represents the result of select operation and contains all nodes "`project`" selected from the database. Analogously, the lists A_2 and A_3 include nodes "`task`" and "`name`" respectively.

The steps of the algorithm for the chosen example are shown in Figure 6. The current node of each list is marked by arrow. For each input list, the algorithm keeps value of a current node *range* of the list. The range points to candidate nodes to be added to the result list. It coincides with the node interval component of the node position, but covers only the nodes from the

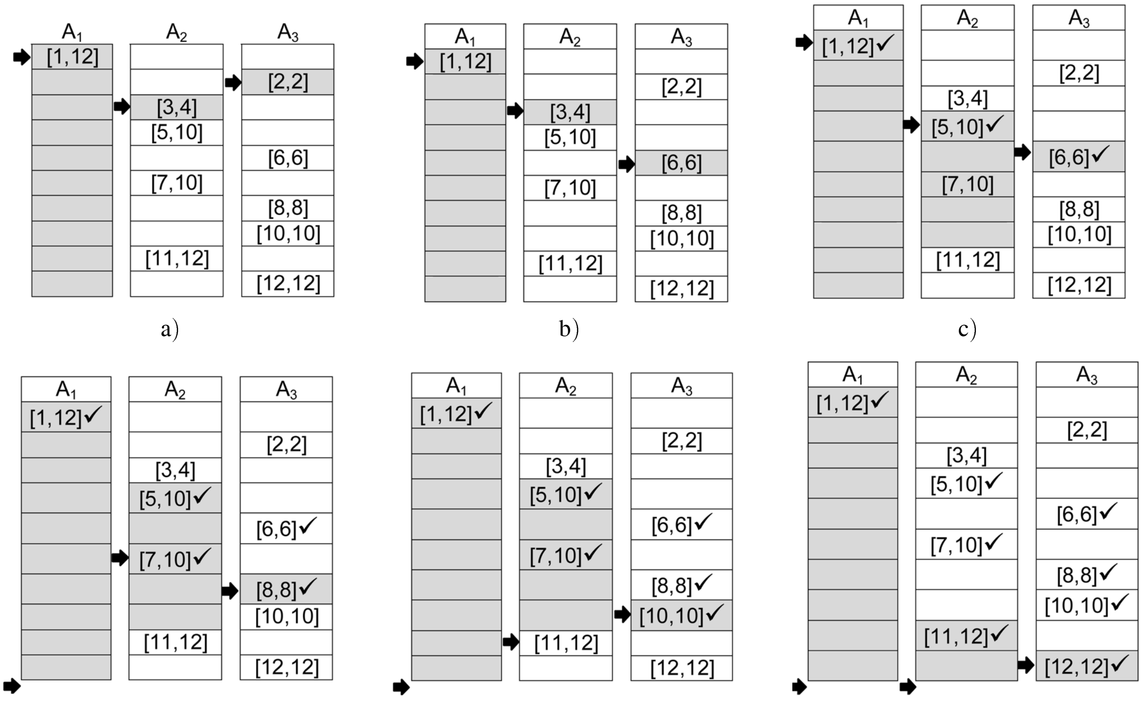


a) b)

Fig. 5. Example of data tree and input lists.

same list. For example, the interval of the node "task [5,10]" in Figure 5 a) is equal to [5,10] and includes six nodes 5 to 10. The range of the same node is equal to [5,10] too, but includes only two "task" nodes 5 and 7. In Figure 6, the range is shown in grey colour. Additionally, each of the lists is visually extended with empty cells to show precedence of the nodes in the source tree. For example, the range [2,2] of the list A_3 in Figure 6 a) is preceding the range [3,4] of the list A_2 and is part of (included into) the range [1,12] of the list A_1.

The basic idea of the algorithm is to synchronously read input lists to find first match of the ranges. Once the matching ranges are found, the current nodes within ranges are put into the result list. If the ranges in two adjacent lists do not match, then one of the ranges changes, based on the result of their comparison. The propagation of changes goes from the last list



a) b) c)

d) e) f)

Fig. 6. Step-by-step example.

back to first. The algorithm stops when no more matches of the ranges can be found.

