Fast Graph Pattern Matching

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Abstract

Due to rapid growth of the Internet technology and new scientific/technological advances, the number of applications that model data as graphs increases, because graphs have high expressive power to model complicated structures. The dominance of graphs in real-world applications asks for new graph data management so that users can access graph data effectively and efficiently. In this paper, we study a graph pattern matching problem over a large data graph. The problem is to find all patterns in a large data graph that match a user-given graph pattern. We propose a new two-step R-join (reachability join) algorithm with filter step and fetch step based on a cluster-based join-index with graph codes. We consider the filter step as an R-semijoin, and propose a new optimization approach by interleaving R-joins with R-semijoins. We conducted extensive performance studies, and confirm the efficiency of our proposed new approaches.

1 Introduction

A graph provides great expressive power to describe and understand the complex relationships among data objects. With the rapid growth of World-Wide-Web, new data archiving and analyzing techniques, there exists a huge volume of data available in public, which is graph structured in nature including hypertext data, semi-structured data [1]. *RDF* also allows users to explicitly describe semantic resource in graphs [7]. In [27], Shasha et al. highlighted algorithms and applications for tree and graph searching including graph/subgraph matching in data graphs. The demand increases to query graphs over a large data graph. In this paper, we study a graph pattern matching problem that is to retrieve all patterns in a large graph, G_D, that match a user-given graph pattern, G_q, based on reachability. As an example, based on business relationships, a graph pattern can be specified as to find `Supplier`, `Retailer`, `Whole-seller`, and `Bank` such that `Supplier` directly or indirectly supplies products to `Retailer` and `Whole-seller`, and all of them receive services from the same `Bank` directly or indirectly over a large data graph which can be obtained from the Web. Similar needs also stem from finding web-services connection patterns in WWW, finding relationships in social networks [3], finding research collaboration patterns, and finding research paper citation connection in archived bibliography datasets.

The graph pattern matching problem can be considered as an extension of finding twig-patterns (tree patterns) over *XML* tree. However, the existing techniques for processing twig-patterns over *XML* tree [8, 14] cannot be effectively applied to handle graph pattern matching over a large directed graph. It is because a graph does not have the nice property such that every two nodes are connected along a unique path. In a large data graph, a node, v_i, can reach another node v_j, while the same v_i is possibly reachable from v_j.

Contributions of this paper: We propose processing graph pattern matching as a sequence of *R*-join (reachability join) upon a graph database which stores a data graph in tables. We propose a new two-step *R*-join algorithm with a filter step and fetch step, based on a new cluster-based join-index with graph codes for reachability checking. Furthermore, we consider the first filter step as an *R*-semijoin, and propose a new optimization approach to optimize a sequence of *R*-joins/*R*-semijoins. We conducted extensive performance studies, and confirm the efficiency of our proposed new approaches.

Organization: We give the problem statement in Section 2. In Section 3. we discuss our *R*-join/*R*-semijoin approach. We propose a new two-step *R*-join algorithm (filter/fetch) based on which an *R*-semijoin is introduced. We propose a new *R*-join/*R*-semijoin order selection approach in Section 4. In Section 5, two existing approaches are discussed. We conducted extensive performance studies using large datasets and report our findings in Section 6. Related work is given in Section 7. Section 8 concludes the paper.

2 Problem Statement

In this section, we give our problem statement following the discussions on data graph and graph pattern.

A data graph is a directed node-labeled graph $G_D = (V, E, \Sigma, \phi)$. Here, V is a set of nodes; E is a set of edges (ordered pairs); Σ is a set of node labels, and ϕ is a mapping function which assigns each node, $v_i \in V$, a label $l_j \in \Sigma$. We use $\mathsf{label}(v_i)$ to denote the label of node v_i. Given a label $X \in \Sigma$, the extent of X, denoted as $\mathsf{ext}(X)$, is the set

