Fast XML Structural Join Algorithms by Partitioning

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An XML structural join evaluates structural relationships (e.g. parent-child or ancestor-descendant) between XML elements. It serves as an important computation unit in XML pattern matching. Several classical structural join algorithms have been proposed such as Stack-tree join and XR-Tree join. In this paper, we consider to answer the problem of structural join by partitioning. The Dietz numbering scheme is used for encoding since nodes with the Dietz encodings could be well distributed on a plane. We first extend the relationships between nodes to the relationships between partitions on a plane and obtain some observations and properties about the relationships between partitions. We then propose a new partition-based method, named P-Join for structural join between ancestor and descendant nodes based on the properties derived from our observations. Moreover, we present an enhanced partitioned-based structural join algorithm and two optimized methods. Extensive experiments show that the performance of our proposed algorithms outperform that of Stack-tree and XR-Tree algorithms. In order to store the partitioning results, we design a simple but efficient index structure, called PSS-tree. The experimental result shows that it has less maintenance overhead than XR-Tree.

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1. INTRODUCTION

XML has been increasingly used in Web applications and become the de facto standard for data exchange over the Internet. Queries in XML query languages (Berglund et al., 2001; Chamberlin et al., 2000; Deutsch et al., 1998) typically specify patterns of selection predicates on multiple elements that have some specified tree structured relationships. These queries can be naturally decomposed into a set of basic parent-child (/) and ancestor-descendant (///) relationships between pairs of nodes, called structural joins.

Structural join is known as an important computation primitive in XML query processing. It is not only the basic unit of the cost-based twig pattern matching (Wu et al., 2003) but also the basis of holistic twig join algorithms (Bruno et al., 2002; Jiang et al., 2003). Therefore, improving the performance of structural joins remains to be an important research issue.

There exists a rich body of work on structural joins. For example, Zhang et al. (2001) proposed a variant of the traditional merge join algorithm, called multi-predicate merge join (MPMGJN).

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However, it may perform a lot of unnecessary computation and disk I/O for matching structural relationship. Similarly, EE-Join and EA-Join in Li and Moon (2001) may scan an element set multiple times. The Stack-Tree-Desc join algorithm proposed by Al-Khalifa et al (2002) improved the merge based structural join algorithms with a stack mechanism. Only one sequential scan is required for two input ordered lists, AList and DList.

Index-based algorithms push the performance of structural joins to a next level (Chien et al., 2002; Jiang et al., 2003). The essential idea is to use indexes on the participating element sets to directly (or near directly) find the matching elements and skip those without matches. Experiments show that index-based algorithms could be faster than merge-based algorithms.

Besides index-based algorithms, partitioning is another way to accelerate structural joins. Li and Moon (2003) proposed three partition-based path join algorithms, namely descendant partition join, segment-tree partition join and ancestor link partition join. These partition-based join algorithms could make better use of the buffer memory by using small in-memory data structures and taking advantage of unevenly sized inputs, but they did not utilize the positional characteristics of the encodings of tree node encodings well.

Furthermore, many numbering schemes have been proposed because with them we could quickly determine the positional relationships between tree nodes. Previous strategies solve the problem of structural joins by using the basic properties of numbering schemes. Specifically, they mainly pay attention to the relationship of node encodings while ignoring the spatial distribution of tree nodes.

In this paper, we first introduce a partition-based structural join method P-Join (Tang et al., 2005) specially designed for XML queries by extending the relationship between nodes to the relationship between partitions. We then present an enhanced partition-based structural join algorithm and two optimized algorithms to further improve the performance of P-Join.

The major contributions of this paper are summarized as follows:

- We extend the relationships between nodes to the relationships between partitions and get some observations and properties about the relationships between partitions. Based on the relationships between partitions, we get 9 observations and 4 properties.
- We present a partition-based structural join method, named P-Join. Previous work (Chien et al., 2002; Jiang et al., 2003) only utilized B*-Tree and XR-Tree on Stack-tree join algorithm to skip ancestor and descendant nodes. With P-Join, however, after filter operation, the ancestor and descendant nodes are further classified into different partitions using positional relationships on a plane. Then some partitions could directly output join results without actual join operation, other partitions could also efficiently produce join results utilizing spatial characteristics.
- We present an enhanced partition-based structural join algorithm and two optimized methods based on P-Join. We also design an efficient structure PSS-tree to index partitioning results.
- We report the result of a performance study which shows that our proposed algorithms outperform previous classical existing structural join algorithms.

The rest of this paper is organized as follows. In Section 2 we introduce the numbering scheme selected and some concepts about partition relationships. Next, in Section 3 we propose a new partition-based structural join method P-Join. Section 4 describes an enhanced partition-based structural join algorithm and two optimized methods based on P-Join. Section 5 gives the performance evaluation. Finally Section 6 concludes this paper.

2. NUMBERING SCHEME AND PARTITION RELATIONSHIPS

XML document is commonly modeled as a data tree. Nodes in the tree correspond to elements, attributes or values, and the edges represent immediate parent-child relationships. A unique feature
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of XML queries is to query the structural relationships between tree nodes.

Efficiently determining the structural relationships between tree nodes is the pivot of XML queries. In this section we first introduce the numbering scheme adopted in this paper to determine the positional relationships of tree nodes. We then describe the spatial positional characteristics of points and partitions.