For the given example, the algorithm starts from the state in Figure 6 a). The ranges are initially assigned to the first nodes of the lists. The comparison of the ranges goes from the list of ancestors to the list of descendants (left-to-right in the figure). The range [3,4] of the descendant list A_2 satisfies the range [1,12] of the ancestor list A_1, but the range [2,2] of the descendant list A_3 is not included into the range [3,4] of the ancestor list A_2. As the descendant range [2,2] precedes the ancestor range [3,4], the algorithm reads a new node from the list A_3 and changes range to [6,6], as it is shown in Figure 6 b).

Now the descendant range [6,6] follows the ancestor range [3,4]. Therefore, the latter is changed to [5,10] (Figure 6 c). At this point, all descendant ranges satisfy the ancestor ranges and their nodes (up to current) are sent to the output list. The nodes added to the output are marked with the tick mark. The algorithm reads new nodes from the lists and changes ranges (Figure 6 d). For the list A_3, the range is changed from [6,6] to [8,8]. The range of the list A_2 is not changed as the new node [7,10] is still within the current range. The range of the list A_1 is not changed in spite the fact that it has reached the end of the list. This is due to the assumption that propagation of changes goes from the last list to the first. The nodes [8,8] and [7,10] are sent to the output.

By analogy to the previous step, the algorithm continues reading the lists (Figure 6 e). For the list A_3, the range is changed from [8,8] to [10,10]. The range [5,10] of the list A_2 is not changed as the range of the list A_3 still satisfies it and no propagation is necessary. The node [10,10] is added to the result.

The next read operation of the node [12,12] of the list A_3 forces to change the range of the list A_2 from [5,10] to [11,12] (Figure 6 f). Nodes [11,12] and [12,12] are appended to the output list. Any further reading from the list A_3 fails and the algorithm stops.

3.3. Algorithm of Sequence Join

The text of the algorithm is presented in Figure 7. The steps of finding match of the ranges and appending result nodes are presented as separate sub-routines.

The algorithm generates the result list in the tree representation. To generate tuple representation the append subroutine should iterate over the range nodes producing each possible combination.

The algorithm uses recursive subroutines. The depth of the recursion is equal the number of input lists which, in its turn, is related the depth of the input XML data tree. The depth of the existing XML databases does not exceed 20 and recursion will not cause consumption of memory resources.

3.4. Time Cost Estimation

In this section we estimate the execution time difference between the proposed join algorithm and the pair-wise join algorithm. As there are multiple ways to break and n-way join into n binary joins, and the decision is chosen at run time, we assume that it is performed sequentially and all intermediate results are materialised.

Consider regular path expression `a1/a2/.../an`. Both approaches require n selection operators resulting in lists of nodes $A_1,\ A_2, \ldots,\ A_n$ respectively. The execution plans for pair-wise join and sequence join are shown in Figure 8 a) and b) accordingly. We consider the total time to perform join operation as the sum of time needed to read input lists (σ) and time necessary to create output list (τ): $\sigma + \tau$.

For pair-wise approach, the task of matching complex query is reduced to performing of one join operation for each binary structural relationship in query expression. For n input lists of nodes, it causes creation of $\frac{n}{2}$ intermediate lists of nodes. The next step is to perform binary join operation over the intermediate lists. It is applied until it results in the only one, result list. Thus, the whole number of intermediate list (including the result list) is $\frac{n}{2} + \frac{n}{4} + \ldots + \frac{n}{2^{\log n}} = \left(1 - \frac{1}{2^{\log n}}\right) n = n - 1$. In Figure 8 a) these lists are denoted as $A_{n+1}, \ldots,\ A_{2n-1}$. If τ_i is the time required to create list i, then the total time necessary for creation of intermediate lists is $\sum_{n+1}^{2n-1} \tau_i$.

sequence-join ({*A*}, *R*)

```
Input:  $A_0$,…,$A_N$ are lists of nodes
  sorted by order
Output: $A_R$ is the result list of
  merged nodes

for (i=0; i≤N; i++) set-range($A_i$);

while(find-range-match(0,{0,∞})=OK)
    append-nodes($A_N$, $A_N$.node);
    change-range($A_N$);
end while
```

append-nodes (*i*, *NODE*)

```
if (i≥0)
while ($A_i$.node « NODE)
      or ($A_i$.node «» NODE)
    if ($A_i$.node «» NODE)
        append-nodes(i-1, $A_i$.node);
        append $A_i$.node to $A_R$;
    end
    $A_i$.next-node;
    if (i = N) break;
end while
```

change-range (*i*)

```
if ($A_i$.range == $A_i$.node) $A_i$.next-
  node;
$A_i$.range = $A_i$.node;
```