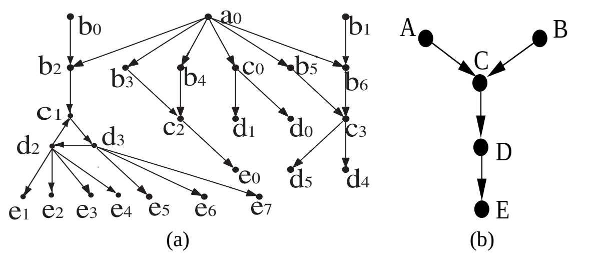


Figure 1. Data Graph (a) & Graph Pattern (b)

of all nodes in G_D whose labels are the same X. A simple data graph, G_D, is shown in Figure 1 (a). There are 5 labels, $\Sigma = \{A, B, C, D, E\}$. In Figure 1 (a), a node in an extent $\mathsf{ext}(X)$ is represented as x_i where x is a small letter of X with a unique number i to distinguish it from others in $\mathsf{ext}(X)$. For example, $ext(C) = \{c_0, c_1, c_2, c_3\}$.

In the following, we use $V(G)$ and $E(G)$ to denote the set of nodes and the set of edges in graph G.

A graph pattern is a connected directed node-labeled graph $G_q = (V_q, E_q)$, where V_q is a subset of labels (Σ), and E_q is a set of edges (ordered pairs) between two nodes in V_q. An edge $(X, Y) \in E(G_q)$ represents a reachability condition, denoted $X \hookrightarrow Y$, for $X, Y \in V_q$. A reachability condition, $X \hookrightarrow Y$, requests two nodes v_i and v_j in G_D, for $\mathsf{label}(v_i) = X$ and $\mathsf{label}(v_j) = Y$, v_j is reachable from v_i, denoted $v_i \rightsquigarrow v_j$. A match in G_D matches graph pattern G_q if it satisfies all the reachability conditions conjunctively specified in G_q. Note: $X \hookrightarrow Y$ and $Y \hookrightarrow Z$ implies $X \hookrightarrow Z$.

A result that matches a n-node graph pattern G_q is a n-ary tuple, $\langle v_1, v_2, \cdots, v_n \rangle$. A graph pattern, G_q, is shown in Figure 1 (b). There are five labeled nodes: A, B, C, D, and E, and there are four edges (reachability conditions), $A \hookrightarrow C$, $B \hookrightarrow C$, $C \hookrightarrow D$ and $D \hookrightarrow E$, which conjunctively specify a graph pattern to be found. Consider the data graph G_D in Figure 1 (a). There is a match in G_D that matches the graph pattern, G_q, shown in Figure 1 (b), $\langle a_0, b_0, c_1, d_2, e_1 \rangle$. In detail, $a_0 \rightsquigarrow c_1$ satisfies $A \hookrightarrow C$, $b_0 \rightsquigarrow c_1$ satisfies $B \hookrightarrow C$, $c_1 \rightsquigarrow d_2$ satisfies $C \hookrightarrow D$, and $d_2 \rightsquigarrow e_1$ satisfies $D \hookrightarrow E$. Note: c_1 is reachable from both a_0 and b_0 and can reach d_2, and $a_0 \rightsquigarrow c_1$ and $c_1 \rightsquigarrow d_2$ imply $a_0 \rightsquigarrow d_2$.

Graph Matching Problem: A graph matching problem is to find all matches in an arbitrary large directed data graph G_D that match all the reachability conditions conjunctively specified in a graph pattern, G_q.

3 A New Join-Based Approach

In this paper, given a graph pattern G_q, we propose graph matching as a sequence of joins, where each reachability condition, $X \hookrightarrow Y \in E(G_q)$, is a join, called *R*-join (for reachability join).

