Multi Reachability Query Processing

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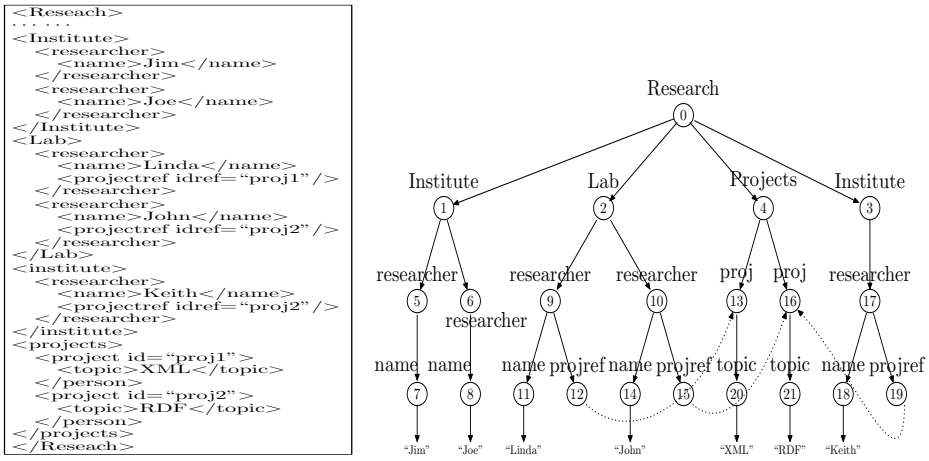
Abstract. There is a need to efficiently navigate on a large graph to find a certain piece of information by some structure constraints. Reachability query could be the main means for such a purpose and existing approaches studied an efficient primitive called reachability join. In this paper, we focus on processing the query containing multi reachability joins (*R*-joins). We studied the processing ability of the up-to-date alternative that extended the wellknown tree-specific method, namely, twig-stack join algorithm, to be applicable on DAGs. Due to the rapid increasing of the transitive closure size for graphs in stead of trees, however, we found the proposed dynamic programming approach that combines *R*-join primitives into an optimized plan based on cost tends to be superior over the alternative and more stable in terms of the density of the underneath DAGs than the alternative. According to the extensive experiments we've done, our method is faster than the existing work by at least two orders of magnitudes.

1 Introduction

With the rapid growth of World-Wide-Web, new data archiving and analyzing techniques bring forth a huge volume of data available in public, which are graph structured in nature including hypertext data, semi-structured data and XML [1]. A graph provides great expressive power for people to describe and understand the complex relationships among data objects. As a major standard for representing data on the World-Wide-Web, XML provides facilities for users to view data as graphs with two different links, the parent-child links (document-internal links) and reference links (cross-document links). In addition, XLink (XML Linking Language) [7] and XPointer (XML Pointer Language) [8] provide more facilities for users to manage their complex data as graphs and integrate data effectively. Besides, RDF [3] explicitly describes semantical resource in graphs.

Upon such a graph, a primitive operation, *reachability join* (or simply *R*-join) was studied [11, 6]. In brief, a reachability join, $A \leftrightarrow D$, denoted *R*-join, is to find all the node-pairs, (a,d), in the underneath large data graph such as d is reachable from a, denoted $a \rightsquigarrow d$, and the labels of a and d are A and D respectively. Such *R*-join helps users to find information effectively without requesting them to fully understand the schema of the underneath graph. We explain the need of such *R*-join using an XML example. In Figure 1, it shows a graph representation (Figure 1 (b)) for an XML data (Figure 1 (a)). In Figure 1 (b), solid links represent document-internal links whereas dashed links represent cross-document links. We consider Figure 1 (b) as a graph with all links being treated in the same way. With *R*-join, we can easily find all the topics that a researcher



(a) XML Data (b) XML Data Graph

Fig. 1. An Example

is interested in using `researcher`↪`topic`. However, it would be difficult for a user to find the same information using XPath queries, because XPath supports document-internal links using a descendants-or-self-axis operator // and cross-document links using value-matching based on a notion called `ID`/`IDREF` in XML. It cannot find such information using an XPath query, `researcher`//`topic`, because `topic` is a child of `proj`, and there is an `ID`/`IDREF` from `researcher` to `proj`. XPath requests users to fully understand the schema and understand that the two different kinds of links are processed in two different ways in XML data. In this paper, we focus ourselves on optimizing and processing multi *R*-join queries.

A query with more than one *R*-joins could be naturally be represented by a query graph. To process such a query graph, there are existing approaches [5, 12] that extended the wellknown tree-specific method, namely, twig-stack join algorithm [4], to be applicable on DAGs. We studied the processing ability of the most up-to-date one method from such a family and found its performance is quite sensitive to the density of the underneath DAG. We give explanation for this observation. This makes our first contribution. For the second contribution, we found the proposed dynamic programming approach that combines *R*-join primitives into an optimized plan based on cost tends to be superior over the alternative and more stable in terms of the density of the underneath DAGs than the alternative. Our last contribution is that we conducted extensive experimental studies on multi *R*-joins queries processing using XMark data [9], which confirms that the efficiency of our approach.