Find-range-match (*i*, *R*)

```
Input: i is the index of current
  input list from the set {$A_0$,…,$A_N$}.
  R is the range of nodes.
Output: returns one of the values:
  OK to indicate that the range is
  found
  OUT if the end of the list is
  reached
  SKIP to indicate that no match has
  been found for the range R

while ()
    if ($A_i$.node = NULL) return OUT;

    if (R »« $A_i$.node)
        $A_i$.next-node;//next child range
        change-range(i);
    end

    if (R » $A_i$.node)
        $A_i$.next-node;//next sibling
        change-range(i);
    end

    if (R « $A_i$.node) return SKIP;

    if (R «» $A_i$.node)
        if (i = N) return OK;
        case find-range-match(i+1,
                 $A_i$.range)
            OK: return OK;
            OUT:return OUT;
            SKIP:     //next sibling
                change-range(i);
        end
    end
end while
```

A « *B*	is-preceding-of
A «» *B*	is-ancestor-of
A »« *B*	is-descendant-of
A » *B*	is-following-of

Fig. 7. Sequence join algorithm.

The total number of list used as an input includes all the lists except the result one: $n + \frac{n}{2} + \frac{n}{4} + \ldots + \frac{n}{2^{(\log n)-1}} = \left(2 - \frac{2}{2^{\log n}}\right) n = 2(n-1)$. If σ_i is the time required to read list *i*, then the time necessary for reading of input lists is $\sum\limits_{1}^{2n-2} \sigma_i$.

The total time necessary to perform multiple pair-wise join is

$$\sum_{1}^{2n-2} \sigma_i + \sum_{n+1}^{2n-1} \tau_i, \tag{1}$$

where τ_i and σ_i is the time required to create

Fig. 8. Execution plans of multiple pair-wise join and sequence join.

and read list i respectively.

The sequence join reads input lists $A_1, \ldots, A_n$ and creates the only one, result list A_{2n-1}, as shown in Figure 8 b). The total time necessary to perform sequence join is

$$\sum_{1}^{n} \sigma_i + \tau_{2n-1}, \tag{2}$$

where σ_i is the time required to read input lists, and τ_{2n-1} is the time needed to create result table.

The time difference between the two approaches is

$$\left(\sum_{1}^{2n-2} \sigma_i + \sum_{n+1}^{2n-1} \tau_i\right) - \left(\sum_{1}^{n} \sigma_i + \tau_{2n-1}\right) = \sum_{n+1}^{2n-2} \sigma_i + \sum_{n+1}^{2n-2} \tau_i, \tag{3}$$

where τ_i and σ_i is the time required to create and read list i respectively.

The parameters τ_i and σ_i depend on the capacity of the list i. If the number of nodes in each list is comparable, then we can assume the times to create and read list are equal: $\forall i,\ i = 1, \ldots, n$; $\tau_i = \tau$. The time cost functions of the algorithms (1) and (2), as well as their difference (3), can be represented in a simpler form:

the time cost of multiple pair-wise join is

$$(2\sigma + \tau)(n - 1), \tag{1a}$$

the time cost of sequence join is

$$(\sigma n + \tau), \tag{2a}$$

and their difference is

$$(\sigma + \tau)(n - 2), \tag{3a}$$

where τ and σ is an average time required to create an output and read an input list respectively, n is the number of original input lists.

The algorithm time cost graphs are presented in Figure 9.

The graph shows that the sequence join algorithm does better over the queries with 3 and more basic structural relationships.