Such an *R*-join is possible based on a graph labeling called 2-hop reachability labeling [17]. A 2-hop reachability labeling over graph G_D assigns every node $v \in V$ a label $L(v) = (L_{in}(v), L_{out}(v))$, where $L_{in}(v), L_{out}(v) \subseteq V$, and $u \rightsquigarrow v$ is true if and only if $L_{out}(u) \cap L_{in}(v) \neq \emptyset$. A 2-hop reachability labeling for G_D is derived from a 2-hop cover of G_D. In brief, given G_D, the 2-hop cover minimizes a set of $S(U_w, w, V_w)$, as a set cover problem. Here, $w \in V(G_D)$ is called a center, and $U_w, V_w \subseteq V(G_D)$. $S(U_w, w, V_w)$ implies that, for every node, $u \in U_w$ and $v \in V_w$, $u \rightsquigarrow w$ and $w \rightsquigarrow v$, and therefore $u \rightsquigarrow v$. Consider Figure 1, an example is $S(L_{in}, w, L_{out}) = S(\{b_3, b_4\}, c_2, \{e_0\})$. Here, c_2 is the center. It indicates: $b_3 \rightsquigarrow c_2$, $b_4 \rightsquigarrow c_2$, $c_2 \rightsquigarrow e_0$, $b_3 \rightsquigarrow e_0$, and $b_4 \rightsquigarrow e_0$. There are several implementations to find such 2-hop cover for G_D [23, 24, 15]. The 2-hop cover update problem is addressed in [24]. We proposed a fast algorithm to compute 2-hop cover [15].

Let $\mathcal{H} = \{S_{w_1}, S_{w_2}, \cdots\}$ be the set of 2-hop cover computed, where $S_{w_i} = S(U_{w_i}, w_i, V_{w_i})$ and all w_i are centers. The 2-hop reachability labeling for a node v is $L(v) = (L_{in}(v), L_{out}(v))$. Here, $L_{in}(v)$ is a set of centers w_i where v appears in V_{w_i}, and $L_{out}(v)$ is a set of centers w_i where v appears in U_{w_i}.

Based on the 2-hop reachability labeling, we store graph G_D into a database, $\mathsf{G_{DB}}$, by taking a node-oriented representation. There are $|\Sigma|$ tables for G_D. A table T_X, for a label $X \in \Sigma$, has three columns named X, X_{in} and X_{out}. For each node $x_i \in \mathsf{ext}(X)$ ($\subseteq V(G_D)$), there is a tuple in table T_X. The X column keeps the node identifier x_i. The X_{in} and X_{out} columns keep its $L_{in}(x_i)$ and $L_{out}(x_i)$, respectively. We assume that the X column is the primary key of the table, because a node in G_D is uniquely identified with a node identifier. We call T_X a base table if it is the table for a label $X \in \Sigma$.

Example 3.1: A graph database $\mathsf{G_{DB}}$ for G_D (Figure 1) is shown in Figure 2 (a). There are five tables: $T_A(A, A_{in}, A_{out})$, $T_B(B, B_{in}, B_{out})$, $T_C(C, C_{in}, C_{out})$, $T_D(D, D_{in}, D_{out})$, and $T_E(E, E_{in}, E_{out})$. For a tuple x_i in table T_X, we make 2-hop reachability labeling compact by removing x_i from its X_{in} and X_{out} columns. Hence, $L_{in}(x_i) = X_{in} \cup \{x_i\}$ and $L_{out}(x_i) = X_{out} \cup \{x_i\}$. Below, we call $L_{in}(x_i)$ and $L_{out}(x_i)$ graph codes for x_i, denoted $\mathsf{in}(x_i)$ and $\mathsf{out}(x_i)$. The reachability, $x_i \rightsquigarrow y_i$, returns true, if $\mathsf{out}(x_i) \cap \mathsf{in}(y_j) \neq \emptyset$. □

3.1 R-Join

Given two base tables in $\mathsf{G_{DB}}$, a reachability condition, $X \hookrightarrow Y$, in a graph pattern G_q, can be processed as an *R*-join between two tables, T_X and T_Y.

$$T_R \leftarrow T_X \underset{X \hookrightarrow Y}{\bowtie} T_Y \tag{1}$$

Here, an *R*-join implies that, for every $x_i \in \mathsf{ext}(X)$ and $y_j \in \mathsf{ext}(Y)$, $x_i \rightsquigarrow y_j$ holds, if the reachability condition, $X \hookrightarrow Y$, is evaluated to be true using the graph codes. A pair, $\langle x_i, y_j \rangle$, appears in the temporal table T_R, if $x_i \rightsquigarrow y_j$ is true ($\mathsf{out}(x_i) \cap \mathsf{in}(y_j) \neq \emptyset$).