There are many proposed numbering schemes for efficiently determining the positional relationships between any pair of tree nodes (e.g. Al-Khalifa et al., 2002; Dietz, 1982; Grust, 2002; Li and Moon, 2001; Min et al., 2003; Wang et al., 2003). In this paper we attempt to make use of a numbering scheme for partitioning data that will in turn make the structural join more efficient. Therefore, the choice of a good numbering scheme is important. We use the Dietz numbering scheme (Dietz, 1982), which uses preorder and postorder values, as a pair, to encode each tree node, where preorder is the order in pre-order traversal of XML data tree, while postorder is the order in post-order traversal.

Dietz numbering scheme expresses the positional relationship as follows:
- For a tree node $e_i$ and its ancestor $e_j$, $\text{PRE}(e_i) < \text{PRE}(e_j)$ and $\text{POST}(e_i) > \text{POST}(e_j)$.
- For two sibling nodes $e_i$ and $e_j$, if $e_i$ is the predecessor of $e_j$ in pre-order traversal, $\text{PRE}(e_i) < \text{PRE}(e_j)$ and $\text{POST}(e_i) < \text{POST}(e_j)$.

Here, $\text{PRE}(e)$ and $\text{POST}(e)$ represent the preorder and postorder of element $e$, respectively. Figure 1 shows a simple XML data tree encoded with the Dietz numbering scheme.

With the Dietz numbering scheme, the structural relationship between tree nodes can be clearly expressed on a plane as shown in Figure 2. The $x$-axis represents the preorder values and the $y$-axis the postorder values. For any XML data tree, no two XML nodes have the same preorder or postorder values. Therefore, no two XML nodes can be placed at the same row or column on a plane. Consider the node $p$ in Figure 2. Any node $e$ on the top left of $p$ is the ancestor of $p$ because $\text{PRE}(e) < \text{PRE}(p)$ and $\text{POST}(e) > \text{POST}(p)$; likewise, the node on the bottom right is the descendant of $p$; the node on the bottom left is the preceding node of $p$; the node on the top right is the following node of $p$.

Figure 1: An XML document example
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The main reason of using the Dietz numbering scheme is simply explained below. In comparison with the region code, which uses \((\text{start}, \text{end})\) pair for coding (Al-Khalifa \textit{et al}, 2002). Consider the XML document example in Figure 1. Figure 3(a) shows the distribution of nodes on a plane under Dietz numbering scheme. Figure 3(b) shows the distribution of nodes using region numbering scheme. For simplicity, in Figure 3, we only show nodes \(a\) and \(d\) while omitting \(b\) and \(c\) from the example XML document shown in Figure 1. As can be seen in Figure 3, nodes with the Dietz numbering scheme are distributed dispersedly, whereas the nodes with the region numbering scheme are rather skewed and only in the upper triangle of a subspace. This distribution character of Dietz numbering scheme is more appropriate for our spatial-partitioning technique introduced in Section 4, thus we choose Dietz numbering scheme.

In this paper, we extend the relationships between nodes as shown in Figure 2 to the relationships between partitions. We show an example in Figure 4, where the whole space is partitioned into 9 disjoint rectangle partitions, \(R_1\) \(R_2\) \(R_9\). Here each \(R_i\) contains a subset of XML elements (or nodes in an XML tree). Consider the partition \(R_5\) in the centre of Figure 4. We made the following observations:
1. All nodes in \(R_1\) are the \textit{ancestors} of all nodes in \(R_5\).
2. All nodes in \(R_3\) are the \textit{following} nodes of all nodes in \(R_5\).
3. All nodes in \(R_7\) are the \textit{preceding} nodes of all nodes in \(R_5\).
4. All nodes in \(R_9\) are the \textit{descendants} of all nodes in \(R_5\).
5. Some nodes in \(R_2\) are the \textit{ancestors} or \textit{following} nodes of some nodes in \(R_5\).
6. Some nodes in \(R_4\) are the \textit{ancestors} or the \textit{preceding} nodes of some nodes in \(R_5\).
7. Some nodes in $R_6$ are the descendants or following nodes of some nodes in $R_5$.
8. Some nodes in $R_8$ are the descendants or preceding nodes of some nodes in $R_5$.
9. Some nodes in $R_5$ may have any positional relationships with nodes in $R_5$.

Note, items 1-4 state that a relationship is always true for all nodes in two different partitions. Items 5-8 state that a relationship may be true for some nodes in two different partitions. The last item 9, states a fact a partition-based positional relationship does not deal with the relationships between nodes inside a single partition.

The observations made above show that we can process structural joins using a partition-based approach. When users query the ancestors of nodes in the partition of $R_5$, (1) we need not do structural join between nodes in $R_5$ and any node in $R_3$, $R_6$, $R_7$, $R_8$ and $R_9$, since none of these partitions includes ancestors of any nodes in $R_5$; (2) we need not do structural join between $R_1$ and $R_5$, since all nodes in $R_1$ are the ancestors of all nodes in $R_5$; and (3) we only need to do structural join between $R_2$, $R_5$ and $R_4$, $R_5$, since some nodes in $R_2$ and $R_4$ are the ancestors of some nodes in $R_5$. The similar techniques can be applied when users query the descendant or other XPath axes in the partition of $R_5$.