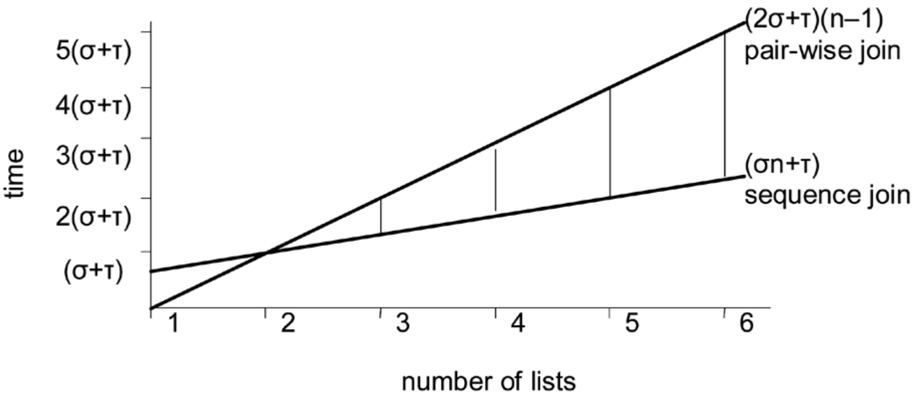


Fig. 9. Time cost difference between the pair-wise join and sequence join.

4. Experimental Evaluation

We have conducted several experiments evaluating the proposed algorithm. The tests involve both real-world and synthetic datasets. This section describes experimental testbed and presents the results of these experiments.

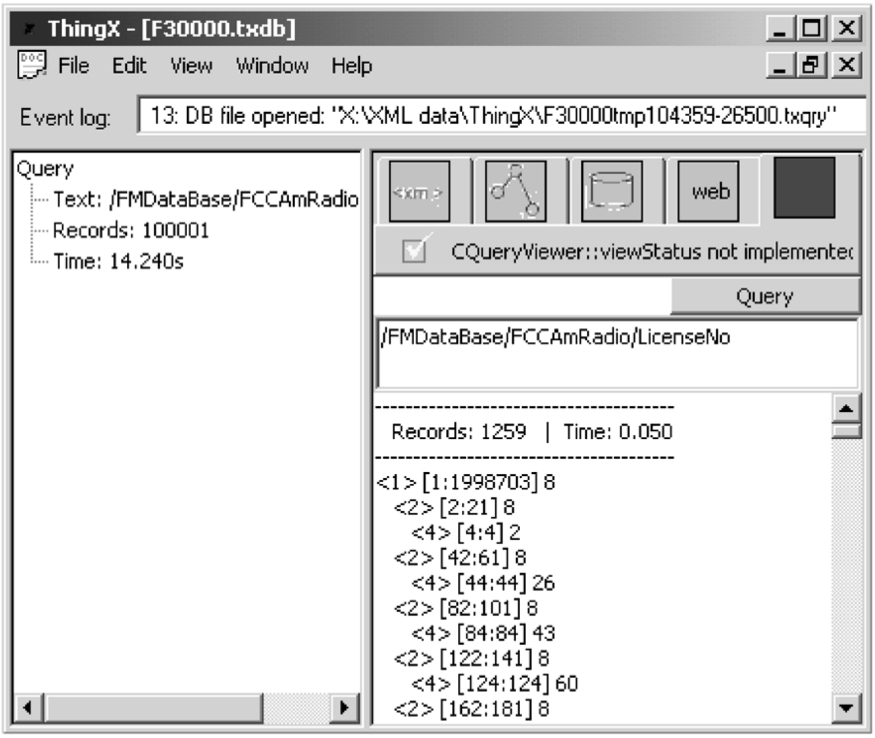
4.1. Experimental Setup

We implemented a prototype system for storing, indexing, and querying XML data. The screenshot of the prototype window is shown in Figure 10. Source XML files are parsed using the Xerces-C++ XML parser [17]. The data is parsed without validation option. The prototype exploits Berkeley DB [18] to store parsed data and index files. The B-tree indexing facility of the package is used to build index files. The system provides a simple query interface for regular path expressions. The interface is XQuery-compliant [11] and directly performs query processing. The overall system is implemented in C++.

All experiments were performed under Windows 2000 workstation software running on a Dell Dimension 8100 computer. The station has 256Mb of memory, 20Gb hard disk, and 1.4 GHz Pentium IV processor.

