Locating Valid SLCAs for XML Keyword Search with NOT Semantics

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ABSTRACT

Keyword search provides an easy way for users to pose queries against XML documents, and it is important to support queries with arbitrary combinations of AND, OR, and NOT operators. The previous RELMN algorithm processed such kind of queries by extending the original SLCA definition in a straightforward way, but it did not work correctly in some cases. In this paper, we propose the concept of *valid SLCAs* as query results. Basically, nodes in an XML document are classified according to their usages, which is further used to define the *scope* affected by a negative keyword. Only *valid* nodes, which are not affected by any negative keyword, are qualified to identify *valid SLCAs*. The experimental results show that the proposed algorithm achieves higher precision and recall, and is more efficient than the previous work.

1. INTRODUCTION

Keyword search provides an easy way for users to obtain desired information from XML documents by just giving some keywords they are interested in, but irrelevant data may be returned due to lacking exact query semantics. Many researchers advocate the idea that each returning result should be based on an LCA (Lowest Common Ancestor), which contains every keyword under its subtree at least once [1][3][4][5][6][7]. Among all the LCA-based techniques, the smallest-LCA (SLCA) [6] concept is particularly popular since it can locate nodes semantically closer to the query keywords. Specifically, a node n is said to be an SLCA node if: (i) n is an LCA node, and (ii) none of n's children are LCA nodes. Consider the sample XML tree depicted in Figure 1, which represents the information about course offerings at a particular school, and each node is identified by a Dewey encoding.

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Table 1: Sample keyword queries.

Q_1	Subject ∧ Friday
Q_2	Subject ∧ Friday ∧ !R101
Q_3	2010 ∧ Subject ∧ !R101
Q_4	Red Wood ∧ Subject ∧ Friday ∧ !R103
Q_5	Subject ∧ Friday ∧ !R102 ∧ !2010
Q_6	Subject ∧ Friday ∧ (R101 ∨ R103)

Query Q_1 in Table 1 is used to retrieve those subjects whose classes are held on Friday. Since only nodes 1.2.2 and 1.3.3 contain $Subject$ and $Friday$ under their subtrees and none of their children do, these two nodes are the SLCAs for Q_1.

The limitation of the works above is that they only concern the keywords with the AND operator. It is therefore an important research issue to process queries with arbitrary combinations of AND, OR, and NOT operators, and the challenge mainly lies in how to identify results satisfying the NOT semantics. A straightforward idea is that the returning SLCA should contain every "positive" keyword but no "negative" keyword (keywords with NOT operators). Consider the sample query Q_2 in Table 1, where the exclamation mark "!" is used to represent the NOT operator. The semantics of query Q_2 is similar to that of query Q_1, except that Q_2 should not output the courses held in room 101. Since the course rooted at node 1.2.2 contains the unwanted negative keyword "R101", only the subtree rooted at 1.3.3 should be returned. Although intuitive, such approach is sometimes too restrictive. Consider query Q_3, asking for subjects whose classes are offered in 2010 but not held in room 101. We cannot find an SLCA satisfying the above definition, but actually node 1.2.3.1, whose class is held in room 103, is an answer reasonable for a human user, which we call *human answers* in short. To avoid the occurrences of such false negatives, when

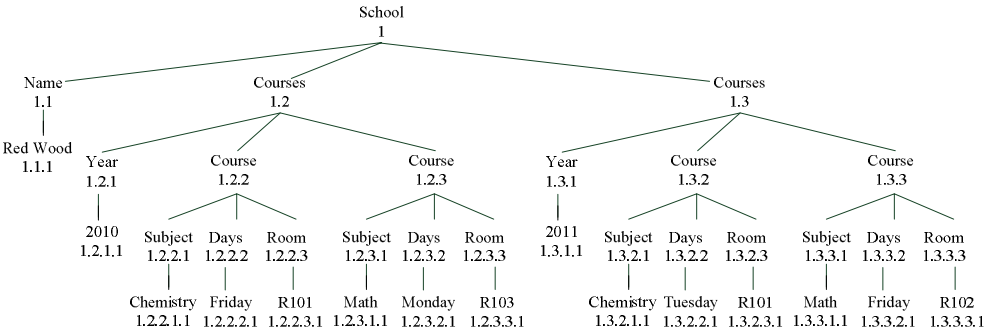


Figure 1: A sample XML tree.

no satisfied nodes are found, our previously proposed RELMN algorithm [2] will identify SLCAs only based on positive keywords, and then *prune out* nodes according to negative keywords.