Consider $T_B \underset{B \hookrightarrow E}{\bowtie} T_E$, $\langle b_0, e_7 \rangle$ appears in the result, because $\mathsf{out}(b_0) = \{b_0, c_1\}$, $\mathsf{in}(e_7) = \{c_1, e_7\}$, and $\mathsf{out}(b_0) \cap \mathsf{in}(e_7) \neq \emptyset$.

In general, an *R*-join over any two tables, T_R and T_S, with a reachability condition, $X \hookrightarrow Y$, can be specified. Note: X (Y) is the column in the base table T_X (T_Y), that may appear in a temporal table because of a previous *R*-join. Here, T_R and T_S can be either a base or temporal table.

$$T_{RS} \leftarrow T_R \underset{X \hookrightarrow Y}{\bowtie} T_S \qquad (2)$$

Therefore, a graph pattern, G_q, can be specified as a sequence of *R*-joins followed by a projection to project the columns for every label $X \in V(G_q)$.

In this paper, we concentrate ourselves on query processing and optimization over multi *R*-joins, and focus on discussions of finding an optimal query plan that is represented as a left-deep tree [29] in which an *R*-join is either between two base tables or between a temporal table and a base table. As shown in Eq. (3) and Eq. (4) below, T_X and T_Y represent base tables, and T_R represents either a base or a temporal table.

$$T_R \underset{X \hookrightarrow Y}{\bowtie} T_Y \qquad (3)$$

$$T_X \underset{X \hookrightarrow Y}{\bowtie} T_R \qquad (4)$$

As a special case, a self-*R*-join is a join that can be processed as a selection,

$$T_R \underset{X \hookrightarrow Y}{\bowtie} T_R \qquad (5)$$

where T_R can be a base/temporal table. The following holds for *R*-joins. $T_R \underset{X \hookrightarrow Y}{\bowtie} T_S \equiv T_S \underset{X \hookrightarrow Y}{\bowtie} T_R$ (**Commutative**), $(T_R \underset{X \hookrightarrow Y}{\bowtie} T_S) \underset{W \hookrightarrow Z}{\bowtie} T_T \equiv T_R \underset{X \hookrightarrow Y}{\bowtie} (T_S \underset{W \hookrightarrow Z}{\bowtie} T_T)$ (**Associative**). Given a table T_R and suppose T_R keeps tuples that satisfy two reachability conditions, $A \hookrightarrow B$ and $B \hookrightarrow D$. Then the tuples in T_R satisfy $A \hookrightarrow D$ (**Transitive**).

3.2 A Cluster-Based R-Join Index

Like a θ-join, an *R*-join needs to check the reachability condition $X \hookrightarrow Y$ at run time, which incurs high cost. We propose a join-index approach, which is to index all tuples x_i and y_j that can join between two tables, T_X and T_Y. With such a join-index, an *R*-join can be efficiently implemented as to fetch the results.

We build a cluster-based *R*-join index for a data graph G_D based on the 2-hop cover computed, $\mathcal{H} = \{S_{w_1}, S_{w_2}, \cdots\}$, using our fast algorithm in [15], where $S_{w_i} = S(U_{w_i}, w_i, V_{w_i})$ and all w_i are centers. It is a B$^+$-tree in which its non-leaf blocks are used for finding a given center w_i. In the leaf nodes, for each center w_i, its U_{w_i} and V_{w_i}, denoted *F-cluster* and *T-cluster*, are maintained. We further divide w_i's *F-cluster* and *T-cluster* into labeled *F-subclusters*/*T-subclusters* where every node, x_i, in an X-labeled *F-subcluster* can reach every node y_j in a Y-labeled *T-subcluster*, via w_i. It is important to note that, in our cluster-based *R*-join index, we keep node identifiers (tuple identifiers) instead of pointers to tuples in base tables. With this arrangement, we can answer some *R*-join without accessing base tables. If there is a need to access a base table, we use the primary index built on the base table.