4.2. Data Sets

We have chosen several data sets, both real-world (DBLP [12], Shakespeare [13], HAM-RADIO [14], Mondial [15]), and synthetic (Xmark [16]). The characteristics of these sources of data are summarised in Table 2. The columns `Files` and `Size` of the Source data section show the number of the source XML documents within the dataset and disk space occupied by them respectively. The field `Size` of the Database section refers to the size of the database obtained after parsing and storing the source documents. The `Element` column represents the number of different element type names. It includes all the attribute names. The `Occurrences` field indicates the total number of element occurrences within the document and includes all attribute occurrences as well. The column `Values` show the total number of different values of the elements. The field `Depth` show the maximum level of element nesting.



Event log: 13: DB file opened: "X:\XML data\ThingX\F30000tmp104359-26500.txqry"

```
Query
  Text: /FMDataBase/FCCAmRadio
  Records: 100001
  Time: 14.240s
```

☑ CQueryViewer::viewStatus not implementec

/FMDataBase/FCCAmRadio/LicenseNo

```
--------------------------------------
  Records: 1259  |  Time: 0.050
--------------------------------------
<1> [1:1998703] 8
  <2> [2:21] 8
    <4> [4:4] 2
  <2> [42:61] 8
    <4> [44:44] 26
  <2> [82:101] 8
    <4> [84:84] 43
  <2> [122:141] 8
    <4> [124:124] 60
  <2> [162:181] 8
```

Fig. 10. Prototype system window.

XML documents	Type	Source data		Database data				
		Files	Size (Mb)	Size (Mb)	Elements	Occurrences	Values	Depth
DBLP books	real	1 407	0.59	1.27	23	11 456	6 846	4
DBLP conf	real	150 885	58.93	125.83	29	1 321 593	567 197	4
DBLP journals	real	99 475	37.19	86.76	23	973 602	374 196	5
HAM-RADIO	real	882	360.96	730.93	23	14 118 079	2 913 795	4
Shakespeare	real	37	7.53	21.51	28	179 696	112 766	6
Mondial	real	1	2.04	5.46	49	85 220	36 929	6
Xmark (100Mb)	synth.	1	113.79	324.98	77	2 048 193	416710	12
Xmark (1Gb)	synth.	1	1 164.79	2 052.00	77	20 532 805	2 043 572	12

Table 2. Datasets characteristics.

A brief description of the data sets content is the following:

- **DBLP** contains computer science bibliography information [12]. It consists of many small files, each representing a single record about publication (conference or journal paper, book).
- **Shakespeare** dataset is the XML version of the plays by Shakespeare [13].
- **HAM-RADIO** is the FCC Ham Radio database of the US Government's Federal Communications Commission [14].
- **Mondial** is freely available geographic database [15].
- **Xmark** datasets are synthetic and were generated by xmlgen generator [16]. The data models an auction website with large number of element and attribute types and high nesting of elements. We have selected standard (100Mb) and large (1Gb) documents.

4.3. Queries and Performance Metrics

In order to study the tradeoffs of the join algorithm we carried out a series of comparative experiments. Query processing time was used as a major performance metric. The experiments evaluate the effect of several parameters on the performance of query processing: the size of the source XML files, number of elements and values, depth of the parsed tree, as well as the size of the query answer, number of elements

#	XQuery expression	Dataset	Records			RPE len
			Input	Output	%	
Q1	/book/isbn	DBLP books	705	621	88%	2
Q2	/inproceedings/cite	DBLP conf	214 837	102 519	48%	2
Q3	/article/author	DBLP journals	245 748	245 216	99%	2
Q4	/FMDataBase/FCCAmRadio/Address/City	HAM-RADIO	2115906	2115906	100%	3
Q5	/PLAY/ACT/SPEECH/LINE	Shakespeare	139 083	138 620	99%	4
Q6	/country/province/city/name	Mondial	26 032	6 616	25%	4
Q7	/person/profile/interest/category	Xmark (.1Gb)	309 588	97 176	31%	4
Q8		Xmark (1Gb)	1723670	977 538	57%	4

Table 3. Description and parameters of the test queries.

selected. The queries and their characteristics are given in Table 3.

