A NEW ALGORITHM FOR TWIG PATTERN MATCHING

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Abstract: Tree pattern matching is one of the most fundamental tasks for XML query processing. Prior work has typically decomposed the twig pattern into binary structural (parent-child and ancestor-descendent) relationships or paths, and then stitch together these basic matches by join operations. In this paper, we propose a new algorithm that explores both the document tree and the twig pattern in a bottom-up way and show that the join operation can be completely avoided. The new algorithm runs in $O(|T|\cdot|Q|)$ time and $O(|Q|\cdot leaf_T)$ space, where T and Q are the document tree and the twig pattern query, respectively; and $leaf_T$ represents the number of leaf nodes in T. Our experiments show that our method is effective, scalable and efficient in evaluating twig pattern queries.

1 INTRODUCTION

In XML, data is represented as a tree; associated with each node of the tree is an element type from a finite alphabet $\sum$. The children of a node are ordered from left to right, and represent the content (i.e., list of subelements) of that element.

To abstract from existing query languages for XML (e.g. XPath, XQuery, XML-QL, and Quilt), we express queries as twig patterns (or say, tree patterns) where nodes are types from $\sum \cup \{*\}$ (* is a wildcard, matching any node type) and string values, and edges are *parent-child* or *ancestor-descendant* relationships. As an example, consider the query tree shown in Fig. 1, which asks for any node of type b (node 2) that is a child of some node of type a (node 1). In addition, the b type (node 2) is the parent of some c type (node 4) and an ancestor of some d type (node 5). Type b (node 3) can also be the parent of some e type (node 7). The query corresponds to the following XPath expression:

$a[b[c \text{ and } //d]]/b[c \text{ and } e//d]$.

In this figure, there are two kinds of edges: child edges (c-edges) for parent-child relationships, and descendant edges (d-edges) for ancestor-descendant relationships. A c-edge from node v to node u is denoted by $v \rightarrow u$ in the text, and represented by a single arc; u is called a *c-child* of v. A d-edge is denoted $v \Rightarrow u$ in the text, and represented by a double arc; u is called a *d-child* of u.

Definition 1. An embedding of a twig pattern Q into an XML document T is a mapping f: $Q \rightarrow T$, from

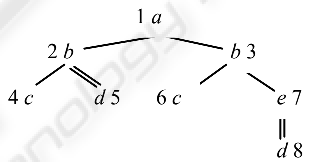

Figure 1: A query tree.

the nodes of Q to the nodes of T, which satisfies the following conditions:

(i) Preserve node type: For each $u \in Q$, u and $f(u)$ are of the same type. (or more generally, u's predicate is satisfied by $f(u)$.)

(ii) Preserve c/d-child relationships: If $u \rightarrow v$ in Q, then $f(v)$ is a child of $f(u)$ in T; if $u \Rightarrow v$ in Q, then $f(v)$ is a descendant of $f(u)$ in T.

If there exits a mapping from Q into T, we say, Q can be imbedded into T, or say, T contains Q. In addition, if label(T's root) = label(Q's root), we say that the embedding is *root-preserving*.

As an example, see the document tree and the twig pattern shown in Fig. 2(a).

There exits a mapping from Q to T as illustrated by the dashed lines, by which each node of Q is mapped to a different node of T. However, according to the definition, an embedding could map several nodes of Q (of the same type) to the same node of T, as shown in Fig. 2(b), by which nodes q_2 and q_5 in Q are mapped onto a single node v_2 in T, and q_3 and q_4 are mapped onto a single node v_3 in T.

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For the purpose of query evaluation, either of the mappings is recognized as a tree embedding.

In fact, almost all the existing strategies are designed to work in this way.

In this paper, we discuss a new algorithm, which works in a bottom-up way and shows that the join or join-like operations can be completely avoided. The algorithm works in $O(|T|\cdot|Q|)$ time and $O(|Q|\cdot leaf_T)$ space, where $leaf_Q$ is the number of the leaf nodes of Q.

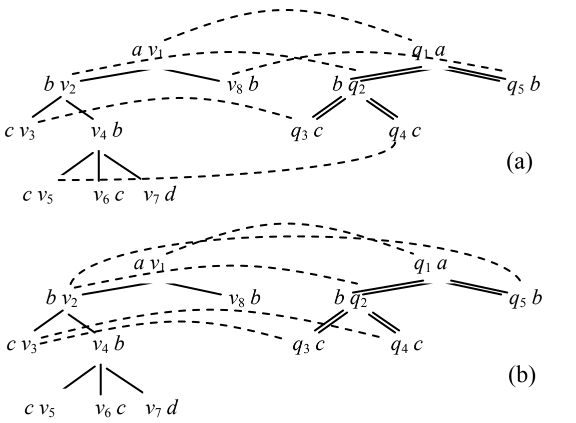


Figure 2: Illustration for tree embedding.

