A Survey Of Algorithms Related To Xml Based Pattern Matching

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Abstract

The New era practitioners are highly depending on the flexible open standard data structures to store and transmit the data in the B2B process, as a part of that, eXtended Markup Language(XML) Patterns are needed for efficient processing of user queries on different XML-enabled (MS-SQL Server, Oracle) Databases. The XML Document can be converted into XML Tree by using different tools like XML DOM. There are four central problems in data management: capture, storage, retrieval, and exchange of data. XML is a tool used for data exchange. Data exchange has been a long issue in information technology, but the Internet has elevated its importance. Electronic Data Interchange (EDI), the traditional data exchange standard for large organizations, is giving way to XML, which is likely to become the data exchange standard for all organizations, irrespective of size. Most of the business and enterprises generate and exchange XML data more often, so there is need for efficient processing of queries on XML data. An XML query pattern can be represented as rooted labeled tree called as twig pattern. The core operation in XML query processing is efficient matching of XML tree patterns. The main reason why this one is introduced here is , it process large XML queries. The existing algorithms process only small queries it includes only P-C and A-D relations. It process large queries with P-C, A-D, wildcards, negation function and order restriction called extended XML tree pattern.

In this paper, we present the survey of the recent works and algorithms related to eXtended Markup Language based Small Patterns Matching. We present an analysis of the Small Patterns Matching algorithms likes Twigstack, Twigstack List, ordered TJ and TJFast. Tree Match Twig pattern Matching algorithm can solve complicated queries and works with good performance.

Keywords: B2B, XML Tree Pattern, XML, database.

1. INTRODUCTION

As the Trend change, the conventional business is transmitting into the form of e-business through the Internet, which is known as B2B (Business-to-Business). It is very clear for us the B2B problem are all website based, same of the B2B websites are company websites, product supply and procurement exchanges, specialized or vertical industry portal, Information sites etc. For any type of e-business the websites is essential in this context the web information is presented in xml format and XML Document contain all the XML components of websites and the determination of XML Patterns are needed to solve the problems in B2B sites and to get more performance.

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In this paper we present the core concepts of Query languages. XML Trees can be Ordered and Unordered Trees. The present XML Trees can understand with a good labeling schemes[5].XPath[1], XQuery[2] are different query languages for XML. We also present the experimental results for pattern search with using the XMLBuilder and SAX parser in Java.

2. OBJECTIVE

The basic idea is searching. It means searching for the occurrence of a tree pattern query in an XML database is a core operation in XML query processing. Previous algorithms search only the small tree patterns in the XML databases. Here the idea for this one is to search large tree patterns and to get optimal answers. It uses matching cross that's a theoretical framework that demonstrates the intrinsic reason in the proof of the optimality of holistic algorithms. The reason behind why we introduce matching cross is the previous algorithm's performs their work in two phases means matching and merging, at matching phase there is a chance to occur many useless intermediate results (path solutions).

3. ALGORITHMS

An algorithm is a step by step procedure to solve a particular problem. The following are the algorithms for pattern matching.

3.1 Algorithm: TreeMatch

Input: The query Q

Output: The tree pattern called as twig pattern

- 1. locateMatchLabel (Q);
- 2. while(notEnd (root)) do
- 3. f_{act}= getNext (topBranchingNode);
- 4. if (f_{act} is a rturn node) then
- 5. addToOutputList (NearestAncestorBraching (f_{act}),cur (T_{fact}));
- 6. advance (T $_{\rm fact}$); // read the next element in T $_{\rm fact}$
- 7. updateSet (f_{act}); // update set encoding
- 8. locateMatchLabel (Q); // locate next element with matching path
- 9. emptyAllSets (root);

The following are the procedures and functions are used in the TreeMatch algorithm:

Procedure locateMatchLabel(Q)

1. for each leaf $q \in Q$, locate the extended Dewey label eq in list Tq such that eq matches the individual rootleaf path

Procedure addToOutputList(q,eqi)

1.for each $e_q \epsilon S_q$ do

2.if(satisfyTreePattern(e_{qi} , e_q)) then 3.outputList(e_q); add(e_{qi});

$Function \ satisfy TreePattern(e_{qi}, e_q)$

1.if(bitVector(e_q , q_i)=='1') then return true
2.else return false;

Procedure updateSet(q,e)

1.cleanSet(q,e)
 2.add e to set S_q; //set the proper bitVector(e)
 3.if(isNotRoot(q) and bitVector(e)=="1...1")) then updateAncestorSet(q);

Procedure cleanSet(q,e)

1.for each element $e_q \in S_q$ do

2.if(satisfyTreePattern(eq,e)) then
3.if(q is a return node) then
4.addToOutputList(NearestAncestorBranching(q),e);
5.if(isTopBranching(q)) then

- 6.if(there is only one element in S_q) then
- 7. output all elements in outputList (e_q) ;
- else merge all elements in outputList (e_q) to outputList (e_a),where e_a=NearestAncestorBranching(e);
- 9. delete e_q from set S_q ;

Procedure updateAncestorSet(q)