Although the RELMN algorithm basically performs well, the process of result identification is complex, and it still might cause false negatives or false positives in some cases, as will be discussed in detail in Section 2. Therefore, we propose a new approach to improve the effectiveness and efficiency of processing XML keyword search with NOT semantics. The main idea is to classify all nodes into several groups based on their usage. This classification is used to define the *scope* that a negative keyword can affect. We then propose to return *valid SLCA* as the query result, where a valid SLCA contains every positive keyword under its subtree, and each of which is not *affected* by any negative keyword. Consider query Q_3 again. Node 1.2 is the only SLCA based on positive keywords. Since its descendant nodes 1.2.1.1 and 1.2.3.1 match the positive keywords, and are not within the scope affected by the negative keyword $R101$, node 1.2 is qualified as a *valid SLCA*, which contains human answers and should be returned. In summary, the contributions of this paper are as follows:

- Based on a simple observation of XML documents, we propose a set of definitions which identify nodes which should not be output due to negative keywords.
- We design an efficient algorithm called ValidSLCA to process queries with arbitrary combinations of AND, OR, and NOT operators.
- We perform an empirical evaluation by measuring the precision, recall, and processing time of two approaches. The experimental results show that the new ValidSLCA algorithm is more efficient and gives better query results than the previous RELMN algorithm [2].

The rest of this paper is organized as follows. Section 2 briefly describes the RELMN algorithm. The basic observation and definitions underlying the new approach are presented in Section 3, and the corresponding algorithm is discussed in Section 4. At last, experimental studies and conclusions are given in Section 5 and Section 6, respectively.

2. THE RELMN APPROACH

We briefly describe the RELMN algorithm in this section, and direct the readers to [2] for detailed discussion.

The RELMN algorithm basically consists of two steps. First, it searches the *satisfied* SLCAs of the input query. Specifically, a node n *satisfies* the query Q if n contains every "positive" keyword under its subtree but does not contain any "negative" keyword. Further, n is a *satisfied SLCA* if n satisfies Q but none of n's children do. As discussed in Section 1, node 1.3.3 is a *satisfied* SLCA for query Q_2. When no satisfied SLCAs are found, the RELMN algorithm will locate SLCAs purely based on positive keywords. Second, for every subtree rooted at the identified SLCAs, it then prunes the unwanted part based on the following rule: node n_1 is able to prune its sibling node n_2 if n_1 contains more positive keywords or contains less negative keywords under its subtree than n_2 does. Consider query Q_3 again. RELMN will first identify node 1.2 based on the positive keywords "2010" and "Subject", and then exclude the subtree rooted at node 1.2.2, since it has the negative keyword $R101$ and is pruned by node 1.2.3.

The time complexity of the above two steps are respectively $O(d|M| \cdot w)$ and $O(\Sigma_{i=1}^{z} b_i)$, where d is the depth of the XML tree, $|M|$ is the sum of the keyword frequencies, w is the number of clauses of query Q in conjunctive normal form, z is the number of nodes in the match tree for Q[1], and b_i is

[1]A match (in RELMN) is a node containing a positive/negative keyword. The match tree for a given query is a subtree of the XML tree, which consists of the nodes along the path from each match up to the root.

the number of siblings of the i^{th} node.

We now discuss the cases where the RELMN algorithm might cause false negatives or false positives. Consider query Q_4 in Table 1, asking for the course information at the school "Red Wood", and only the subjects whose classes are held on Friday but not in room 103 should be returned. Note that nodes 1.2.2 and 1.3.3 represent human answers. Nevertheless, RELMN will only return 1.3.3. The reason is that RELMN will first identify node 1 as the only SLCA, and then prune node 1.2 by node 1.3 because it contains the negative keyword $R103$. Hence, node 1.2.2 is excluded too. Take query Q_5 as another example, asking for subjects whose classes are held on Friday, but not in room R102, and not in year 2010. Observe that the human answer is empty. However, RELMN will return both nodes 1.2.2 and 1.3.3, since they are both identified as SLCAs based on positive keywords and cannot prune each other.

3. BASIC OBSERVATIONS AND DEFINITIONS

In this section, we explain the observation on XML documents which is underlying the new approach, and deliver the basic definitions. The main idea is to identify the *scope* which is affected by a negative keyword according to node types. Since the entity-relationship (ER) model has been widely used for data modeling, we borrow some terms from that model to classify the nodes in an XML tree based on their usage as follows:

1. A node is a *text* node if it is a value.
2. A node is an *attribute* node if it has only one child, which is a text node.
3. A node denotes an *entity* if its tag name is identical to its siblings, such as a *-node in the XML DTD (Document Type Definition).
4. A node is a *dummy* node if it is none of the three nodes mentioned above.