The remainder of the paper is organized as follows. In Section 2, we review the related work. In Section 3, we discuss our main algorithm. Section 4 is devoted to the implementation and experiments. Finally, a short conclusion is set forth in Section 5.

2 RELATED WORK

With the growing importance of XML in data exchange, the tree pattern queries over XML documents have been extensively studied recently. Most existing techniques rely on indexing or on the tree encoding to capture the structural relationships among document elements.

XISS (Li and Moon, 2001) is a typical method based on indexing, by which single elements/attributes are indexed as the basic unit of query and a complex path expression is decomposed into a set of basic path expressions. Then, atom expressions (single elements or attributes) are recognized by direct accessing the index structure. All other kinds of expressions need join operations to stitch individual components together to get the final results.

Paths are also used as the basic indexing unit as done by DataGuide (Goldman and Widom, 1997) and Fabric (Cooper and *et al*., 2001). By DataGuide, a concise summary of path structures for a semi-structured database is provided, but restricted to row paths. No complex path expressions or regular expression queries can be handled. Fabric works better in the sense that the so-called *refined paths* are supported. Such queries may contain branches, wild-cards (*) and ancestor-descendent operators (//). However, any query not in the set of refined paths has to resort to join operations. Another two strategies based on the path indexing are APEX (Chung and *et al*., 2002) and F^+B (Kaushik and *et al*., 2002). APEX is an adaptive path index and uses data mining technique to summarize paths that frequently appear in the query workload. It has to be updated as the query workload changes. In stead of maintaining all paths starting from the root, it keeps every path segment of length 2. Obviously, to get the final results, the join operations have to be conducted. F^+B (Kaushik and *et al*., 2002) shares the flavour of Fabric (Cooper and *et al*., 2001). It is based on the so-called forward and backward index (F&G index (Abiteboul and *et al*., 1999)), which covers all the branching paths. It works well for pre-defined query types. In normal cases, however, such a set of F&B indexes tends to be large and therefore the performance suffers. The method discussed in (Wang and *et al*., 2003) can be considered as a quite different method, by which a document is stored as a sequence: (a_1, p_1), ..., (a_i, p_i), ..., (a_n, p_n), where each a_i is an element or a word in the document, and p_i a path from the root to it. Using this method, the join operations are replaced by searching a trie structure (called suffix tree in (Wang and *et al*., 2003)). The drawback of this method is that a relatively large index structure has to be created. Another problem of this method is that a document tree that does not contain a query pattern may be designated as one of the answers due the *ambiguity* caused by identical sibling nodes. This problem is removed by the so-called *forward prefix* checking discussed in (Wang and Meng, 2005). Doing so, however, the theoretical time complexity is dramatically increased.

All the above methods need to decompose a twig pattern into a set of binary relationships between pairs of nodes, such as parent-child and ancestor-descendant relations, or into a set of paths. The sizes of intermediate relations tend to be very large, even when the input and final result sizes are much more manageable. As an important improvement, *TwigStack* was proposed by Bruno *et al.* (Bruno and *et al*., 2002), which compress the intermediate results by the stack encoding, which represents in linear space a potentially exponential number of answers. However, *TwigStack* achieves optimality only for the queries that contain only *d*-edges. In the case that a query contains both *c*-edges and *d*-edges, some useless path matchings have to be performed. In addition, in the worst case, *TwigStack* needs $O(|D|^{|Q|})$ time for doing the merge joins as shown by Chen *et al*. (see page 287 in (Chen and *et al*., 2006)), where D is a largest data stream associated with a node q in Q, which contains all the document nodes that match q. Since then, several methods that improve *TwigStack* in some way have been reported. For instance, *iTwigJoin* (Chen and *et al*., 2005) exploits different data partition possibilities while *TJF*ast (Lu and *et al*., 2005) accesses only leaf nodes of document trees by using Dewey IDs. But both of them still need to do some useless matchings as shown by the theoretical analysis made in (Choi and et al., 2003). *Twig*^{2}*Stack* (Chen and *et al*., 2006) is the most recent method that improves *TwigStack*. By this method, the stack encoding is replaced with the *hierarchical stack encoding*, by which each stack associated with a query node contains an ordered sequence of stack trees. In this way, the path joins are replaced by the so called *result enumeration*. In (Chen and *et al*., 2006), it is claimed that *Twig*^{2}*Stack* needs only $O(|D|\cdot|Q| + |subTwigResults|)$ time. But a careful analysis shows that the time complexity of the method is actually bounded by $O(|D|\cdot|Q|^2 + |subTwigResults|)$. It is because each time a node is inserted into a stack associated with a node in Q, not only the position of this node in a tree within that stack has to be determined, but a link from this node to a node in some other stack has to be constructed, which requires to search all the other stacks. The number of these stacks is $|Q|$ (see Fig. 4 in (Chen and *et al*., 2006) to know the working process.)