Together with the cluster-based *R*-join index, we design a W-table in which, an entry $W(X, Y)$ is a set of centers. A center w_i will be included in $W(X, Y)$, if w_i has a non-empty X-labeled *F-subcluster* and a non-empty Y-labeled *T-subcluster*. It helps to find the centers, w_i, in the cluster-based *R*-join index, that have an X-labeled *F-subcluster* and a Y-labeled *T-subcluster*.

Example 3.2: The $\mathsf{G_{DB}}$ for G_D (Figure 1) is shown in Figure 2. Figure 2 (a) shows the five base tables, Figure 2 (c) shows the clustered-based *R*-join index, and Figure 2 (b)

A	A_{in}	A_{out}
a_0	$\emptyset$	$\{c_1, c_3\}$

B	B_{in}	B_{out}
b_0	$\emptyset$	$\{c_1\}$
b_1	$\emptyset$	$\{c_3, b_6\}$
b_2	$\{a_0, b_0\}$	$\{c_1\}$
b_3	$\{a_0\}$	$\{c_2\}$
b_4	$\{a_0\}$	$\{c_2\}$
b_5	$\{a_0\}$	$\{c_3\}$
b_6	$\{a_0\}$	$\{c_3\}$

C	C_{in}	C_{out}
c_0	$\{a_0\}$	$\emptyset$
c_1	$\emptyset$	$\emptyset$
c_2	$\{a_0\}$	$\emptyset$
c_3	$\emptyset$	$\emptyset$

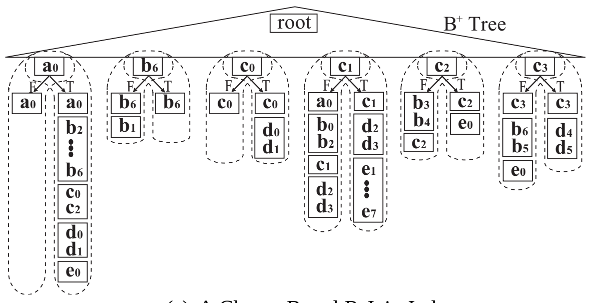
D	D_{in}	D_{out}
d_0	$\{a_0, c_0\}$	$\emptyset$
d_1	$\{a_0, c_0\}$	$\emptyset$
d_2	$\{c_1\}$	$\{c_1\}$
d_3	$\{c_1\}$	$\{c_1\}$
d_4	$\{c_3\}$	$\emptyset$
d_5	$\{c_3\}$	$\emptyset$

E	E_{in}	E_{out}
e_0	$\{a_0, c_2\}$	$\emptyset$
e_1	$\{c_1\}$	$\emptyset$
$\vdots$	$\vdots$	$\vdots$
e_7	$\{c_1\}$	$\emptyset$

(a) Five Base Tables

(A,B)	$\{a_0\}$
(A,E)	$\{a_0, c_1\}$
(B,E)	$\{c_1, c_2\}$
(B,D)	$\{c_1, c_3\}$
(B,B)	$\{b_0, b_6\}$
(A,C)	$\{a_0, c_1, c_3\}$
(B,C)	$\{c_1, c_2, c_3\}$
(C,D)	$\{c_0, c_1, c_3\}$
(A,D)	$\{a_0, c_1, c_3\}$
(C,C)	$\{c_0, c_1, c_2, c_3\}$
(D,E)	$\{c_1\}$
(C,E)	$\{c_1, c_2\}$
(D,C)	$\{c_1\}$
(D,D)	$\{c_1\}$

(b) W-table



(c) A Cluster-Based R-Join-Index

Figure 2. A Graph Database for G_D (Figure 1)