Based on the above observations, we define two predicates namely, all $(S, R_i, R_j)$ and some $(S, R_i, R_j)$ where $R_i$ and $R_j$ are partitions and $S$ is a type indicator including ancestor, descendant, following, and preceding. Here, all$(S, R_i, R_j)$ means that all nodes in $R_i$ satisfy the given relationship $S$ with $R_j$, and some $(S, R_i, R_j)$ means some nodes in $R_i$ satisfy the given relationship $S$ with $R_j$. For example, as shown in Figure 4, all (ancestor, $R_1$, $R_5$) is true, all (ancestor, $R_5$, $R_1$) is false, and all (ancestor, $R_4$, $R_5$) is false. It is worth noting that, given a partition $R_i$, only those partitions that are at top left of $R_i$ satisfy all (ancestor, $R_i$, $R_i$), and only those partitions that are at bottom right of $R_i$ satisfy all (descendant, $R_i$, $R_i$).

PROPERTY 1. Given two partitions $R_i$ and $R_j$ such as up$(R_j, R_i)$ is true. Assume that there are three nodes $x \in R_i$, $y \in R_j$ and $z \in R_j$. If $y$ is an ancestor of $x$, then $z$ is an ancestor of $x$ if PRE$(z) <$ PRE$(y)$.

PROPERTY 2. Given two partitions $R_i$ and $R_j$ such as left$(R_j, R_i)$ is true. Assume that there are three nodes $x \in R_i$, $y \in R_j$ and $z \in R_j$. If $y$ is an ancestor of $x$, then $z$ is an ancestor of $x$ if POST$(z) >$ POST$(y)$.

Figure 4: Partitions
PROPERTY 3. Given two partitions $R_i$ and $R_j$ such as $\text{down}(R_j, R_i)$ is true. Assume that there are three nodes $x \in R_i, y \in R_j$ and $z \in R_j$. If $y$ is a descendant of $x$, then $z$ is a descendant of $x$ if $\text{PRE}(z) > \text{PRE}(y)$.

PROPERTY 4. Given two partitions $R_i$ and $R_j$ such as $\text{right}(R_j, R_i)$ is true. Assume that there are three nodes $x \in R_i, y \in R_j$ and $z \in R_j$. If $y$ is a descendant of $x$, then $z$ is a descendant of $x$ if $\text{POST}(z) < \text{POST}(y)$.

These properties can be used to reduce the overhead of evaluating structural joins, when nodes are sorted in a partition. Note that Grust (2002) and Grust et al. (2003) use the Dietz numbering scheme, as an index structure to support XPath location steps including ancestor, following, preceding, sibling, descendant-or-self, etc. However, they process joins node-at-a-time. We focus on joining partitions, which processes joins set-at-a-time.

3. A NEW PARTITION-BASED STRUCTURAL JOIN

In this section, we propose a new partition-based method for structural join between ancestors and descendants. Our method can be easily extended to support other XPath axes including following, preceding and sibling, etc.

We use the cases depicted in Figure 5 to illustrate our partition-based structural join algorithm. Figure 5(a) shows a general case where a plane is partitioned into 4 partitions, i.e., $A_1, A_2, A_3$ and $A_4$, according to partition $D$, where $D$ is a minimal partition (rectangle) which contains all descendant nodes. $D$ is always located the same as $A_4$ for ancestor/descendant relationship.

One technique we use in our partition-based join is to dynamically adjust the partitions of $A_1, A_2, A_3$ and $A_4 (= D)$ when we attempt to find ancestors for every $d$ in $D$. In other words, the four partitions are conceptually redrawn for any $d$ in $D$. Two ascending $B^+$-Tree indices on the preorder and postorder value are created for $A$, respectively. Note that we only need to scan every $d$ in $D$ once. The details are given below. We assume that elements in partitions are sorted by their preorder values in ascending order. The adjustment of partitions has the following three cases for a descendant $d$ in $D$.

1. $d$ is in the middle of the boundary between $A_2$ and $D$(Figure 5(b)).
2. $d$ is at the top of the boundary between $A_2$ and $D$(the top-left corner of $D$) (Figure 5(c)).
3. $d$ is at the bottom of the boundary between $A_2$ and $D$(Figure 5(d)).

For the first case, we output $d$ with all $a$ in $A_1$, then traverse each $ai$ in $A_2$ in the reverse order, and compare it with $d$, if $ai$ is not an ancestor of $d$, then all elements $di$ after $d$ cannot be the descendant of $ai$, we do not need to join this $ai$ with any such $di$ in $D$. Otherwise, if $ai$ is an ancestor of $d$, all $aj$ before $ai$ are ancestors of $d$ according to Property 2. Suppose that after processing $d$, we need to process the
next descendant $d_i$ in the sorted list (Figure 5(b)). Because $d$ is on the boundary between $A_2$ and $D$, the boundary between $A_3$ and $d_i$ will remain unchanged. We can find those elements $a$ in $A_3$ such as $\text{PRE}(a) < \text{PRE}(d_i)$. Note that when processing $d_i$ in Figure 5(b), those nodes $a$ in $A_4$ such as $\text{PRE}(a) < \text{PRE}(d_i)$ are adjusted to $A_2$. It is important to note that the area of $A_1$ and $A_2$ are expanded while the area of $A_3$ and $A_4$ are shrunk. This adjustment process is shown in Figure 5(b).

The second case is simple, since only all nodes in $A_1$ are the ancestors of $d$. All nodes in $A_2$ are the preceding nodes of $d$, all nodes in $A_3$ are the following nodes of $d$, and all nodes in $A_4$ are the descendants of $d$. We can simply output $d$ with every $a$ in $A_1$ as join results. After processing $d$, we need to adjust the boundaries of $D$, when we process the next descendant $d_i$ which has the smallest preorder value. In the first step, we identify a node $d_j$ in $D$ with the largest postorder value from the unprocessed descendants. In the second step, we adjust the following nodes to $A_1$.