The method discussed in (Aghili and et al., 2006) incorporates a *binary labeling* as a pre-processing filtration step to reduce the search space. This method is effective only for the case that selective key words at leaf nodes are specified in queries.

Finally, we point out that the bottom-up tree matching was first proposed in (Hoffmann and O'Donnell, 1982). But it concerns a very strict tree matching, by which the matching of an edge to a path is not allowed. In (Gottlob and *et al*., 2005), an XPath is transformed into a parse tree and then evaluated bottom-up or top-down. Both the bottom-up and top-down strategies need $O(|T|^5\cdot|Q|^2)$ time and $O(|T|^4\cdot|Q|^2)$ space. In (Miklau and Suciu, 2004), an algorithm for tree homomorphism is discussed, which is able to check whether a tree contains another and returns only a boolean answer. But our algorithms show all the subtrees than match a given twig pattern query.

In comparison with the above methods, our methods have the following advantages:

- Our first algorithm needs less time than *Twig*^{2}*Stack*. Concretely, our algorithm runs in $O(|D|\cdot|Q|)$ time.
- Neither matching paths nor tree stacks are generated. Therefore, the costly path joins (Aghili and *et al*., 2006), as well as the result enumeration, a join-like operation (Chen and *et al*., 2006), are not needed.
- The runtime memory usage is minimum. During the process, our algorithm transforms (dynamically) the data streams to a tree structure T with all the matching patterns recognized. To represent the results, each node v in T is associated with a set of nodes in Q (denoted as $M(v)$) such that for each $q \in M(v)$ the subtree rooted at q can be embedded in the subtree rooted at v. If $M(v)$ contains the root of Q, it indicates an answer and v will be stored in a global variable (or report the subtree rooted at v as an answer). Later on, $M(v)$ will be removed once $M(v$'s parent) is established since $M(v)$ will not be accessed any more.

3 ALGORITHM

In this section, we discuss our algorithm according to Definition 1. The main idea of this algorithm is to search both T and Q bottom-up and checking the subtree embedding by generating dynamic data structures. In the process, a tree labeling technique is used to facilitate the recognition of nodes' relationships. Therefore, in the following, we will first show the tree labeling in 3.1. Then, in 3.2, we discuss the main algorithm. In 3.3, we prove the correctness of the algorithm and analyze its computational complexities.

3.1 Tree Labeling

Before we give our main algorithm, we first restate how to label a tree to speed up the recognition of the relationships among the nodes of trees.

Consider a tree T. By traversing T in *preorder*, each node v will obtain a number (it can an integer or a real number) $pre(v)$ to record the order in which the nodes of the tree are visited. In a similar way, by traversing T in *postorder*, each node v will get another number $post(v)$. These two numbers can be used to characterize the ancestor-descendant relationships as follows.

Proposition 1. Let v and v' be two nodes of a tree T. Then, v' is a descendant of v iff $pre(v') > pre(v)$ and $post(v') < post(v)$.

Proof. See Exercise 2.3.2-20 in [34].

If v' is a descendant of v, then we know that $pre(v') > pre(v)$ according to the preorder search. Now we assume that $post(v') > post(v)$. Then, according to the postorder search, either v' is in some subtree on the right side of v, or v is in the subtree rooted at v', which contradicts the fact that v' is a descendant of v. Therefore, $post(v')$ must be less than $post(v)$. The following example helps for illustration.