Algorithm 1 *HPSJ* $(T_X, T_Y, X \hookrightarrow Y)$

```
1: $\mathcal{C} \leftarrow \mathsf{W}(X, Y)$ using the $W$-table;
2: $\mathcal{R} \leftarrow \emptyset$;
3: for each $w_k \in \mathcal{C}$ do
4:     $X_k \leftarrow \mathsf{getF}(w_k, X)$ using the cluster-based R-join index;
5:     $Y_k \leftarrow \mathsf{getT}(w_k, Y)$ using the cluster-based R-join index;
6:     $\mathcal{R} \leftarrow \mathcal{R} \cup (X_k \times Y_k)$;
7: end for
8: return $\mathcal{R}$;
```

Algorithm 2 *HPSJ+* $(T_R, T_Y, X \hookrightarrow Y)$

```
1: $T_W \leftarrow \mathsf{Filter}(T_R, X \hookrightarrow Y)$;
2: $T_{RS} \leftarrow \mathsf{Fetch}(T_W, X \hookrightarrow Y)$;
3: return $T_{RS}$;

4: Procedure $\mathsf{Filter}(T_R, X \hookrightarrow Y)$
5: $T_W \leftarrow \emptyset$;
6: for each tuple, $r_i$, in $T_R$ do
7:     $X_i \leftarrow \mathsf{getCenters}(x_i, X, Y)$ where $x_i$ is in $X$ column in $r_i$;
8:     insert $(r_i, X_i)$ into $T_W$ if $X_i \neq \emptyset$;
9: end for
10: return $T_W$;

11: Procedure $\mathsf{Fetch}(T_W, X \hookrightarrow Y)$
12: $T_{RS} \leftarrow \emptyset$;
13: for each $(r_i, X_i) \in T_W$ do
14:     for each $w_k \in X_i$ do
15:         $Y_i \leftarrow \mathsf{getT}(w_k, Y)$ using the cluster-based R-join index;
16:         $T_{RS} \leftarrow T_{RS} \cup (\{r_i\} \times Y_i)$;
17:     end for
18: end for
```

shows its W-table. The cluster-based *R*-join index (Figure 2 (c)) has six centers, a_0, b_6, c_0, c_1, c_2, and c_3. The W-table (Figure 2 (b)) tells where *R*-join can find its centers in the cluster-based *R*-join index.

Consider $T_A \underset{A \hookrightarrow B}{\bowtie} T_B$. The entry $W(A, B)$ keeps $\{a_0\}$, which suggests that the answers can only be found in the clusters at the center a_0. As shown in Figure 2 (c), the center a_0 has an A-labeled *F-subcluster* $\{a_0\}$, and a B-labeled *T-subcluster* $\{b_2, b_3, b_4, b_5, b_6\}$. The answer is the Cartesian product between these two labeled subclusters. □

3.3 R-Join Algorithms

We first outline an *R*-join algorithm (Algorithm 1) between two tables discussed in [16], and then discuss a new two-step *R*-join algorithm (Algorithm 2) between a temporal table and a base table proposed in this paper.

The *HPSJ* algorithm (Algorithm 1) processes an *R*-join between two base tables, $T_X \underset{X \hookrightarrow Y}{\bowtie} T_Y$. First, it gets all centers, w_k, that have a non-empty X-labeled *F-subcluster* and a non-empty Y-labeled *T-subcluster*, using the W-table, and maintains it in $\mathcal{C}$ (line 1). Second, for each center $w_k \in \mathcal{C}$, it conducts three things. (1) It obtains its X-labeled *F-subcluster*, using $\mathsf{getF}(w_k, X)$, and stores them in X_k (line 4). (2) It obtains its Y-labeled *T-subcluster*, using $\mathsf{getT}(w_k, Y)$, and stores them in Y_k (line 5). Both (1) and (2) are done using the cluster-based *R*-join index. (3) it conducts Cartesian product between X_k and Y_k, and saves them into the answer set $\mathcal{R}$ (line 6). The output of an *R*-join between two base tables is a set of pairs $\langle x_i, y_j \rangle$ for $x_i \rightsquigarrow y_j$. It is important to note that there is no need to access base tables because all the nodes are maintained in the cluster-based *R*-join index to answer the *R*-join.