- $a$ in $A_2$ if $\text{PRE}(a) > \text{POST}(d_j)$,
- $a$ in $A_4$ if $\text{PRE}(a) > \text{POST}(d_j)$,
- $a$ in $A_3$ if $\text{PRE}(a) < \text{PRE}(d_i)$, and
- $a$ in $A_4$ if $\text{PRE}(a) < \text{PRE}(d_i)$.

In the third step, we adjust those nodes $a$ in $A_4$ such as $\text{POST}(a) > \text{POST}(d_j)$ to $A_3$. This adjustment process is shown in Figure 5(c).

For the third case, all nodes in $A_1$ and $A_2$ are ancestors of $d$, and no nodes in $A_3$ and $A_4$ are ancestors of $d$. After processing $d$, we get the next element $d_i$ in $D$ following the sorted order. We can determine a node $d_j$ which has the minimum postorder value from the left elements. Because $d$ is at the bottom of the boundary between $A_2$ and $D$, the boundaries need to be adjusted. Here, we first remove those elements $a$ in $A_2$ and $A_4$ if $\text{POST}(a) < \text{POST}(d_j)$, since these nodes $a$ will not be ancestors of any descendants $d_i$ in $D$. Second, we adjust those elements $a$ in $A_3$ if $\text{PRE}(a) < \text{PRE}(d_i)$ to $A_1$. Third, we adjust those elements $a$ in $A_4$ if $\text{PRE}(a) < \text{PRE}(d_i)$ to $A_2$. This adjustment process is shown in Figure 5(d).

The partition-based structural join algorithm, P-JOIN($A$, $D$), is outlined below.

Algorithm 1 P-Join ($A$, $D$)

1: $A_1, A_2, A_3, A_4 \leftarrow \text{PARTITION}(A, D)$
2: for each $d$ in $D$(sorted) do
3: if $d$ is in case 1 then
4: \hspace{1em} posFlag $\leftarrow$ MIDDLE
5: else if $d$ is in case 2 then
6: \hspace{1em} posFlag $\leftarrow$ TOP
7: else if $d$ is in case 3 then
8: \hspace{1em} posFlag $\leftarrow$ BOTTOM
9: end if
10: OUTPUT ($A_1, d$)
11: if posFlag = MIDDLE then
12: \hspace{1em} LOCATE ($A_2, d$); OUTPUT ($A_2, d$); ADJUSTMIDDLE ($A, d$)
13: else if posFlag = TOP then
14: \hspace{1em} ADJUSTTOPLEFT ($A, D$)
15: else if posFlag = BOTTOM then
16: \hspace{1em} OUTPUT ($A_2, D$); ADJUSTBOTTOMLEFT ($A, D$)
17: end if
18: end for
The main advantage of algorithm \( P-Join \) is that it does not necessarily join every ancestors and descendants using a dynamic boundary adjustment technique.

In fact, as a pre-processing technique, we can filter those nodes that cannot be matched before calling \( P-Join \). Filtering operation is extensively used in database system to save I/O cost, consequently improve the system performance. Traditional bit filter (Babb, 1979; Valduriez and Gardarin, 1984) techniques in relational database utilize the equal relationship between attributes of two relations for filtering. For semistructured data like XML, however, bit filter techniques cannot be applied well, thus we filter nodes with their spatial positional characters.

We explain filtering using Figure 3(a). First, we use the minimum rectangle containing all descendants \( d \) to filter \( A \), all ancestors \( a \) in the area that cannot be an ancestor of any \( d \) are filtered. Thus, \( a_2 \) and \( a_9 \) are filtered, where \( a_2 \) is the preceding node of all nodes \( d \) and \( a_9 \) is the following node of all nodes \( d \). We can remove \( a_2 \) and \( a_9 \) from \( A \), and then we use the minimum rectangle containing the left \( A \) to filter \( D \), all nodes \( d \) in the area that will not be a descendant of any \( a \) will be filtered. In this example, no \( d \) is filtered because any \( d \) will produce the structural join result of \( ad \). It is easy to see that the filtering order of \( A \) and \( D \) is arbitrary and the results are the same. Moreover, one mutually filtering of \( A \) and \( D \) is enough and there is no need to recursively filter.

4. OPTIMIZATION TECHNIQUES

In this section, we further investigate optimization techniques on how to partition \( A \) and \( D \) when querying the ancestor-descendant relationship \( ad \). We will present a spatial partitioning approach and two optimization techniques, and will discuss the data structure for indexing the partitioning results. On top of the spatial partitioning approach, two new partition based structural join algorithms are proposed.

4.1 Spatial-Partitioning

Partitioning \( A \) and \( D \) for minimizing structural join is challenging, and is itself complex and time consuming. To find an efficient partitioning method, we are now left with the challenge to find a method which considers the spatial characters of \( A \) or \( D \) first, and then partition the leftover \( D \) or \( A \) for structural join.

When the size of \( D \) is large, the nested level is high and the distribution is poorly proportioned, the partitioning methods that mainly consider \( D \) will get good performance. On the contrary, the methods that pay attention to \( A \) will be better. The partitioning order of \( A \) or \( D \) is symmetrical. In this section, we mainly discuss the partitioning method for \( D \), the method for \( A \) can be applied in a similar manner.