Example 1. See the pairs associated with the nodes of the tree shown in Fig. 3. The first element of each pair is the preorder number of the corresponding node and the second is its postorder number. With

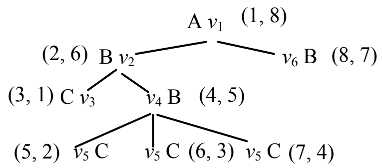


Figure 3: Illustration for tree encoding.

such labels, the ancestor-descendant relationships can be easily checked.

For instance, by checking the label associated with v_2 against the label for v_6, we see that v_2 is an ancestor of v_6 in terms of Proposition 1. Note that v_2's label is (2, 6) and v_6's label is (6, 3), and we have 2 < 6 and 6 > 3. We also see that since the pairs associated with v_8 and v_5 do not satisfy the condition given in Proposition 1, v_8 must not be an ancestor of v_5 and *vice versa*.

Definition 1. (*label pair subsumption*) Let (p, q) and (p', q') be two pairs associated with nodes u and v. We say that (p, q) is subsumed by (p', q'), denoted (p, q) (p', q'), if $p > p'$ and $q < q'$. Then, u is a descendant of v if (p, q) is subsumed by (p', q').

In the following, we also use $T[v]$ to represent a subtree rooted at v in T.

3.2 Algorithm for Twig Pattern Matching

Now we discuss our algorithm for twig pattern matching. During the process, both T and Q are searched bottom-up. That is, the nodes in T and Q will be accessed along their postorder numbers. Therefore, for convenience, we refer to the nodes in T and Q by their postorder numbers, instead of their node names.

In each step, we will check a node j in T against all the nodes i in Q.

In order to know whether $Q[i]$ can be embedded into $T[i]$, we will check whether the following two conditions are satisfied.

1. label(j) = label(i).
2. Let $i_1, ..., i_k$ be the child nodes of i. For each i_a (a = 1, ..., k), if (i, i_a) is a c-edge, there exists a child node j_b of j such that $T[j_b]$ contains $Q[i_a]$; if (i, i_a) is a d-edge, there is a descendent j' of j such that $T[j']$ contains $Q[i_a]$.

To facilitate this process, we will associate each j in T with a set of nodes in Q: $\{i_1, ..., i_j\}$ such that for each $i_a \in \{i_1, ..., i_j\}$ $Q[i_a]$ can be root-preservingly embedded into $T[j]$. This set is denoted as $M(j)$. In addition, each i in Q is associated with a value $\beta(i)$, defined as below.

i) Initially, $\beta(i)$ is set to ϕ.

ii) During the computation process, $\beta(i)$ is dynamically changed. Concretely, each time we meet a node j in T, if i appears in $M(j_b)$ for some child node j_b of j, then $\beta(i)$ is changed to j.

In terms of above discussion, we give the following algorithm.

Algorithm *Twig-pattern-matching*(T, Q)

Input: tree T (with nodes 0, 1, ..., $|T|$) and tree Q (with nodes 1, ..., $|Q|$)

Output: a set of nodes j in T such that $T[j]$ contains Q.

```
begin
1.    for j := 1, ..., |T| do
2.    {let j_1, ..., j_k be the children of j;
3.      for l := 1, ..., k do
4.        {for each i' ∈ M(j_l) do β(i') ← j;
5.            remove M(j_l);}
5.            for i := 1, ..., |Q| do
6.            if label(i) = label(j) then
7.     {let i_1, ..., i_g be the children of i;
8.          if for each i_l (l = 1, ..., g) we have
9.            (i, i_l) is a c-edge and β(i_l) = j, or
10.           (i, i_l) is a d-edge and β(i_l) is subsumed by j;
11.   then {insert i into M(j);
12.             if i is the root of Q, then report the subtree
                rooted at j as an answer;}
13.  }
end
```

In the above algorithm, each time we meet an j in T, we will establish the new β values for all those nodes of Q, which appear in $M(j_1)$, ..., $M(j_k)$, where $j_1, ..., j_k$ represent the child nodes of j (see lines 1 - 4). Then, all $M(j_l)$'s (l = 1, ..., k) are removed. In a next step, we will check j against all the nodes i in Q (see lines 5 - 13). If label(i) = label(j), we will check $\beta(i_1)$, ..., $\beta(i_g)$, where $i_1, ..., i_g$ are the child nodes of i. If (i, i_l) ($l \in \{1, ..., g\}$) is a c-edge, we need to check whether $\beta(i_l) = j$ (see line 9). If (i, i_l) ($l \in \{1, ..., g\}$) is a *d*-edge, we simply check whether $\beta(i_l)$ is subsumed by *j* (see line 10). If all the child nodes of *i* survive the above checking, we get a root-preserving embedding of the subtree rooted at *i* into the subtree rooted at *j*. In this case, we will insert *j* into *M*(*j*) (see line 11) and report *j* as one of the answers if *i* is the root of *Q* (see line 12).