- 1. /*assume that q' = NearestAncestorBranching (q)*/
- 2. for each $e \in Sq'$ do
- 3. if (bitVector (e, q) = 0) then
- 4. bitVector (e, q) = 1;
- 5. if (isNotRoot (q) and (bitVector (e)="1...1")) then
- 6. updateAncestorSet (q');

Procedure emptyAllSets(q)

- 1. if (q is non-leaf node) then
- 2. for each child c of q do emptyAllSets (c);
- 3. for each element $e \in Sq$ do cleanSet (q, e);

3.2 Algorithm for getNext(n):-

- 1. if (isLeaf (n)) then
- 2. return n
- 3.else
- 4. for each ni \in NearestDescendantBranching(n) do
- 5. $f_i = getNext(n)$
- 6. if (isBranching(n_i) and notEmpty (S_{ni})) then
- 7. return f_i
- 8. else ei = max {p | $p \in MB(n_i, n)$ }
- 9.end for

10. max = maxarg_i $\{e_i\}$

11. for each $n \in NearestDescendantBranching (n) do$

12. if (ForAll (e) $\in MB$ (n,, n) : e is not belongs to Ancestors (e_max)) then

- 13. return f_i;
- 14. end if
- 15.end for
- 16. min = minarg_i { $f_i | f_i$ is not a return node}

17. for each $e \in MB(n_{\min}, n)$

18. if (e \in ancestors (e_{max})) then updateSet (S_n,e)

19.end for

20. return f_{min}

21.end if

Function MB(n,b)

1. if (isBranching(n)) then

2. Let e be the maximal element in set S_n

3.else

4. Let $e = cur(T_n)$

5.end if

6.Return a set of elements **a** that is an ancestor of **e** such that **a** can match node **b** in the path solution of **e** to path pattern p_n .

4. EXPERIMENTAL RESULTS

Our experiment uses a concise encoding to present matching results, which leads to the reduction of useless intermediate results. We have an extensive set of experiment on synthetic and real data set for performance comparison. We compared TreeMatch with previous holistic XML tree pattern algorithms. The experimental results show that our algorithm can correctly process XML tree patterns called twigs. It achieves performance speedup. This is because of reduction of useless intermediate results during XML query processing.

Table 4.1: Number of output elements(O) and thepercentage(P) of useful elements for TreeMatch algorithm

Query	D1		D2		D3	
	0	Р	0	Р	0	Р
Q1	660	100%	3276	100%	6702	100%
Q2	1775	100%	8757	100%	17325	100%
Q3	4575	98.8%	47290	99.9%	80145	94.5%
Q4	3335	100%	16054	100%	32012	100%
Q5	148	100%	606	100%	1302	100%
Q6	3275	100%	47100	100%	67478	99.9%

Table 4.2: Number of required buffered elements

Query D1	D2	D3
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Q1	5	6	6
Q2	9	10	11
Q3	260	13030	45001
Q4	6	7	8
Q5	7	8	10
Q6	260	13304	44989

The purpose of this is to simulate the application where the available main memory is large so that a big portion of documents can fit in the main memory. Table 4.2 shows the maximal number of elements buffered in order to avoid outputting any useless intermediate results. An obvious observation is that Q3 and Q6 (Queries) need to buffer many elements, but all other queries only need to buffer very small number of elements. This can also be explained that all queries except Q3, Q6 belong to the optimal query class. We compared the performance of three algorithms (D1,D2 and D3) .From this one TreeMatch is better than the other algorithms because it reaching 20%-90% improvement in execution time for all queries.

4.1 SCREENS

The following screen allows to select XML file for viewing XML Tree

ML Tree Viewer	using SAX Parser in JAVA	
File :	Selected File Name Here	Select File
Gen file		
Look In:	Documents	
abc		
CSS		
project		
Camsung		
Scanned	Documents	
	00 2008	
File Name:		
Files of <u>T</u> ype:	xml files	•
		Open file Cancel
[

Fig:1:XML file selection

After selecting the location of an XML file the XML Tree will appears as follows



Fig:2:XML Tree

Small XML query patterns can be search in the XML as follows

🖻 • 🔕 🤣 🔚 🕒 🛍 🔍 💽	2 🖩 💶 🗞 🗄 🥹 💆 🔴
/Employee/Email	Evaluate Evaluate Evaluate when typing Evaluate on button click
auto-expand Email Santhoshi@gmail.com	<pre>employeexml </pre> <pre> </pre>
D:\employee.xml	

Fig:3:Searching small patterns in XML

The following is one of the application to search the XML queries for XML tree pattern.

	Image: Second
auto-expand	<pre>employee.xml </pre>
D:\employee.xml	

Fig:4:XPath Builder for searching

5. CONCLUSION

In this paper, we presented the survey results of XML based pattern matching algorithms . The TreeMatch algorithms with different query classes are introduced. TreeMatch has an overall good performance in terms of running time and the ability to process extended XML tree patterns (twigs). The previous twig pattern matching algorithms (*TwigStack, TwigStackList, OrderedTJ, and TJFast*) requires bounded main memory for small queries. But, the *TreeMatch* works on one-phase query evaluation and it requires bounded main memory for larger queries.

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BIOGRAPHIES

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