The rest of paper is organized as follows. Section 2 gives our problem statement on multi reachability join query processing. Section 3 introduces the existing processing technique extended from tree-specific join approach. Together with the motivation for our approach, we discuss drawbacks of such an approach for multi *R*-joins queries processing . In Section 4, we briefly introduces the multiple interval encoding for DAGs, followed by a detailed description about fitting the existing *R*-join primitive and dy-

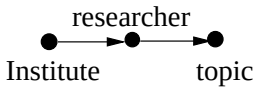


Fig. 2. An *R*-join Query

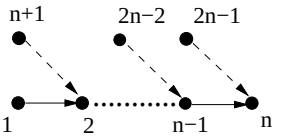


Fig. 3. A Example DAG for *TwigStackD*

namic programming paradigm into a cost-based optimizer for multi *R*-join queries. Section 5 reports the performance evaluation on our proposed method. Section 6 concludes this paper.

2 Multi Reachability Joins

We consider a database as a directed node-labeled data graph $G = (V,E,L,\phi)$.Here, V is a set of elements, E is a set of edges, L is a set of labels, and ϕ is a mapping function which assigns a node a label. Given a label $l \in L$, the extent of l is defined as a set of nodes in G whose label is l, denoted $ext(l)$. Below, we use $V(G)$ and $E(G)$ to denote the set of nodes and the set of edges of a graph G, respectively. Such a data graph example is shown in Figure 1 (b).

A reachability join, $A \hookrightarrow D$, called *R*-join, is to find all the node-pairs, (a,d), in the data graph G such that d is reachable from a, denoted $a \rightsquigarrow d$, and $\phi(a) = A$ and $\phi(d) = D$. We also use $D \hookleftarrow A$, instead of $A \hookrightarrow D$, if needed. $A \hookrightarrow D \equiv D \hookleftarrow A$. In this paper, we concentrate on processing conjunctive multi *R*-join queries in the form of

$$A \hookrightarrow B \wedge B \hookrightarrow C \wedge \cdots \wedge X \hookrightarrow Y$$

The following holds for *R*-joins.

- **Asymmetric**: $A \hookrightarrow B \not\equiv B \hookrightarrow A$.
- **Transitive**: If $A \hookrightarrow B \wedge B \hookrightarrow C$ hold, then $A \hookrightarrow C$.
- **Associative**: $(A \hookrightarrow B) \hookrightarrow C \equiv A \hookrightarrow (B \hookrightarrow C)$[1]

A multi *R*-joins query can be represented as a directed query graph, $G_q(V_q,E_q,L_q,\lambda)$. Here, V_q is a set of nodes. The node-label of a node $v \in V_q$ is represented as $\lambda(v)$. An edge $v \rightarrow u$ represents a *R*-join $A \hookrightarrow D$, where the labels of v and u are A and D, respectively. A graph representation of a multi *R*-joins query, $A \hookrightarrow C \wedge B \hookrightarrow C \wedge C \hookrightarrow D$, is shown in Figure 2.

We evaluate a query graph $G_q(V_q,E_q,L_q,\lambda_q)$ over a data graph $G(V,E,L,\phi)$. The result of the query graph, G_q, denoted $R(G_q)$, consists of a set of n-ary tuples. A tuple consists of n nodes in the data graph G, if the query graph G_q has n nodes ($|V(G_q)| = n$), in the form of $t = [v_1, v_2, \cdots, v_n]$, where there is a one-to-one mapping between v_i in t and u_i in $V(G_g)$ such that $\phi(v_i) = \lambda(u_i)$. In addition, all nodes in the n-ary tuple r satisfy all the reachability join conditions specified in the query graph G_q.

Example 1 *Fig. 2 represents a simple multi R-joins query as a directed graph. This query graph has a node labeled* ***Institute****, a node labeled* ***researcher*** *and a node label*

[1] The chain query $A \hookrightarrow B \wedge B \hookrightarrow C \wedge \cdots \wedge X \hookrightarrow Y$ is abbreviated to $A \hookrightarrow B \hookrightarrow C \hookrightarrow \cdots \hookrightarrow X \hookrightarrow Y$.

l	v	po_v	I_v
Institute	1	5	[1 : 5]
Institute	3	20	[12 : 13][17 : 20]
researcher	5	2	[1 : 2]
researcher	6	4	[3 : 4]
researcher	9	10	[6 : 10]
researcher	10	15	[11 : 15]
researcher	17	19	[12 : 13][17 : 19]
topic	20	7	[7 : 7]
topic	21	12	[12 : 12]

Table 1. Graph Encoding of [2]

(a) Tree Interval Encoding (b) SSPI Index

v	Interval	v	Interval
1	[2 : 11]	13	[17 : 20]
3	[34 : 41]	16	[27 : 30]
4	[42 : 43]	17	[35 : 40]
5	[3 : 6]	19	[38 : 39]
6	[7 : 10]	20	[18 : 19]
9	[13 : 22]	21	[28 : 29]
10	[23 : 32]		

v	preds
13	{4}
16	{19, 4}
20	{13}
21	{16}

Table 2. Graph Encoding of [5]

topic. *And two edges are in the query graph. The edge from* ***Institute*** *node to* ***researcher*** *node requires that the data node pair* (i,r), $i \in$***ext***$($***Institute***$)$ *and* $r \in$***ext***$($***researcher***$)$, *such that* $i \rightsquigarrow r$, *should be returned; in the same time, the edge from* ***researcher*** *node to* ***topic*** *node requires that the data node pair* (r,t), $r \in$***ext***$($***researcher***$)$ *and* $t \in$***ext***$($***topic***$)$, *such that* $i \rightsquigarrow r$, *should be returned.*