Example 2. Consider the document tree *T* and the twig pattern query *Q* shown in Fig. 2(a) once again. When applying the above algorithm to *T* and *Q*, we will find that *Q* can be root-preservingly embedded into *T*. Fig. 4 shows the whole computation process.

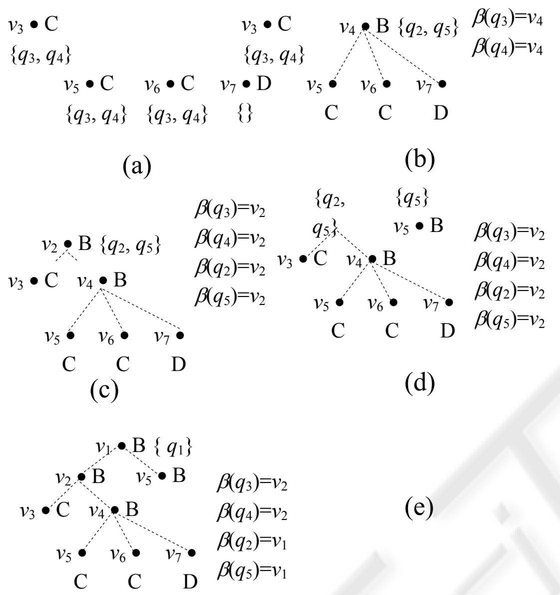


Figure: 4: A sample trace.

In the first four steps, we check respectively v_3, v_5, v_6, and v_6 against *Q*, generating a data structure as shown in Fig. 4(a), in which $M(v_3) = M(v_5) = M(v_6) = \{q_3, q_4\}$ and $M(v_7) = \{\ \}$. In a next step, we meet v_4 and generate a data structure as shown in Fig. 4(b). In more detail, in this step, we first set $\beta(q_3) = v_4$ and $\beta(q_4) = v_4$, and then try to find any subtree in *Q*, which can be embedded into $T[v_4]$. Since label(v_4) = label(q_2) = B and both $\beta(q_3)$ and $\beta(q_4)$ are equal to v_4, it shows that $T[v_4]$ contains $Q[q_2]$. So $M(v_4)$ contains q_2. In addition, since q_5 is a leaf node (no children) and label(v_4) = label(q_5), $M(v_4)$ also contains q_5. In the sixth step, we will meet v_2 and the data structure generated is shown in Fig. 4(c). Here, we should remark that not only $\beta(q_2)$ and $\beta(q_5)$ are set to v_2, but $\beta(q_3)$ and $\beta(q_4)$ are also changed to v_2. It is because in this step we have $M(v_3) = \{q_3, q_4\}$ and v_3 is a child node of v_2. Therefore, we have $M(v_2) = \{q_2, q_5\}$. In the seventh step, we meet v_8 and generate a data structure as shown in Fig. 4(d). Although we have label(v_8) = label(q_2), we cannot insert q_2 into $M(v_8)$ since in this step both $\beta(q_3)$ and $\beta(q_4)$ are equal to v_2, not to v_8. So $M(v_8)$ contains only q_5. In the final step, we meet v_1. The corresponding data structure is shown in Fig. 4(e). Since $M(v_1)$ contains q_1, the root of *Q*, we know that *Q* can be embedded into *T*.

4 CORRECTNESS AND COMPUTATIONAL COMPLEXITIES

In this subsection, we show the correctness of the algorithm given in 3.2 and analyze its computational complexity.

- *Correctness*

The correctness of the algorithm consists in a very important property of postorder numbering described in the following lemma.

Lemma 1. Let v_1, v_2, and v_3 be three nodes in a tree with $post(v_1) < post(v_2) < post(v_3)$. If v_1 is a descendent of v_3. Then, v_2 must also be a descendent of v_3.

Proof. We consider two cases: i) v_2 is to the right of v_1, and ii) v_2 is an ancestor of v_1. In case (i), we have $post(v_1) < post(v_2)$. So we have $pre(v_3) < pre(v_1) < pre(v_2)$. This shows that v_2 is a descendent of v_3. In case (ii), v_1, v_2, and v_3 are on the same path. Since $post(v_2) < post(v_3)$, v_2 must be a descendent of v_3.