Logically, an element node should be potentially distributed in any area of a plane. In practice, however, for a general XML data tree, element nodes are mainly distributed near the area from the bottom left to top right of a plane. The root node will exist on the top left. Only when the whole
XML data tree is a linear structure, the node will appear on the bottom right, which is obviously an abnormal case. Based on the characteristics of the general distribution of XML data trees, we propose an efficient spatial partitioning method, denoted as SPATIAL-PARTITIONING.

The basic idea of SPATIAL-PARTITIONING is first to find two data marks that have the largest distance in $d$ and search the nearest $|d|/N$ nodes of each data mark with a NEAREST method. Spatial-Partitioning will recursively call the NEAREST method until the size of a group is 1 or 2. The two data marks are chosen from the edges of the minimum rectangle containing all $d$. The selection of the $|d|/N$ nearest nodes is implemented as shown in Figure 6. The NEAREST() procedure is given below.

**Algorithm 2 NEAREST** ($x$, $n$)

1: $nX \leftarrow x$'s nearest $n$ points in $x$-axis
2: $e \leftarrow$ FURTHERMOST ($x$, $nX$)
3: $r \leftarrow$ DISTANCE ($e$, $x$)
4: $p \leftarrow$ minPreorder node in the left nodes
5: while $X$-DISTANCE($p$, $x$) $< r$ do
6: if DISTANCE ($p$, $x$) $< r$ then
7: $nX \leftarrow nX- e+ p$
8: $e \leftarrow$ FURTHERMOST($x$, $nX$)
9: $r \leftarrow$ DISTANCE($e$, $x$)
10: $p \leftarrow p.next$
11: end if
12: end while
13: return $nX$

In the NEAREST procedure, the FURTHERMOST($x$, $nX$) searches the furthermost point of $x$ in $nX$, the DISTANCE($e$, $x$) is the $2D$ distance between $e$ and $x$, the $X$-DISTANCE($p$, $x$) is their horizontal distance.

We give an example for searching five nearest nodes of $x$ including $x$ in Figure 6. We first search five nearest nodes on the $X$-axis distance of $x$, which are $x$, $e_1$, $e_2$, $e_3$ and $e_4$. The furthermost node is $e_1$, and $r_1$ is the distance between $x$ and $e_1$, any node whose horizontal distance with $x$ is less than $r_1$ may be in the result. We choose node according to its preorder, so next we get $e_4$, which is nearer than $e_1$, so we remove $e_1$ and add $e_4$. Now the five nodes are $x$, $e_2$, $e_3$, $e_4$ and $e_5$. And then, we get $e_6$ and remove $e_3$, now the furthermost node is $e_4$ and the furthermost distance is $r_3$, other nodes' horizontal distance with $x$ are all larger than $r_3$. Now we get $x$ five nearest nodes $x$, $e_2$, $e_4$, $e_5$ and $e_6$.

Compared with computing all nodes to find their nearest $n$ nodes, this partitioning method only need to compute a small part of nodes to get the results. Furthermore, along with the progress of partitioning, the nodes will be less and the search speed will be quicker. The efficiency of NEAREST procedure benefits from the particular plane distribution characters of tree nodes. With above example, we can easily see that our partitioning method could quickly partition $D$ into $N$ groups, each has $D_N$ nodes. We show SPATIAL-PARTITIONING algorithm below.

**Algorithm 3 SPATIAL-PARTITIONING** ($d$, $n$, $I=1$)

1: if $N = 1$ then
2: return $D_i$
3: else if $N=2$ then


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4: choose p₁ and p₂ in D
5: \( D_i \leftarrow \text{NEAREST}(p_1, |D|/N) \)
6: \( D_{i+1} \leftarrow \text{NEAREST}(p_2, |D|/N) \)
7: return \( D_i, D_{i+1} \)
8: else if \( N>2 \) then
9: choose p₁ and p₂ in D
10: \( D_i \leftarrow \text{NEAREST}(p_1, |D|/N) \)
11: \( D_{i+1} \leftarrow \text{NEAREST}(p_2, |D|/N) \)
12: \( D \leftarrow D - D_i - D_{i+1} \)
13: \( N \leftarrow N-2 \)
14: \( i \leftarrow i+2 \)
15: \( \text{GROUP}(D, N, i) \)
16: return \( D_1 \ldots D_N \)
17: end if

In our SPATIAL-PARTITIONING() method, if \( N = 1 \), we just distribute all D to one group. Otherwise, we choose two enough remote datum marks on the edges of minimum rectangle containing all D, and search each datum mark’s \(|D|/N\) nearest points and distribute them to one group. And then, we recursively call the spatial partitioning method until all D are distributed to N groups. With this procedure, the number of d in each group is \(|D|/N\).

To make the result simple and concrete, suppose partitioning number \( N=2 \). We partition the D as shown in Figure 3(a), we first choose two enough remote points \( d_1 \) and \( d_{10} \). Then choose \( d_1 \)’s \(|D|/N = 5\) nearest points \( d_1, d_3, d_4, d_5, d_6 \) to first group \( D_1 \) and \( d_4, d_7, d_8, d_9, d_{10} \) to the second group \( D_2 \). The partitioning result is shown in Figure 7. \( D_1 \) is the minimum rectangle containing all \( d \) nodes inside \( D_1 \), and \( D_2 \) is the minimum rectangle containing all \( d \) nodes inside \( D_2 \).

4.2 Optimized Partitioning Methods

Under the precondition of average partition of D, however, we should further optimize the partitioning results to improve the performance. To get this requirement, we propose two optimized methods based on the partitioning results of SPATIAL-PARTITIONING() method.