3 Twig-Join-Extended Approach and Our Motivation

In this section, we briefly review an existing approaches to process multi R-joins based on an interval-based coding scheme and give the motivation for our method. The Interval-based encoding scheme is widely used for processing queries over an XML tree, where a node v is encoded with a pair $[s,e]$ where s and e together specifies an interval. Given two nodes, u and v in an XML tree, u is an ancestor of v, $u \rightsquigarrow v$, if $u.s < v.s$ and $u.e > x.e$ or simply u's interval contains v's. Twig-Join is proposed in [4] to efficiently find all matches for a twig query against XML trees.

3.1 *TwigStackD* for Directed Acyclic Graphs

Recently, as an effort to extend Twig-Join in [4] to be workable on graphs, Chen et al. studied multi R-join query processing(called pattern matching) over a directed acyclic graph (DAG) in [5].

The test of a reachability relationship in [5] is broken into two parts. First, like the existing interval-based techniques for processing pattern matching over an XML tree, they first check if the reachability relationships can be identified over a spanning tree generated by depth-first traversal of a DAG. Table 2(a) lists the intervals from a spanning tree over the DAG of our running example. Second, for the reachability relationship that may exist over DAG but not in the spanning tree, they index all non-tree edges(named **remaining edges** in [5]), and all nodes being incident with any such non-tree edges in a data structure called SSPI in [5]. Thus, all predecessor/successor relationships that could not be identified by the intervals alone could be found with the help of SSPI. For our running example, Table 2(b) shows SSPI.

For example, the whole procedure to find the predecessor/successor relationship of $17 \rightsquigarrow 21$ in the DAG of Fig. 1 is like this. First, we check the containment of tree intervals for 17 and 21, but we could not identify $17 \rightsquigarrow 21$. Then, because 21 has entries

of predecessor in SSPI, we again try to find a reachability relationship between 17 and all 21's predecessors in SSPI by checking the containment of tree interval for 17 and that of each of 21's predecessors in SSPI. However, we still could not identify such a relationship relationship that far. Again, we recursively repeat the last step and we finally find that the tree interval of 17 contains that of 19. So we successfully identified $17 \rightsquigarrow 21$. Note that in this method, the reachability relationship between two nodes does not exist only if none reachability relationship could be found recursively for all predecessors throughout the whole SSPI .

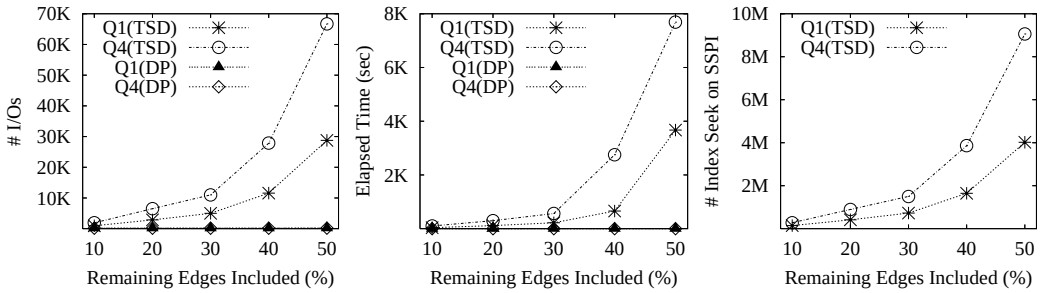
To process *R*-joins over a DAG, Chen et al. proposed a stack-based approach, denoted *TwigStackD*, overall in two parts.

1. Using Twig-Join algorithm in [4] to find all matches exist in the spanning tree of a give DAG for a twig/DAG query. In the mean while,
2. for each nodes popped out from stacks used in Twig-Join algorithm, *TwigStackD* buffers all nodes which participate in any partial solution in a bottom-up fashion, and maintains all reachability links among those nodes. When a top-most node that participates a solution found, *TwigStackD* enumerates in the buffer pool and outputs all full solutions headed by that node.

Example 2 *For our running example, we use the query in Fig. 2 to demonstrate TwigStackD algorithm, which uses SSPI index and operate on three interval lists for* ***Institute****,* ***researcher****, and* ***researcher****. The Twig-Join part of TwigStackD will found no solution. Consider the point when the cursor from Twig-Join part arrives to node* 17*, which is the last node to be scanned in the* ***researcher*** *list with minimum start value. At that time, the buffer pool for* ***topic*** *contains node* 20 *and* 21 *(Recall that TwigStackD grows up solutions in a bottom-up fashion and so* 20 *and* 21 *are partial solutions). When the Twig-Join part of TwigStackD still could not find matches on* 17 *and pop out it, the second part of TwigStackD check if* 17 *could reach any nodes in the buffer pool of* ***topic****, that is,* 20 *and* 21*. TwigStackD finds* $17 \rightsquigarrow 20$ *does not exist. Because entries in SSPI relevant to node* 20 *are recursively traversed, that is,* 20, 13 *and* 4*, and for all of them, no associated intervals found to be contained in that of* 17*. Then TwigStackD continues to check if* $17 \rightsquigarrow 21$ *and it is true known from the above description. So* 17 *is added to the* ***researcher*** *buffer pool. Similar procedure goes for node* 3 *upon which TwigStackD find the top-most node that leads to the solution* $[3, 17, 21]$.