For example, nodes 1.1.1 (*Red Wood*), 1.2.3.2.1 (*Monday*), and 1.3.1.1 (2011) are text nodes. Nodes 1.2.1 (*Year*) and 1.2.2.3 (*Room*) are attribute nodes. Nodes 1.2 (*Courses*) and 1.2.3 (*Course*) are entity nodes. In addition, the *closest entity* of node n refers to the lowest entity node that are the ancestor of n. For instance, node 1.3 (*Courses*) is the closest entity of node 1.3.1.1 (2011), and node 1.2.3 (*Course*) is the closest entity of node 1.2.3.2.1 (*Monday*).

We observe that a text node is generally used as the attribute value of its closest entity. For example, node 1.1.1 (*Red Wood*) is used to describe the name of the school (node 1), node 1.3.1.1 (2011) indicates the courses (node 1.3) belonging to year 2010, and node 1.2.3.2.1 (*Monday*) represents that the course (node 1.2.3) is held on Monday. Therefore, if a negative keyword matches a text node n, it is reasonable to assume that the subtree rooted at n's closest entity is unwanted. For instance, if the negative keyword is $!R101$, we assume that the subtrees rooted at nodes 1.2.2 and 1.3.2 should not be returned. In other words, we propose that the query result is composed of the subtrees which represent positive keywords and are not "affected" by the negative keywords. For ease of discussion, we assume that the query is in DNF in the rest of this section. Hence, the clauses in a query are connected with the OR operators, and keywords in the same clause are connected with the AND operators. The formal definitions are then given as follows:

Definition 1. If node n is a text node and corresponds to a given negative keyword, the closest entity of n is termed a *negator*.

Definition 2. A node is a *match* of keyword k if its tag name or content contains k. Moreover, a match is *valid* if it has no ancestors that are negators formed within the same clause.

Consider the positive keyword *Friday* in query Q_2. Among the two matches 1.2.2.2.1 and 1.3.3.2.1, the former one will become *invalid* due to the negator (node 1.2.2) caused by the negative keyword $!R101$.

Definition 3. For a given clause c, a node n is said to be an SLCA if n contains every positive keyword of c at least once under its subtree and none of n's children do. Furthermore, n is a candidate valid SLCA (VSLCA) if n contains at least one valid match for every positive keyword of c.

Continuing the running example, both nodes 1.2.2 and 1.3.3 are SLCAs in our framework, but only node 1.3.3 is a candidate VSLCA since node 1.2.2 has no valid matches for both *Friday* and *Subject* under its subtree.

Definition 4. Given a keyword query in DNF with only one clause, all the candidate VSLCAs n are *valid SLCAs*. If there is more than one clause, n is a *valid* SLCA only if n has no descendants that are also candidate VSLCAs formed by other clauses.

The proposed new approach will return all identified valid SLCAs as the query result. Consider query Q_6, which searches the subjects whose classes are held on Friday and in room 101 or 103. The

DNF of Q_6 has two clauses: $(Subject \wedge Friday \wedge R101)$ and $(Subject \wedge Friday \wedge R103)$, and the candidate VSLCAs of these two clauses are node 1.2.2 and node 1.2, respectively. The query result will be node 1.2.2, since it is the descendant of node 1.2.

Note that in Definition 1, we only consider text nodes for negative keywords. The reason is that a negative non-text keyword is mainly used to describe unnecessary information, and does not affect the validity of an SLCA. For instance, suppose the negative non-text matches have no ancestor-descendant relationships with other positive keywords, such as in the query (Subject ∧ R101 ∧ !Days). We can see that the SLCA node, 1.2.2 (Course), is a human answer and should not be affected by $!Days$. Even if the negative non-text matches have ancestor-descendant relationships with other positive keywords, such as in the query (Subject ∧ R101 ∧ !Room), node 1.2.2 (Course) should still be returned.

4. THE VALIDSLCA ALGORITHM

The proposed ValidSLCA algorithm is listed in Figure 2. Briefly, for the input query Q, we will convert it into DNF Q' (line 1). To get the candidate VSLCAs of each clause, we first identify the SLCAs based only on positive keywords by the approach given in [6] (line 5). We then collect the negators in line 6. The negators are used to determine the valid matches by procedure $ValidateMatches$. Namely, some of the matches will be removed if they are the descendants of the negators. Next, we identify candidate VSLCAs by ensuring that there exists at least one valid match for each positive keyword (lines 9-12). At last, those candidate VSLCAs that are ancestors of others are removed (line 13).