We chose several test queries based on the length of the regular path expression and number of matches. The column `Input Records` indicates the total number of processed records. The `Output` and "%" columns show the number of records that match the query expression and their relative number against the processed records respectively. The `RPE length` represents the length of the query expression path. If all single element subexpressions of the query expression are different, then this number coincides with the number of select operations for the query, i.e. the number of input lists.

4.4. Experimental Results

The elapsed query time for the test datasets are shown in Figure 11. The cases with the query path length of more than 2 (queries Q4–Q8) demonstrate improved performance of the sequence algorithm against the pair-wise algorithm.

The sequence join performs less effectively than the pair-wise join for the queries with the path length of 2 (queries Q1–Q3). This fact is in accordance with our time cost estimation shown in Figure 9.

For queries Q5-Q7, results are presented for different ways to break an n-way join into multiple binary joins. Sequential join algorithm has shown good performance against each of them. All the intermediate results for binary joins are materialised.

5. Conclusion

The structural join operation is intensely exploited for finding structural patterns within an XML database. Thus, an effective implementation of the structural join operation is essential for effective XML query processing.

We have developed the sequence join algorithm for regular path expressions. In contrast to pair-wise approach, the algorithm takes several lists of elements as an input. It exploits the position of the element within XML document to compute structural relationships between elements fast. The algorithm checks structural pattern matching through all the input lists at once. Due to this, it does not generate nonexistent sub-results and hence eliminates creation of excessive intermediate data. Experimental evaluation of the algorithm shows that sequence join performs better than multiple binary joins for the queries with the expression length of 3 or more. It is true for the synthetic and real-world data queries of both small and large cardinality.

As a direction for future activities, it is worth to consider sequence joins in context of graph-based queries. This area poses many interesting

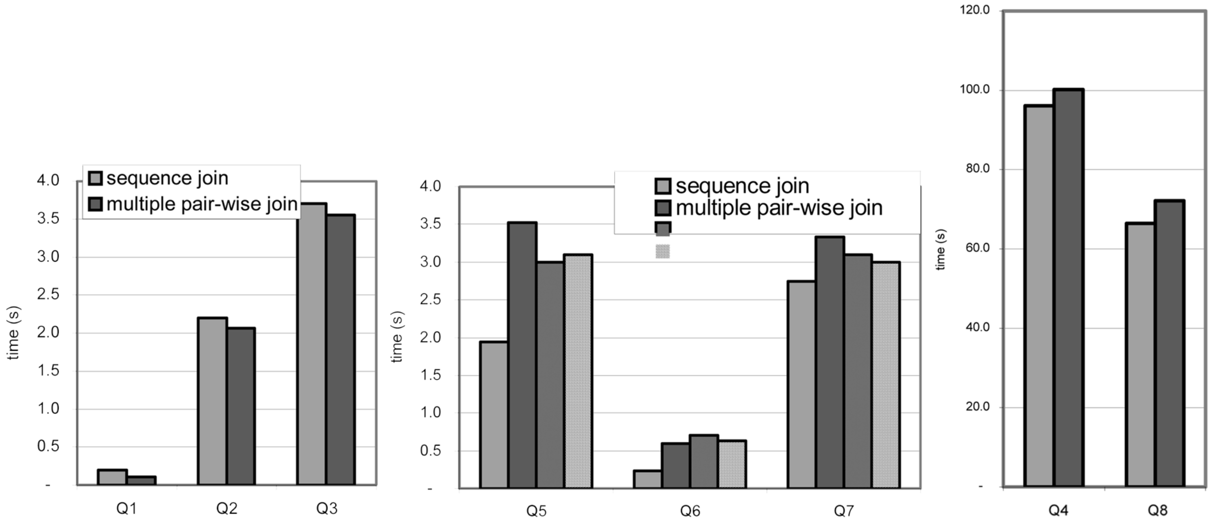


Fig. 11. Query performance comparison.

problems, like handling graph-cycles (that are usually represented in the tree model as values of the link nodes). Another issue is processing the whole variety of XPath axes rather than ancestor-descendant or parent-child only.

6. Acknowledgements

This project is partly supported by ORS award. The authors would like to thank Jonathan Smith for his helpful comments on this paper.

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Received: January, 2004
Accepted: June, 2004

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