The first optimized method is to minimize the maximum area of D. Minimizing the maximum rectangle of D could increase the possibility that sibling element nodes fall into the same rectangle, which could reduce the chance that the same ancestor \( a \) be duplicated in different groups. Thus save the additional disk I/O cost. The method MINMAXD(D1 ... DN) is given below:

![Figure 7: Partition D](image-url)
Algorithm 4 MINMAXD \((D_1, \ldots, D_N)\)

1: \(D_i\) MAXAREA\((D_i)\) \((i = 1 \ldots N)\)
2: \(D_j = \text{NEARESTAREA}(\text{CENTER}(D_i))\)
3: \(d = \text{NEARESTPOINT}(D_i, D_j)\)
4: \(\text{if } \text{AREA}(D_i + d) < \text{AREA}(D_i) \text{ then}
5: \quad \text{MERGE}(D_i, d)
6: \quad \text{CUT}(D_i, d)
7: \quad \text{return} \text{MINMAXD}(D_1, \ldots, D_N)
8: \text{else}
9: \quad \text{return} D_1, \ldots, D_N
10: \text{end if}

This method first searches the rectangle area \(D_i\) from \(D_1\) to \(D_N\) having the maximum area. Next we try to reduce the area of \(D_i\). We search the area \(D_j\) whose centre is the nearest to the centre of \(D_i\). Then we choose the point \(p\) on the edge of \(D_i\), which could guarantee that after removing \(p\) from \(D_i\), the area of \(D_i\) will reduce. Now we just need to judge if the area of new \(D_j\) with \(p\) is larger than the area of old \(D_i\). We aim at minimizing the maximum area of \(D\), therefore, we recursively call this method if this optimization could further reduce the maximum area. Otherwise, we terminate this method and return the partitioning result after optimization.

The second optimized method is to minimize each overlay area. Any element \(d\) in the overlay area will be distributed to just one group. Compared with the whole rectangle, the overlay area is a smaller area and elements in it are more likely to be the sibling elements. If sibling elements are distributed to distinct groups, their common ancestor are sure to be distributed to corresponding groups, which need redundant duplication overhead. Minimizing the overlay area of rectangles and the number of \(d\) in the overlay area may, therefore, reduce the entire duplication overhead. The optimized method MINOVERLAY\((D_1, \ldots, D_N)\) is given below:

This method first checks if there are overlay areas from \(D_1\) to \(D_N\). If there is not any overlay area from \(D_1\) to \(D_N\), no optimization is needed. Otherwise, there are three cases for each overlay area \(O\) as the followings:

- There is no point in the overlay area \(O\), then, we do nothing to adjust it.
- There are some points in the overlay area \(O\), nevertheless, no points are on the edge of \(O\). In this case, adjusting these points will not effect the area of \(O\). Therefore, we do not adjust these points, either.
- There are some points in the overlay area \(O\) and at least one point is on the edge of \(O\). Then we
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could adjust the points on the edge of \( O \) to the other \( D_i \) it does not belong to originally, with which to reduce the area of overlay \( O \).

When no point is on the edge of any overlay area, this optimization process is performed.

**Algorithm 5 MINOVERLAY** \((D_1, \ldots, D_N)\)

1: if \((D_i \cap D_j) = \text{NULL} \ (i \neq j)\) then
2: \quad return \(D_1, \ldots, D_N\)
3: end if
4: \(\text{SELECTUNDISPOSED} (O) = D_i \cap D_j\)
5: if no point in \( O \) then
6: \quad do nothing
7: else if points are not on the edge of \( O \) then
8: \quad return \(D_1, \ldots, D_N\)
9: else if points are on the edge of \( O \) then
10: \quad for each \( p \in \text{EDGE} \ (O) \) do
11: \quad \quad if \( p \in D_i \) then
12: \quad \quad \quad \( D_i \leftarrow D_i - p; D_j \leftarrow D_j + p \)
13: \quad \quad else
14: \quad \quad \quad \( D_j \leftarrow D_j - p; D_i \leftarrow D_i + p \)
15: \quad \quad end if
16: \quad end for
17: end if
18: return MINOVERLAY(D_1, \ldots, D_N)

4.3 Indexing Partitioned Groups

We now introduce the data structure to index partitioning results \( D \) and \( A \). There is much research on indexing and querying spatial data. R-tree (Guttman, 1984), R*-tree (Beckmann et al., 1990) and M-tree (Ciaccia et al., 1997) are popular index mechanisms for indexing spatial data and spatial join (Arge et al., 2004; Brinkhoff et al., 1993; Huang and Rundensteiner, 1997; Proietti and Faloutsos, 2000; Zezula et al., 1998). R-tree and M-tree families have good search performance, which could be used in our data partition method. XML has inherent structural characters distinct from other spatial data, therefore, we adopt a more simple but effective method for partition.

We use \( B^+\)-Tree to index the groups of \( D \), after spatial partitioning of \( D \), into \( N \) groups, \( D_1, D_2, \ldots, D_N \). For each \( D_i \), we index its corresponding \( A \) which may produce join results with \( D_i \). They

![Figure 9: Modify Overlay](image-url)
are $A_1$, $A_2$, $A_3$ and $A_4$. We call this structure partitioned spatial structural index tree (PSS-tree). The structure of PSS-tree is shown in Figure 10. All data in PSS-tree are clustered.