Observe that the procedures ValidateMatches and CombineSLCA are variants of merge sort algorithms and are therefore linear to the input. Besides, two B-tree indices are maintained for efficient processing. In the first index, the data associated with each keyword k is a sorted list of Dewey numbers of all the nodes which contain keyword k. If a node is a text-node, we additionally record its closest entity. Hence, we can efficiently retrieve the match array of the keyword (lines 3-4) and negators (line 6). The second index is used to output meaningful answers for users (line 14), which retrieves the tag name by a given Dewey number. Both indices are created and accessed based on the Oracle Berkeley DB[2].

We next give the time complexity of ValidSLCA. The details are omitted due to space constraints. Let d be the maximum depth of the XML tree and

[2]http://www.oracle.com/database/

Input: A keyword query Q of arbitrary combination with AND, OR, and NOT operators.
Output: All of the valid SLCAs of Q.

ValidSLCA(Q)
1 convert Q into DNF Q'
2 **for** each clause c_i of Q' **do**
3 **for** each positive keyword k_j of c_i **do**
4 $M_j \leftarrow$ all the matches of k_j
5 $S_i \leftarrow$ compute SLCAs by { $M_1, M_2, M_3 \ldots$}
6 $E \leftarrow$ collect the negators by the negative keywords of c_i
7 **for** each M_j **do**
8 $M'_j \leftarrow ValidateMatches(M_j, E)$
9 **for** each $n \in S_i$ **do**
10 **for** each M'_j **do**
11 if n has no descendants belongs to M'_j **then**
12 remove n from S_i
13 $S \leftarrow CombineSLCA(S_1, S_2, S_3 \ldots)$
14 Output S /* all the valid SLCAs of query Q */

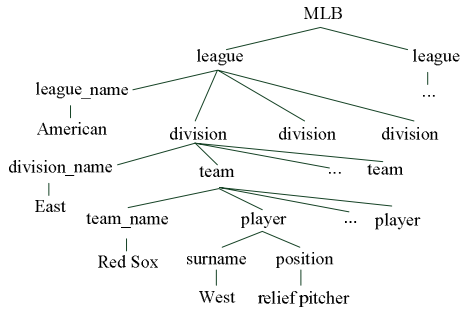
ValidateMatches(M, E)
1 $i \leftarrow 1, j \leftarrow 1$
2 **while** $i \leq |M|$ **and** $j \leq |E|$ **do**
3 **if** $M[i]$ precedes $E[j]$ **then**
4 $i \leftarrow i + 1$ /* $M[i]$ is valid */
5 **else if** $E[j]$ is the ancestor of $M[i]$ **then**
6 remove $M[i]$ from M /* $M[i]$ is invalid */
7 $i \leftarrow i + 1$
8 **else**
9 $j \leftarrow j + 1$
10 return M

CombineSLCA($S_1, S_2, S_3 \ldots$)
1 $S \leftarrow$ merge $(S_1, S_2, S_3 \ldots)$ by their Dewey Numbers
2 $i \leftarrow 1, j \leftarrow 2$
3 **while** $j \leq |S|$ **do**
4 **if** $S[i]$ is the ancestor of $S[j]$ **then**
5 remove $S[j]$ from S
6 **else**
7 $i \leftarrow j$
8 $j \leftarrow j + 1$
9 return S

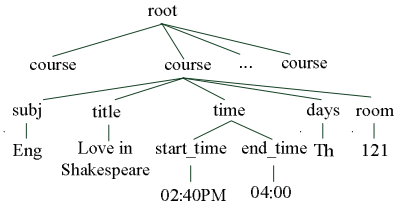
Figure 2: The *ValidSLCA* algorithm.

Q' be the DNF of the original input query Q. Suppose Q' has k clauses, and the i^{th} clause has p_i positive keywords and n_i negative keywords. That is, the matches of positive keywords of c_i are $M_1, M_2, ..., M_{p_i}$, and the matches of negative keywords of c_i are $N_1, N_2, ..., N_{n_i}$. Let $|M_i^{sum}| = \Sigma_{j=1}^{p_i} M_j$ and $|N_i^{sum}| = \Sigma_{j=1}^{n_i} N_j$ be the sum of the size of positive and negative matches. The overall time complexity of algorithm ValidSLCA is $O(\Sigma_{i=1}^{k} \Sigma_{j=1}^{p_i} (|M_j| + |N_i^{sum}|) \cdot d)$.