3.2 Processing Ability of *TwigStackD*— Our Motivation

In order to identify a reachability relationship between two nodes, say, a and d, *TwigStackD* need to recursively search on SSPI to check if an ancestor of d could be reached by a. This overhead over a DAG can be costly. Consider the DAG of $2n-1$ nodes in Fig. 2, where the solid line is edges in the spanning tree generated by a depth-first search, and dashed lines are the remaining edges. Then the processing for the reachability relationship from node $n+1$ to node n will require the check if n is reachable, one by one, from node $n+1$ to node $2n-1$, and there are total $n-2$ times checking, since all of them are listed as the predecessors of n in SSPI. So, the time for such an operation is in $O(|V|)$. Recall the second step of *TwigStackD*, where relying on SSPI, the reachability relationship between every node popped from stacks and every nodes in the buffer pool



(a) Number of I/Os (b) Elapsed Time (sec) (c) Number of Index Seek

Fig. 4. The Test on DAGs with Increasing Densities

are checked. Therefore, the I/O cost of using *TwigStackD* to process *R*-joins queries is considerable.

Fig. 4 shows the performance of *TwigStackD* on 5 DAGs, which are obtained by including in the resulting spanning tree 10%, 20%, 30%, 40% and 50% of the remaining edges that are not in the spanning tree from an original DAG. The original DAG is obtained by collapse all strong connected components in a graph that is from a small XMark dataset with a factor 0.01 (16K nodes) and take both XML tree edge and ID/IDREF links as the edges in the graph. Queries `Q1` and `Q4` listed in Fig. 7 (a) and (d) were used here. For the *TwigStackD* processing, all curves are titled `Q1(TSD)` and `Q4(TSD)`.

Fig. 4 (a) shows the I/O number to process each query increased dramatically as more edges being added to the underlying DAG. As an example, for query `Q4`, the I/O number increased by 4606 from 10% to 20% on the y-axis, while it increased by 38881 from 40% to 50% on the y-axis. When 5 times number of remaining edges being included, the I/O number increased about 35 times. As for the number of index seek of SSPI, namely the number of times to seek an leaf page from the B+-Tree that implements the SSPI, which is showed in Fig. 4 (c), this value increased by 616052 from 10% to 20% on the y-axis, while it increased by 5201991 from 40% to 50% on the y-axis. The correlation coefficient for such two types of measurements is as hight as above 0.999, which speaks such an behavior for the number of I/Os during processing is mainly coursed by the number of index seek of SSPI. Similar situation for processing time could also be observed in Figure 4 (c), since the I/O number is the dominating factor for total processing cost. This test empirically showed that *TwigStackD* performs better for DAGs with fewer remaining edges, but its performance degrades rapidly when more edges being included in the underneath DAG.

One reason of the drawbacks of SSPI could be that to avoid storage of transitive closure of a DAG, *TwigStackD* trades time efficiency for space optimality. Thus, we choose to use a multiple interval encoding scheme for a DAG proposed in [2] which tries to efficiently manage the transitive closure for a DAG on both time and space. Besides, there exists efficient join algorithm[11] that processes a size 2 *R*-join query. Therefore, the main motivations to our approach is as follows,

– Using more efficient encoding scheme in [2] that requires not so large space as much as the transitive closure but still efficiently handles reachabililty queries for DAGs;
– Extending the existing size 2 *R*-join query processing scheme to be applicable to multi *R*-join queries with arbitrary size.
– Using long-established dynamic programming techniques to combine efficient *R*-join primitives into an optimized plan that evaluates multi *R*-join queries.

Fig. 4 (a) and (b) gives us a preliminary view on the efficiency of our approach, where curves are titled `Q1(DP)` and `Q4(DP)`. It is obvious that our approach is by far not so sensitive as *TwigStackD* is to the density of the DAG and the overall performance of our approach is far better than *TwigStackD*. For example, for `Q4` processing over the five DAGs, all numbers of I/Os are below 200 and the elapse times are below 1 second.

4 A New Dynamic Programming Approach

Dynamic programming has been widely used and studied as an effective paradigm for query optimization [10] and the query optimizers of nowadays commercial systems such as DB2 still depend on this paradigm. In this section, we show how to use dynamic programming to optimize and process multi *R*-joins queries.

4.1 A Multiple Interval Encoding

Agrawal et al. proposed an interval-based coding for encoding DAG [2]. Unlike the approaches that assign a single code, $[s:e]$, for every node in tree, Agrawal et al. assigned a set of intervals and a postorder number for each node in DAG. Let $I_u = \{[s_1:e_1],[s_2:e_2],\cdots,[s_n:e_n]\}$ be a set of intervals assigned to a node u, there is a path from u to v, $u \rightsquigarrow v$, if the postorder number of v is contained in an interval, $[s_j:e_j]$ in I_u. The interval-based coding for the graph in Figure 1 (b) is given in Table 1. For the same example of $17 \rightsquigarrow 21$ in the DAG of Fig. 1, it could be identified by the 21's *poId*, 12, and one interval associated with 17, $[12:13]$, since 12 is contained in $[12:13]$.