### 4.4 Partitioned Spatial Structural Join Algorithms

Based on the SPATIAL-PARTITIONING method, spatial partitioning methods and PSS-tree, in this section, we propose two partitioned spatial structural join algorithms, PSSJ and OPSSJ.

Partitioned spatial structural join algorithm (PSSJ) first filters most ancestors and descendants which will not be join results. Then it uses the basic SPATIAL-PARTITIONING method to partition $D$. Next we use a PSS-tree to index all partitioning groups of $D$ and corresponding $A$s. As to each group, we call SPATIAL-PARTITIONING method to perform the join operation. Now we give the PSSJ algorithm.

**Algorithm 6 PSSJ** $(A, D, N)$

1. FILTER $(A, D)$
2. SPATIAL-PARTITIONING $(D, N)$
3. for each $D_i \in D_1, \ldots, D_N$ do
4.   PSSTree.insert($D_i$, $A_i$)
5. end for
6. for each $I \in 1 \ldots N$ do
7.   P-J OIN $(A_i, D_i)$
8. end for

The process of the optimized partitioned spatial structural join algorithm OPSSJ is similar to PSSJ. The only difference is that after partitioning $D$, OPSSJ calls two optimized methods to optimize the partitioning result. The optimized algorithm OPSSJ are given below:

**Algorithm 7 OPSSJ** $(A, D, N)$

1. FILTER $(A, D)$
2. SPATIAL-PARTITIONING $(D, N)$
3. MINMAX $(D_1, \ldots, D_N)$
4. MINOVERLAY $D_1, \ldots, D_N$
5. for each $D_i \in D_1, D_2, \ldots, D_N$ do
6.   PSSTree.insert($D_i$, $A_i$)
7. end for
8. for each $I \in 1 \ldots N$ do
9.   P-J OIN $(A_i, D_i)$
10. end for
5. PERFORMANCE ANALYSIS
In this section, we present the experimental evaluation that yields a sense for the efficacy of our novel partitioned structural join algorithms. We start with a description of our experiment platform and test data set in Section 5.1. The following sections present a result evaluation and performance evaluation of our partitioned spatial structural join algorithm.

5.1 Experiment Setting
We ran experiments on a PC with Intel Pentium 2.0 GHz CPU, 512M RAM and 40G hard disk. The operating system is Microsoft Windows XP. We employ an OODBMS FISH (Yu et al., 1996) to store XML data. The testing programs were written in Forte C++ and INADA conformed to ODMG (The Object Database Standard, 2000) C++ binding. We have implemented partitioned SpatialStructuralJoin (PSSJ) and its optimized algorithm(OPSSJ), StackTreeJoin (STJ) and XR-Tree algorithm (XR-Tree).

We utilize synthetic data for all our experiments in order to control the structural and consequent join characteristics of the XML documents. We use the IBM XML data generator (Diaz and Lovell, 1999) to generate XML document. The two DTDs adopted are shown in Figure 11. Different sized documents that scale from 20M to 100M are generated with each DTD.

Experiments were performed to study the comparative performance on our two partitioned spatial structural join algorithm. Table 1 shows the set of queries for all data set on two DTDs. Table 2 presents the nested case of our query set. Q1 is selected to test the case that both ancestor and descendant are highly nested. Q2 is selected to test the case that ancestor is highly nested but descendant is less nested. Q3 is selected to test the case that ancestor is less nested but descendant is highly nested. Q4 is selected to test the case that both ancestor and descendant are less nested. The test query set contains all possible nested case of ancestor and descendant for thoroughly analyzing the performance of partitioned spatial structural join algorithms.

<table>
<thead>
<tr>
<th>QUERY</th>
<th>DESCRIPTION</th>
<th>DTD</th>
</tr>
</thead>
<tbody>
<tr>
<td>Q1</td>
<td>department/employee</td>
<td>Department</td>
</tr>
<tr>
<td>Q2</td>
<td>employee/name</td>
<td>Department</td>
</tr>
<tr>
<td>Q3</td>
<td>section/subsection</td>
<td>Library</td>
</tr>
<tr>
<td>Q4</td>
<td>section/title</td>
<td>Library</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>QUERY</th>
<th>ANC NESTED</th>
<th>DESC NESTED</th>
</tr>
</thead>
<tbody>
<tr>
<td>Q1</td>
<td>highly</td>
<td>highly</td>
</tr>
<tr>
<td>Q2</td>
<td>highly</td>
<td>less</td>
</tr>
<tr>
<td>Q3</td>
<td>less</td>
<td>highly</td>
</tr>
<tr>
<td>Q4</td>
<td>less</td>
<td>less</td>
</tr>
</tbody>
</table>

Table 1: Query Set

Table 2: Query Nested Case
5.2 Varying Partitioning Number
The objective of this set of experiments is to test the query performance of PSSJ and OPSSJ with varying partitioning numbers. We adopt one 100M document for each DTD. The performance curves of testing varying partitioning numbers are given in Figure 12.

Figure 12(a) shows the performance of Q1 with partitioning numbers varying from 10 to 60. Figure 12(b) shows the performance of Q2 with partitioning numbers varying from 10 to 60. Figure 12(c) shows the performance of Q3 with partitioning numbers varying from 20 to 120. Figure 12(d) shows the performance of Q4 with partitioning numbers varying from 30 to 180.