This section is concluded by showing how Algorithm ValidSLCA can correctly process queries Q_4 and Q_5. Recall that nodes 1.2.2 and 1.3.3 are two



(a) Baseball



(b) Reed College

Figure 3: Portions of the XML trees.

Table 2: The information for the data sets.

Data Set	Doc. Size	Nodes	Max/Avg Depth
Baseball	1.01 MB	51,599	7/6.5
Reed	277 KB	18,855	5/3.7
Mondial	1.7 MB	124,736	7/4.6
DBLP	127 MB	7,146,530	7/3.5

courses that should be returned by Q_4, but RELMN only identifies one, as discussed in Section 2. In ValidSLCA, only node 1.2.3.3.1 (R103) matches the negative keyword and the corresponding negator is node 1.2.3. This negator will not affect the positive matches under the subtrees rooted at 1.2.2 and 1.3.3, so we will identify node 1 as the valid SLCA and return both courses. Consider another query Q_5, where the answer should be empty. The two negative keywords (R102 and 2010) yield two negators (nodes 1.2 and 1.3.3) in total. Besides, the positive keyword $Friday$ has two matches 1.2.2.2.1 and 1.3.3.2.1. Since both of them are descendants of negators, our approach will correctly return empty.

5. EXPERIMENTAL EVALUATION

In this section, we compare the performance of RELMN and ValidSLCA algorithms. Both of them were implemented in C++, and the experiments were performed on a 1.67GHz dual-core CPU with 1.5GB RAM. Note that in order to be fair with the RELMN approach, after identifying valid SLCAs, we further adopt the pruning rules described in [5] to remove subtrees containing less positive keywords than their siblings. The time complexity of ValidSLCA therefore becomes $O(\Sigma_{i=1}^{k}\Sigma_{j=1}^{p_i}(|M_j|+|N_i^{sum}|)\cdot d) + O(\Sigma_{i=1}^{k}|M_i^{sum}|\cdot d\cdot 2^{p_i})$.

Table 3: Test queries.

No.	query
QB_1	(Indians ∨ Tigers) ∧ Starting Pitcher ∧ SURNAME
QB_2	SURNAME ∧ !Starting Pitcher ∧ !Relief Pitcher
QB_3	American ∧ TEAM_NAME ∧ !Central
QB_4	!American ∧ TEAM_NAME
QB_5	Yankees ∧ SURNAME ∧ !Starting Pitcher ∧ !Relief Pitcher
QB_6	East ∧ !Yankees ∧ Second Base ∧ HOME_RUNS
QB_7	American ∧ (East ∨ West) ∧ TEAM_NAME
QB_8	Red Sox ∧ HITS ∧ !Outfield
QR_1	subj ∧ 04:10PM ∧ !T ∧ !W
QR_2	subj ∧ !T
QR_3	subj ∧ room ∧ 301 ∧ !M
QR_4	instructor ∧ CHEM ∧ M ∧ 01:10PM
QR_5	instructor ∧ CHEM ∧ !M ∧ 01:10PM
QR_6	room ∧ Love in Shakespeare ∧ !02:40PM
QR_7	room ∧ Love in Shakespeare ∧ !F
QR_8	title ∧ (M ∨ W) ∧ !01:10PM

We used four data sets, DBLP.xml[2], Mondial.xml[2], Reed.xml[3], and Baseball.xml[4], to perform the experiments. Some statistics about these data sets, including their sizes, are listed in Table 2 for comparison. Besides, the metrics to compare the two algorithms are precision, recall, and processing time. The first two are calculated based on *human answers*, which are obtained from three human experts with differences resolved by voting.