We illustrate Lemma 1 by Fig. 5, which is helpful for understanding the proof of Proposition 2 given below.

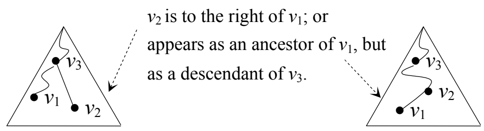


Figure 5: A matching subtree with *M*'s.

Proposition 2. Let *Q* be a twig pattern containing only *d*-edges. Let *v* be a node in the document tree *T*. Let *q* be a node in *Q*. Then, *q* appears in *M*(*v*) if and only if *T*[*v*] contains *Q*[*q*].

Proof. If-part. A query node *q* is inserted into *M*(*v*) by executing lines 6 - 11 in Algorithm *Twig-pattern-matching*( ). Obviously, for any *q* inserted into *M*(*v*) we must have *T*[*v*] containing *Q*[*q*].

Only-if-part. Assume that there exists a *q* in *Q* such that *T*[*v*] contains *Q*[*q*] but *q* does not appear in *M*(*v*). Then, there must be a child node q_i of *q* such that (i) $\beta(q_i) = \phi$, or (ii) $\beta(q_i)$ is not subsumed by *v*. Obviously, case (i) is not possible since *T*[*v*] contains $Q[q]$ and q_i must be contained in a subtree rooted at a node *v'* which is a descendent of *v*. So $\beta(q_i)$ will be changed to a value not equal to ϕ. Now we show that case (ii) is not possible, either. First, we note that during the whole process, $\beta(q_i)$ may be changed several times since it may appear in more than one *M*'s. Assume that there exist a sequence of nodes v_1, ..., v_k for some $k \geq 1$ with $post(v_1) < post(v_2) <... < post(v_k)$ such that q_i appears in $M(v_1)$, ..., $M(v_k)$. Without loss of generality, assume that $v' = v_i$ for some $i \in \{1, ..., k\}$ and there exists an *j* such that $post(v_j) < post(v) < post(v_{j+1})$. Then, at the time point when we check *q*, the actual value of $\beta(q_i)$ is the postorder number for v_j's parent, which is equal to *v* or whose postorder number is smaller than $post(v)$. If it is equal to *v*, then $\beta(q_i)$ is subsumed by *v*, contradicting (ii). If $post(\beta(q_i)$ is smaller than $post(v)$. Thus, we have

$$post(v') < post(\beta(q_i) < post(v).$$

In terms of Lemma 1, the value of $\beta(q_i)$ is a descendent of *v* and therefore subsumed by *v*. The above explanation shows that case (ii) is impossible. This completes the proof of the proposition.

Lemma 1 helps to clarify the *only-if* part of the above proof. In fact, it reveals an important property of the tree encoding, which enables us to save both space and time. That is, it is not necessary for us to keep all the values of $\beta(q_i)$, but only one to check the ancestor-descendent relationship. Due to this property, the path join (Bruno and *et al*., 2002), as well as the result enumeration (Chen and *et al*., 2006), can be completely avoided.

Concerning the correctness of the general case that *Q* contains both *c*-edges and *d*-edges, we have to answer a question: whether any *c*-edge in *Q* is correctly checked.

To answer this question, we note that any *c*-edge in *Q* cannot be matched to any path with length larger than 1in *T*. That is, it can be matched only to a *c*-edge in *T*. It is exactly what is done by the algorithm. See Fig. 6 for illustration.

Each time we meet a node *v*, we will set β values for all those q_j's that appear in an *M* associated with some child node of *v* (see lines 3 - 4). Then, in lines 9 - 10, when we check whether *q* can be inserted into $M(v)$, any outgoing *c*-edge of *q* is correctly checked. As shown in Fig. 6, after the value of $\beta(q_1)$ is set to be *v*, *q* is checked and the value of $\beta(q_1)$ indicates that *v*' is a child of *v*. Since (*v*, *v*')is also a *c*-edge, it matches (q, q_1). Although the value of $\beta(q_1)$ is changed from v_1 to *v* during the process, it does not impact the correctness of *c*-edge checkings which use only the newly set β values that are always the parent of the corresponding nodes.

In conjunction with Proposition 2, the above analysis shows the correctness of the algorithm. We have the following proposition.