Based on [2], Wang et al. studied processing *R*-join over a directed graph [11]. In brief, given a directed graph, G. First, it constructs a DAG G' by condensing a maximal strongly connected component in G as a node in G'. Second, it generates codes for G' based on [2]. All nodes in a strongly connected component in G share the same code assigned to the corresponding representative node condensed in G'. Given a *R*-join, $A \hookrightarrow D$, two lists *Alist* and *Dlist* are formed respectively. *Alist* encodes every node v as $(v, s{:}e)$ where $[s:e] \in I_v$. A node of A has n entries in the *Alist*, if it has n intervals. *Dlist* encodes each node v as (v, po_v) where po_v is the postorder number. Note: *Alist* is sorted on the intervals $[s:e]$ by the ascending order of x and then the descending order of y, and *Dlist* is sorted by the postnumbers in ascending order. Wang et al. proposed to merge-join the nodes in *Alist* and *Dlist* and scans the two lists once.

4.2 System Overview

The join algorithm in [11] is not ready to be extended to process multi *R*-joins. Consider $A \rightsquigarrow D \wedge D \rightsquigarrow E$. For processing $A \rightsquigarrow D$, *Dlist* needs to be sorted based on the postnumbers, because D is descendant. For processing $D \rightsquigarrow E$, *Dlist* needs to be sorted based on

s followed by e for all $(v,s{:}e)$, because D is an ancestor. Also, recall, for $A \rightsquigarrow D$, *Alist* needs to encode every node v as $(v,s{:}e)$ where $[s:e] \in I_v$. The intervals of I_v list for all v in *Alist* must be maintained in multi R-joins processing. We will give out system overview first and then explain that how we remedy this problem. Overall, our R-Joins query processing could be divided into three functioning parts, estimation, planning and execution. The database stores Interval Lists, that is, all *Alist*s and *Dlist*s, Encoding Dict, which supports retrieval of I_v and po_v for any node, and some statistics about the data, which is mainly used to estimate the cost of a given R-join.

The execution part of our query engine contains another 3 types of operations besides the join primitive for $A \hookrightarrow D$,

$\alpha(A)$: Given a list of node vectors in the form of $(v_1, v_2, \ldots, v_l)$ and each v_i is in the extension associated with A, it attaches each interval $[s,e] \in I_{v_i}$ and obtain a number of $(v_1, v_2, \ldots, v_l, s:e)$ from every vector $(v_1, v_2, \ldots, v_l)$ and sorts the resulting list to obtain an *Alist* from these vector.

$\delta(D)$: Similarly, it results an temporary *Dlist*.

$\sigma(A,D)$: Given a list of node vectors in the form of $(v_1, v_2, \ldots, v_l)$ and each v_i/v_j is in the extension associated with A/D, it select out those vectors satisfying $v_i \hookrightarrow v_j$.

We explain the other parts for our R-Joins query processing in the following sections.

4.3 R-join Size Estimation

We introduce a simple but effective way to estimate the answer size for a sequence of R-joins. We need two presumption for our estimation: (1) For any pair-wise R-join, say $A \hookrightarrow D$, every pair of instance (a,d), where $a \in ext(A)$ and $d \in ext(D)$, is joinable with the same probability. (2) Consider two R-joins, say $A \hookrightarrow B$ and $B \hookrightarrow C$, for any three instance (a,b,c), where $a \in ext(A)$, $b \in ext(B)$, and $c \in ext(C)$, the two events $E_1 = \{a \text{ is joinable with } b\}$ and $E_2 = \{b \text{ is joinable with } c\}$ are independent.

Suppose the answer size for R-joins $(R_1 \hookrightarrow \ldots \hookrightarrow R_i)$ is M and the answer size for the pairwise R-join $R_h \hookrightarrow R_{i+1}$ is N, we will show the answer size for $(R_1 \hookrightarrow \ldots \hookrightarrow R_i) \wedge (R_h \hookrightarrow R_{i+1})$ $(1 \le h \le i)$,could be estimated as $\frac{M \times N}{|R_h|}$, where $|R_h|$ is the cardinality for the extension of R_h.