We first use the Baseball and Reed data sets to analyze the precision and recall of RELMN and ValidSLCA. Figure 3 shows the portions of these two data sets to assist in analyzing the outcomes of experiments. The test queries of these two data sets are listed in Table 3, and the precision and recall on the Baseball data set is displayed in Figure 4. We can see that ValidSLCA gets better precision than RELMN in QB_2. In RELMN algorithm, all the nodes with "surname" tag names satisfy QB_2 and will be returned. Since some of the players are starting pitchers or relief pitchers, it gets imperfect precision and 100% recall. However, those players who are starting pitchers or relief pitchers are considered as invalid matches in ValidSLCA. Hence, ValidSLCA gets 100% precision and recall in QB_2. RELMN also gets imperfect precision in QB_4 due to the same reason. On the other hand, the precision and recall on the Reed data set is displayed in Figure 5. The semantics of QR_6 is to search the room of course "Love in Shakespeare" which does not start at 02:40PM. However, there only exists one course titled "Love in Shakespeare", and it coincidentally starts at 02:40PM. That is, the answer should be empty. Refer to Figure 3 (b). The closest entity of !02:40PM is the node with tag name *course*. Hence, ValidSLCA returns empty while RELMN still returns course "Love in Shakespeare". The similar situation happens in QR_7, which makes RELMN get poor precision and recall, too.

The processing time is measured with four data sets mentioned above. Since the query result may be different between RELMN and ValidSLCA, we only consider those queries which yield the same

[3]http://www.cs.washington.edu/research/xmldatasets/
[4]http://www.cafeconleche.org/books/biblegold/examples/

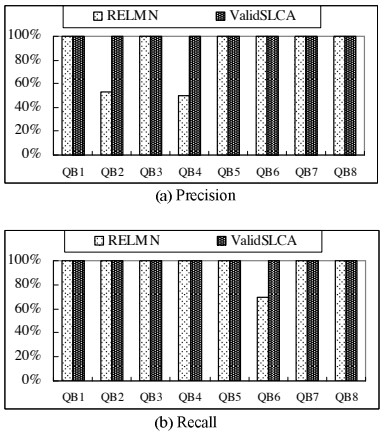


Figure 4: The Baseball data set.

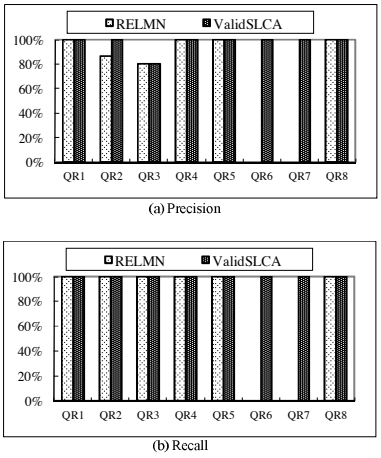


Figure 5: The Reed data set.

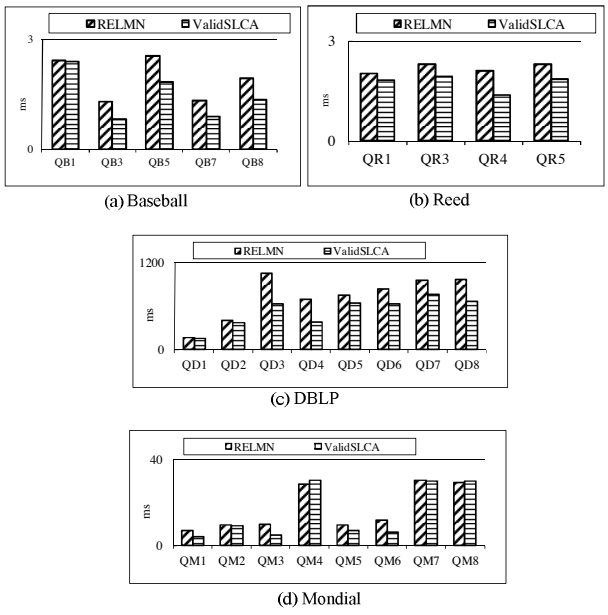


Figure 6: The processing time.

query results by the two algorithms. Due to space limitation, we do not explicitly list the test queries. As shown in Figure 6, we can see that our new approach is more efficient than the previous work in most cases. One reason is that the pruning rules defined in RELMN are very complex to process. Besides, as shown in the time complexity of the two algorithms, RELMN is affected by the branch factor of the XML trees (b_i), which may be very large. On the other hand, ValidSLCA is affected by the number of the query keywords (p_i), which is comparably small. Hence, the RELMN algorithm often takes more time than ValidSLCA does.

6. CONCLUSIONS

In this paper, we propose an algorithm to process keyword search with NOT semantics. The idea is to classify matches as valid or invalid based on negative keywords, and only valid nodes are qualified to identify valid SLCAs as query outputs. We empirically evaluate the precision, recall, and processing time by comparing the previous work and our new approach. The experiments show that our new approach gives more reasonable query results and is even more efficient. As part of our future work, we are interested in designing a novel ranking scheme to order the query results so that users can focus on most desirable ones.

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