Proposition 3. Let *Q* be a twig pattern containing only both *c*-edges and *d*-edges. Let *v* be a node in *T*. Let *q* be a node in *Q*. Then, *q* appears in $M(v)$ if and only if $T[v]$ contains $Q[q]$.

Proof. See the above discussion.

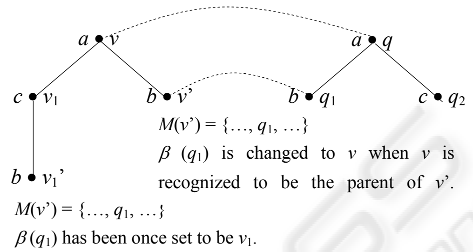


Figure 6: Illustration for *c*-edge checking.

- Computational complexities

The time complexity of the algorithm can be divided into two parts:

1. The first part is the time spent on generating β values (see lines 2 - 5). For each node *j* in *T*, we will access $M(j_l)$ for each child node j_l of *j*. Therefore, this part of cost is bounded by
$$O(\sum_{j=1}^{|T|} d_j \cdot |M(j)|) \leq O(\sum_{j=1}^{|T|} d_j \cdot |Q|) = O(|T|\cdot|Q|),$$
where d_j is the outdegree of *j*.
2. The second part is the time used for constructing $M(j)$'s. For each node *j* in *T*, we need $O(\sum_i c_i)$ time to do the task, where c_i is the outdegree of *i* in *Q*, which matches *j*. So this part of cost is bounded by
$$O(\sum_j \sum_i c_i) \leq O(\sum_{j=1}^{|T|} |Q|) = O(|T|\cdot|Q|).$$

The space overhead of the algorithm is easy to analyze. During the processing, each *j* in *T* will be associated with a $M(j)$. But $M(j)$ will be removed later once *j*'s parent is encountered and for each $i \in M(j)$ its β value is changed. Therefore, the total space is bounded by

$$O(leaf_T|Q| + |T| + |Q|),$$

where $leaf_T$ represents the number of the leaf nodes of *T*. It is because at any time point for any two nodes on the same path in *T* only one is associated with a *M*.

5 EXPERIMENTS

We conducted our experiments on a DELL desktop PC equipped with Pentium III 864Mhz processor, 512MB RAM and 20GB hard disk. We use Oracle-

9i Enterprise Edition as the working platform and implement the algorithms in Oracle PL/SQL language. We set the size of the buffer cache of Oracle-9i to be 8 MBytes and the B+-tree built in the system is used as the index.

- *Tested methods*

In the experiments, we have tested three methods:

TwigStack (*TS* for short) [4],

Twig²Stack (*T²S* for short) [10],

Twig-pattern-matching (discussed in this paper; *TPM* for short),

and compare their execution times.

- *Data*

The data set used for this test is DBLP data set [24] and a synthetic *XMARK* data set. The quantitative characteristics of the sets are described below.

- DBLP. It is a computer science bibliography database. In this data set, each author is represented by a name, a homepage, and a list of papers. In turn, each paper contains a title, the conference or the journal title where it was published, and a list of coauthors. In the version we downloaded, there are 3,332,130 elements and 404,276 attributes, totaling 127 MBytes of data. Each record in DBLP corresponds to a publication which is a simple tree structure of maximum depth 6. The average length of a structure-encoded sequence derived through the reference mechanism in a tree is around 31. The B+-tree established on individual publications is about 2 MBytes of data.
- *XMARK*. It is a popular database in benchmarking XML index methods. It is a very large and complicated tree structure, containing some substructures such as regions, items (objects for sale), people, open-auction, closed-auction, etc. In our experiment, we generate an XMARK set by using *xmlgen* with scaling factor 1.0. It contains about 108 MBytes of data. The B+-tree established on individual sales is about 1.3 MBytes of data.

- *Queries*

As we know, XML queries may have different patterns and may or not be with parameters being specified. To study the performance impact of these two characteristics, we have tested 10 queries against DBLP database, which are divided into two groups. In the first group all the 5 queries are with a constant while in the second group (another 5 queries) no parameter is specified. Over XMARK database, we have also tested 10 queries, divided into 2 groups with each containing 5 queries. In the first group, each query contains a constant. In the second group, for each query no constant is specified. All the queries are shown in Table 1 - Table 4.