Suppose r_j is an instance from $ext(R_j)$, and let $Join(\cdot)$ denote the event that instances are joinable. Then because presumption (2), we have

$$\begin{aligned} & \mathbf{Pr}(Join(r_1, r_2..r_i, r_{i+1})) \\ = \ & \mathbf{Pr}(Join(r_1..r_i) \wedge Join(r_i, r_h)) \\ = \ & \mathbf{Pr}(Join(r_1..r_i)) \cdot \mathbf{Pr}(Join(r_i, r_h)). \end{aligned}$$

And because of presumption (1), we have

$$\begin{aligned} \mathbf{Pr}(Join(r_1..r_i)) &\approx \frac{M}{|R_1| \cdot |R_2| .. |R_i|} \\ \mathbf{Pr}(Join(r_i, r_h)) &\approx \frac{N}{|R_h| \cdot |R_{i+1}|}. \end{aligned}$$

So the estimated answer size of $(R_1 \hookrightarrow \ldots \hookrightarrow R_i) \hookrightarrow R_{i+1}$ can be

$$\begin{aligned} EST &= |R_1||R_2|..|R_i||R_{i+1}|\mathbf{Pr}(Join(r_1, r_2..r_i, r_{i+1})) \\ &= |R_1|..|R_{i+1}| \frac{M}{|R_1||R_2|..|R_i|} \frac{N}{|R_h||R_{i+1}|} \\ &= \frac{M \times N}{|R_h|}. \end{aligned}$$

So we will be able to estimate the answer size for all such R-joins by conveniently memorizing all pairwise R-join size and all label's extension cardinalities in the database catalog.

Example 3 *For our running example, the first join is* ***I*nstitute**$\hookrightarrow$ ***r*esearch**, *thus* $M = 3$. *For* ***I*nstitute**$\hookrightarrow$ ***r*esearch**$\hookrightarrow$***t*opic**, *since* $N = 3$ *and* $|$**ext(research)**$|$=5, *so the estimated result set size is* $\frac{3\times3}{|5|} = 1.8$. *The same result could be calculated if* ***r*esearch**$\hookrightarrow$ ***t*opic** *is taken as the first join.*

4.4 R-join Plan Enumeration

We use dynamic programming style optimization to enumerate a set of equivalent plans that combine the operations mentioned in Sec. 4.2 to evaluate a query graph G_q against a database graph G. We briefly outline the procedure of searching such plans and its execution to evaluate G_q.

Given a query graph G_q, only left-deep tree plans are searched as a common practice for a reasonable search space. Recall: in G_q, a node represent a label and an edge represents $\hookrightarrow$. An R-join, $A \hookrightarrow D$, is represented as an edge from A to D. Initially, subgraphs G_2 with two nodes connected by an edge are considered. Here, $V(G_2) = \{v,u\}$ and $E(G_2) = \{(v,u)\}$ or $E(G_2) = \{(u,v)\}$ depending on whether it is for $v \hookrightarrow u$ or $u \hookrightarrow v$. In the next step, it considers to add one more edge. That is, it considers a subgraph G_3 with three nodes and two edges, such as $V(G_3) = V(G_2) \cup \{u\}$ and E_3 includes all the edges in $E(G_2)$ plus one edge with at least one incident node in $V(G_2)$. The last step repeats until it includes all the nodes and edges in the original query graph G_q and we could get a sequence of subgraphs $(G_2, G_3, ..., G_m)$ and a sequent of edges being added

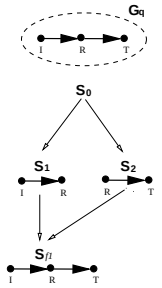


Fig. 5. Searching for an Optimal Plan using DP

Start	End	R-join	Result Size	Cost
s_0	s_1	$I \hookrightarrow R$	3	10
s_0	s_2	$R \hookrightarrow T$	3	10
s_1	s_{f1}	$R \hookrightarrow T$	1	21
s_2	s_{f1}	$I \hookrightarrow R$	1	19

Fig. 6. *DP* on G_q

$(e_2, e_2, ..., e_m)$. Regarding a subgraph in the sequence, say, G_i and the edge to be added to the subgraph, which should be e_i or more specifically, (u_i, v_i), there are 3 cases:

- Only u_i exists in $V(G_i)$, in this case, an α operation is needed and followed by a join for $u_i \hookrightarrow v_i$ and the cost is calculated as

$$C_I = C_\alpha \cdot |R(G_i)| + C_{\hookrightarrow}(\varepsilon \cdot |R(G_i)| + |Dlist_{v_i}|)$$

- Only v_i exists in $V(G_i)$, in this case, an δ operation maybe needed and followed by a join for $u_i \hookrightarrow v_i$, since the *Dlist* for v_i maybe obtained by the output from the preceding join. When δ operation is needed, the cost is calculated as

$$C_{II} = C_\delta \cdot |R(G_i)| + C_{\hookrightarrow}(|R(G_i)| + |Alist_{u_i}|)$$

  The first term in C_{II} can be eliminated if no δ operation needed.
- Both u_i and v_i exist in $V(G_i)$, in this case, an σ operation is needed. The cost is calculated as

$$C_{III} = C_\sigma \cdot |R(G_i)|)$$

In these cost formulae, values for $|Alist_{u_i}|$ and $|Dlist_{v_i}|$ are obtained from the statistics in database catalog. The intermediate result by evaluating the query graph G_i is represented as $R(G_i)$. We estimate the value of $|R(G_i)|$ according to section 4.3. The explanation for other factors are as follows,

C_α: factor to approximate the cost of α operation by the cardinality of the node vectors;
C_δ: factor to approximate the cost of δ operation by the cardinality of the node vectors;
C_σ: factor to approximate the cost of σ operation by the cardinality of the node vectors;
$C_{\hookrightarrow}$: factor to approximate the cost of *R*-join operation by the sum of two lists' length;
ε: factor to approximate the length of an *Alist* by the cardinality of the node vectors.