It can be seen from Figure 12 that PSSJ algorithm and OPSSJ algorithm can get better performance along with the increase of the partitioning number, which demonstrates the effectiveness of our partitioning methods. And in each case, the optimized algorithm OPSSJ outperforms the basic PSSJ algorithm. We can also see that when the partitioning number gets to some value in each case, the amplitude of performance will be slow. This value is closely relative to the number and the nested case of ancestors and descendants. The more the number of ancestors and descendants, the more the partitioning number is needed to get a good performance.

5.3 Varying Join Selectivity Test
In the second group of experiments, we study the capabilities of various algorithms to skip elements under different join selectivity. We keep the document size 100M and partitioning number...
unchanged for each query in this test. We test the case when the ancestor join selectivity and descendant join selectivity are varying. For this purpose, we change the document elements with dummy elements so that the desired selectivity on ancestors or descendants can be obtained.

Figure 13 shows the performance of the four algorithms tested when varying join selectivity. Figure 13(a) tests Q1 and Figure 13(b) tests Q2. The nested levels of ancestors are high in both queries. We can clearly see from them that in this case, the join selectivity has great influence on XR-Tree algorithm, while it has little influence on Stack-Tree join algorithm and our two partitioned spatial join algorithms. And in this case, XR-Tree has bad performance. Stack-Tree join algorithm has similar good performance as PSSJ and OPSSJ.

Figure 13(c) tests Q3 and Figure 13(d) tests Q4. The nested level of ancestors is low. We can see from (c)(d) that join selectivity has great influence on all tested algorithms. And in this case, XR-Tree is better than Stack-Tree join and has similar performance as our two partitioned spatial structural join algorithms.

5.4 Sizeup Test
In the third set of experiments, we vary the document size to compare the performance of different structural join algorithms. We kept the join selectivity at 30%, we also give the fixed partitioning number for PSSJ and OPSSJ algorithms. We vary the document size from 20M to 100M.

Figure 14 gives this group of performance tests.

We can see that in all cases, our partitioned spatial structural join algorithms PSSJ and OPSSJ get better performance than XR-Tree and XR-Tree is better than Stack-Tree join algorithm. But 14(b) is an exception, when the nested level of ancestor is high and the nested level of descendant is low,
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Figure 14: Sizeup Test

XR-Tree get a worse performance than Stack-Tree join algorithm.

We can also observe from this figure that all four tested structural join algorithms have good sizeup performance. Along with the increase of the document size, the elapsed time of each algorithm increases well-proportioned.

5.5 Partitioning vs Workload

In this subsection, we analyze the impact of partitioning on the workload of structural join.

Table 3 shows the workload of the sample XML document in Figure 1 under a different number of partitions.

\( A_{\text{output}} \) is the part which could directly output join results without join operation. Thus we omit the workload of this part of \( A \). \( A_{\text{join}} \) is the part which needs structural join with corresponding partition \( D \), we simply compute the workload as \( na \times nd \) where \( na \) is the number of \( a \).

As shown in Table 3, along with the increasing number of partitions, the total number of \( a \) that falls in the \( A_{\text{output}} \) increases, the number which takes part in the join decreases correspondingly. Thus the total workload of \( A_{\text{join}} \) decreases. For example, when the number of partitions is 1, the join workload is 60. When the number of partitions is 2, the join workload turns to 25. When the number of partitions is 3, the join workload decreases to 12, but when the number of partitions is 4, the join workload is still 12 because the number of \( a \) and \( d \) participating in the join is changeless. So in this case, we need no further partitioning operation.

Figures 15 and 16 give the impact of partitioning on the workload of structural joins of \( \text{section/title} \) and \( \text{department/employee} \). From the tables, we can see that with the increasing of the number of partitions the workload of structural join is decreasing while the number of nodes in the partition which can be used to output the join results is increasing.
5.6 Maintenance Overhead Test
In the last experiment, we test the maintenance overhead of XR-Tree and our basic partitioned spatial structural join algorithm PSSJ. We mainly test the elapsed time of constructing index structures. Figure 17 gives the maintenance cost with documents of different size.

Table 3: Workload of A//D in the sample XML document

<table>
<thead>
<tr>
<th># OF PARTITIONS</th>
<th>Output</th>
<th>Join</th>
<th>WORKLOAD</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1</td>
<td>6 × 10</td>
<td>60</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>1</td>
<td>25</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>1 × 3</td>
<td>12</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>0 × 4</td>
<td></td>
</tr>
<tr>
<td></td>
<td>1</td>
<td>3 × 3</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>3</td>
<td>1 × 3</td>
<td>12</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>0 × 2</td>
<td></td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>0 × 2</td>
<td></td>
</tr>
<tr>
<td></td>
<td>1</td>
<td>3 × 3</td>
<td></td>
</tr>
</tbody>
</table>

Figure 15: Workload of section/title

Figure 16: Workload of department/employee

Figure 17: Maintenance Cost(department vs. employee)
We only take Q1 for example because the other performance curves have the similar trend. Observe from this figure, we can see that the maintenance cost of PSSJ is always less than that of XR-Tree. With the increase of the document size, this trend is more obvious.

6. CONCLUSIONS
In this paper, we first extend the relationships between nodes to the relationships between partitions and get some observations about the relationships between partitions. We then introduce a partition-based method P-Join (Tang et al., 2005), for structural join between ancestors and descendants based on the properties derived from these observations. Moreover we present an enhanced partition-based structural join algorithm and two optimized methods. In order to store the partitioning results, we designed a simple but efficient index structure called PSS-tree. Extensive experiments show that our approaches outperform previous methods and we could also get low maintenance costs.

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