Queries over DBLP:

Table 1: Group I.

query	Xpath expression
Q1	//inproceedings/[author]//year [text() = '1999']
Q2	//inproceedings/[author and /title]//year [text() = '1999']
Q3	//inproceedings/[author and /title and //pages]//year [text() = '1999']
Q4	//inproceedings/[author and /title and //pages and //url]//year [text() =
Q5	//articles/[author and /title and //volume and //pages and //url]//year [text() = '1999']

Table 2: Group II.

query	Xpath expression
Q6	//inproceedings/[author]//year
Q7	//inproceedings/[author and /title]//year
Q8	//inproceedings/[author and /title and //pages]//year
Q9	//inproceedings/[author and /title and //pages and //url]//year
Q10	//articles/[author and /title and //volume and //pages and //url]//year

Queries over XMARK:

Table 3: Group III.

query	Xpath expression
Q11	/site//open_auction[seller/person]//date [text() = '10/23/1999']
Q12	/site//open_auction[//seller/person and //bidder]//date [text() =
Q13	/site//open_auction[//seller/person and //bidder/increase]//date [text() = '10/23/1999']
Q14	/site//open_auction[//seller/person and //bidder/increase and //initial]//date [text() = '10/23/1999']
Q15	/site//open_auction[//seller/person and //bidder/increase and //initial and //description]//date [text() = '10/23/1999']

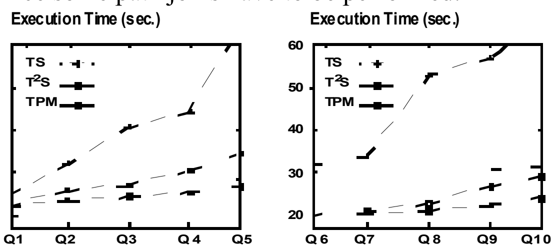
Table 4: Group IV.

query	Xpath expression
Q16	/site//open_auction[seller/person]//date
Q17	/site//open_auction[//seller/person and //bidder]//date
Q18	/site//open_auction[//seller/person and //bidder/increase]//date
Q19	/site//open_auction[//seller/person and //bidder/increase and
Q20	/site//open_auction[//seller/person and //bidder/increase and //initial and //description]//date

- *Test results*

Now we demonstrate the execution times of all the four strategies when they are applied to the above queries.

In Fig. 7(a), we show the test results of the first group. From these we can see that our first algorithm outperforms all the other strategies. It is because this algorithm works only in one scan of the data streams and neither the path join nor the result enumeration is involved. *TwigStack* has the worst performance since some path joins have to be performed.

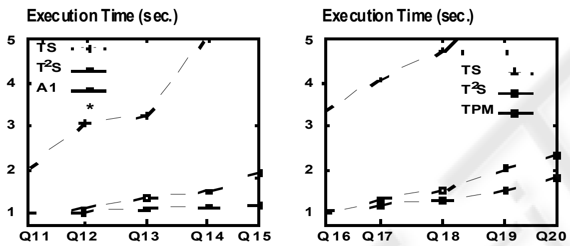


(a) (b)

Figure 7: Results of Group I and Group.

Fig. 7(b) shows the test results of the second group. The execution time of all the strategies are much worse than Group 1 since the queries are all of quite low selectivity and thus almost all the data set has to be downloaded into main memory. In this case, I/O dominates the cost. Again, our first algorithm has the best performance. Especially, when the size of queries becomes larger, this algorithm is 3 - 4 times better than *Twig*^{2}*Stack*. First, the time for constructing a matching tree is much less than that for constructing the hierarchical stacks. Secondly, the space used by our first algorithm is much smaller than *Twig*^{2}*Stack*. It is because our algorithm removes useless data structures earlier than *Earlier Result enumeration* utilized by *Twig*^{2}*Stack*. *TwigStack* shows an exponential-time behavior since for each path in a query a great many matching paths will be produced and the cost of join operations increases exponentially.

In Fig. 8, the test results over the XMARK database are demonstrated. From these, we can see that our first algorithm still has the best performance for this data set.



(a) (b)

Figure 8: Results of Group III and Group IV.

6 CONCLUSIONS

In this paper, a new algorithm is proposed to evaluate twig pattern queries in XML document databases. The algorithm works in a bottom-up way, by which an important property of the postorder numbering is used to avoid join or join-like operations. The time complexity and the space complexity of the algorithm are bounded by O($|T|\cdot|Q|$) and O($|Q|\cdot leaf_T$), respectively, where T is the document tree and Q the twig pattern query, and $leaf_T$ represents the number of leaf nodes in T. Experiments have been done to compare our method with some existing strategies, which demonstrates that our method is highly promising in evaluating twig pattern queries.

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