4.5 The Algorithm

In our dynamic programming style optimization, two basic components in the solution space are *statuses* and *moves*.

Algorithm 1 *DP Algorithm to Generate Plan*

l is a priority queue of status, sorting statues in the increasing order of $cost(S)$.

```
1:  Initialize queue l as ∅;
2:  Add S_0^+ into l;
3:  while l is NOT empty do
4:    S = l.first;
5:    Delete l.first from l;
6:    if S is a Final Status then
7:      Output plan P backward from l; Terminate this Algorithm;
8:    for each move from S to S' do
9:      if S' ∉ l then
10:       Insert S' into l;
11:     else
12:       Update cost(S') and l;
```

– A status, S, specifies a a subquery, G_s, as an intermediate stage in generating a query plan. To be more specific, a subquery of G_q is a subgraph G_s, where $V(G_s) \subseteq V(G_q)$ and $E(G_s) \subseteq E(G_q)$. Note: G_s does not necessarily be a connected graph if without the left-deep tree restriction.
– A move from one status (subquery G_{s_i}) to another status (subquery G_{s_j}) considers an additional R-join in G_{s_j} that does not appear in G_{s_i}, toward finding the entire query plan for G_q. The next status is determined based on a cost function which results in the minimal cost, in comparison with all possible moves. The process of moving from one status to another results in a left-deep tree which is the R-join order selection result.

We could estimate the cost for each move by those cost formulae in Sec. 4.4. Each status S is associated with a cost function, denoted $cost(S)$, which is the minimal accumulated estimated cost to move from the initial status S_0 to the current status S. Such accumulated cost of a sequence of moves from S_0 to S is the estimated cost for evaluating the subquery G_S being considered under the current status S. The goal of dynamic programming is to find the sequence of moves from the initial status S_0 toward the final status S_f with the minimum cost, $cost(S_f)$, among all the possible sequences of moves.

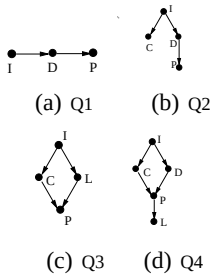
The rest task is to find a sequence of moves, namely a plan P, from the start status S_0^+ to a final status S_f^+, and minimize the cost $cost(P)$. Our algorithm is outlined in Algorithm 1. We simply apply Dijkstra's algorithm for the shortest path problem into our search space, aiming to find a "shortest" path from S_0 to any S_f^+, where nodes represent statues, edges represent moves, and the length of an edge is the cost of one move. We omit further explanation about Algorithm 1.

Example 4 *For our running example, Figure 5 shows two alternative plans for evaluating the query $I \hookrightarrow R \hookrightarrow T$, both containing two moves. The status S_0 is associated with a NULL graph, while S_1 and S_2 are respectively associated with two two graphs with two connected nodes, and S_3 is associated with the G_q and thus to be a final status. Details steps in the searching for an optimal plan is showed in Figure 6, where each row of the table lists a move in the solution space. The first column is the status where to start the move and the second column is the status where the move reaches. The third column is the R-join that will be processed in that move, while the number of results generated after the R-join is the fourth column.*

5 Performance Evaluation

In this section, we use two sets of tests to show the efficiency of our approach. The first set of tests is designed to compare our dynamic programming approach(denoted `DP`) with algorithm [5] (denoted `TSD`). The second set of tests further confirms the the ability to scale of our approach. We implemented all the algorithms using C++ on top of an experimental database system as done in [6]. We configure the buffer of the database system to be 2MB. A PC with a 3.4GHz processor, 2GB memory, and 120G harddisk running Windows XP is used to carry out all tests.

We generated 20M, 40M, 60M, 80M and 100M size XMark datasets [9] using 5 different factors, 0.2, 0.4, 0.6, 0.8, and 1.0 respectively, and named each dataset by its



(a) Q1 (b) Q2

(c) Q3 (d) Q4

Fig. 7. R-join Query Graphs

Dataset	$\|V\|$	$\|E\|$	$\|I\|$	$\|I\|/\|V\|$
20M	307,110	352,214	453,526	1.478
40M	610,140	700,250	901,365	1.477
60M	916,800	1,003,437	1,360,559	1.484
80M	1,225,216	1,337,378	1,816,493	1.483
100M	1,666,315	1,756,509	2,269,465	1.485

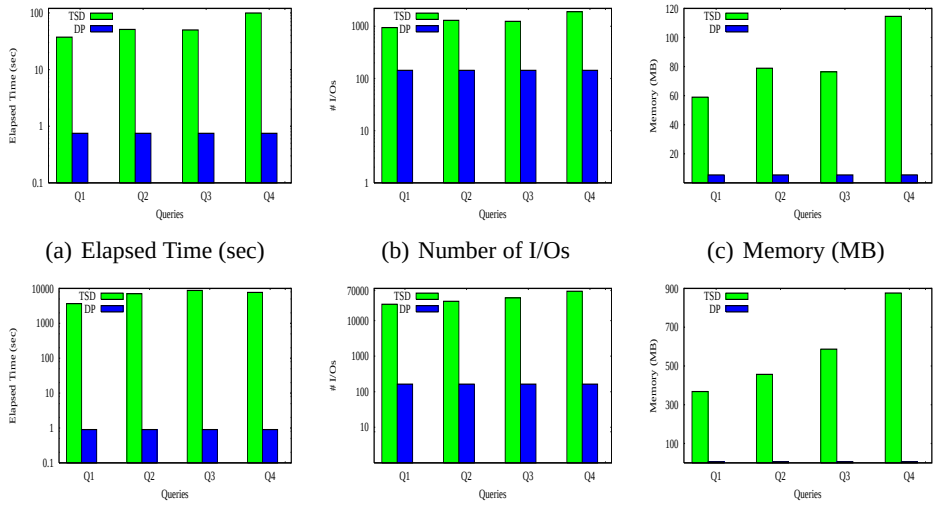
Fig. 8. Datasets Statistics

size. In these XML documents, we treat parent-child edges and ID/IDRE edges without difference to obtain graphs and collapse the strong connected components in graphs to get DAGs. The details of the datasets are given in Fig. 8. In Fig. 8, the first column is the dataset name. The second and third columns are the node number and edge number of the resulting DAG respectively. The forth column is the multiple interval labeling size, while the last column shows the average number of intervals per node in the DAG. Throughout all experiments, we use the 4 multi *R*-join join queries listed in Fig. 7, where the label *I* stands for *interest*, *C* for *category*, *L* for *listitem*,*D* for *description* and *P* for *parlist*.

5.1 *TwigStackD* v.s. Our Approach

We test all queries over the same dataset described in Section 3.2 for the purpose of compare *TwigStackD* algorithm to our approach. We show two set of figures that show the elapsed time, number of I/Os and memory used to process each query. The first set of figures show the performance on the DAG with 10 percent remaining edges added, which are listed in Fig. 9 (a)-(c), and the second set of figures show the performance on the DAG with 50 percent remaining edges added 50 percent, which are listed in Fig. 9 (d)-(f).

As shown in Fig. 9, our approach significantly outperformed *TwigStackD*, in terms of elapsed time, number of I/O accesses, and memory consumption. The sharp difference becomes even greater for the denser DAG, due to the fast performance degradation of *TwigStackD* when the edge number in the DAG increased. For example, consider Q3, *TwigStackD* used 16.7 times of elapsed time and 8.7 times of I/O accesses than those for our approach when 10 percent remaining edges being added, but when 50 percent remaining edges being added, they two rate becomes 2922.3 and 266.4 respectively. The memory usage of *TwigStackD* is unstable, and can range from 60MB to 900MB for the 4 queries, because needs to buffer every node that can potentially be in one final solution and thus largely depends on the solution size. And it could also be observed that generally, the larger query needs more memory for the increased needs of buffer pools by *TwigStackD*.



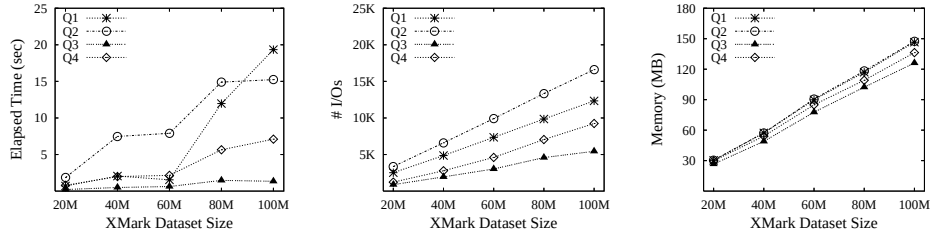
(a) Elapsed Time (sec) (b) Number of I/Os (c) Memory (MB)

(d) Elapsed Time (sec) (e) Number of I/Os (f) Memory (MB)

Fig. 9. Compare on the DAG with 10% and 50% Remaining Edge Included

5.2 Scalability Test of Our Approach

With the size of the dataset increasing from 20M to 100M, we tested the scalability performance for our approach and Fig. 10 shows the results. Both the number of I/Os and memory usage increase evenly as the size of underlying DAGs increases. However, for the processing time of each query when the data size increased, its variation is not so uniformly. A main reason for this observation is the CPU overhead caused by sorting in α and δ operations, for different distribution of the data may result different number of those operations for the same query. However, there is no abrupt change for the processing and the overall performance is still acceptable and query could be done within tens of seconds.



(a) Elapsed Time (sec) (b) Number of I/Os (c) Memory

Fig. 10. Scalability Test

6 Conclusion

In this paper, we study processing multi reachability joins (*R*-joins) queries on DAGs. For the most up-to-date existing approach, the *TwigStackD* algorithm processes the reachability relationships in a spanning tree and those induced by remaining edges a DAG using different procedures. The performance of this method degrades rapidly when the edges in a DAG increase. manage the transitive closure of DAGs [2] and efficient *R*-join primitives that developed in [11], we extend he existing size 2 *R*-join query processing scheme to be applicable to multi *R*-join queries with arbitrary size. The dynamic programming algorithm is employed to combine efficient *R*-join primitives into an optimized plan that evaluates multi *R*-join queries. We conducted extensive performance studies and confirmed the efficiency of our approach.

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