In order to process multi *R*-joins, we need a way to process an *R*-join between a temporal table and a base table. In general, a temporal table T_R has columns which are all the labels that are involved in the previous *R*-joins. Its tuples satisfy all the previous *R*-joins. We propose a new two-step *R*-join algorithm in Algorithm 2, called *HPSJ+*. It processes $T_R \underset{X \hookrightarrow Y}{\bowtie} T_Y$, where T_R is a temporal table that has an X column, and T_Y is a base table that has a Y column. Below, we discuss the *HPSJ+* algorithm in detail. A join algorithm can be implemented in a similar manner like Algorithm 2 to process $(T_R \underset{X \hookrightarrow Y}{\bowtie} T_X)$, where T_R is a temporal table that has a Y column, and T_X is a base table that has an X column.

The *HPSJ+* algorithm takes three inputs, a temporal table T_R, a base table T_Y, and an *R*-join condition $X \hookrightarrow Y$. In *HPSJ+*, first, it calls a procedure $\mathsf{Filter}(T_R, X \hookrightarrow Y)$ to filter T_R tuples that cannot be possibly joined with T_Y using W-table, and stores them into T_W (line 1). Second, it calls a procedure $\mathsf{Fetch}(T_W, X \hookrightarrow Y)$ to fetch the *R*-join results using the cluster-based *R*-join index. We do not need to access the base table T_Y, because the needed nodes are stored in the cluster-based *R*-join index. The details of the two procedures are given below.

In $\mathsf{Filter}(T_R, X \hookrightarrow Y)$, first, it initializes T_W to be empty (line 5). Second, in a for-loop, it processes every tuple r_i in T_R iteratively (line 6-9). In every iteration, it obtains a set of centers, X_i, for x_i in the X column in r_i, where every center w_k in X_i must have some $y_j \in T_Y$ in its *T-cluster* (line 7). It is done using $\mathsf{getCenters}(x_i, Y)$ below.

$$\mathsf{getCenters}(x_i, X, Y) = \mathsf{out}(x_i) \cap \mathsf{W}(X, Y) \tag{6}$$

As shown in Eq. (6), $\mathsf{out}(x_i)$ is a set of centers w_k that x_i can reach. It needs to access the base table T_X using the primary index. We use a working cache to cache those pairs of $(x_i, \mathsf{out}(x_i))$, in our implementation to reduce the access cost for later reuse. $\mathsf{W}(X, Y)$ is the set of all centers, w_k, such that some X-labeled nodes can reach w_k and some Y-labeled nodes can be reached by w_k. The intersection of the two sets is the set of all centers such that x_i must be able to reach some $y_j \in \mathsf{ext}(Y)$. If $X_i \neq \emptyset$, it implies that x_i must be able to reach some y_j (line 6), and therefore the pair of (r_i, X_i) is inserted into T_W (line 8). Otherwise, it can be pruned.

In $\mathsf{Fetch}(T_W, X \hookrightarrow Y)$, it initializes T_{RS} as empty (line 12). For each pair of $(r_i, X_i) \in T_W$, it obtains its Y-labeled *T-subcluster*, using $\mathsf{getT}(w_k, Y)$, stores them in Y_i (line 15), conducts Cartesian product between $\{r_i\}$ and Y_i, and puts them into T_{RS} (line 16).

As an example, consider $(T_B \underset{B \hookrightarrow C}{\bowtie} T_C) \underset{C \hookrightarrow D}{\bowtie} T_D$

to access $\mathsf{G_{DB}}$ (Figure 2). First, Algorithm 1, processes $T_B \underset{B\hookrightarrow C}{\bowtie} T_C$ and results in a temporal table, $T_{BC} = \{(b_0, c_1), (b_2, c_1), (b_3, c_2), (b_4, c_2), (b_5, c_3), (b_6, c_3)\}$. Note: only the clusters maintained in the three centers $W(B, C) = \{c_1, c_2, c_3\}$ need to be used (Refer to Figure 2 (b)). Next, Algorithm 2 processes $T_{BC} \underset{C\hookrightarrow D}{\bowtie} T_D$. In the Filter, the two tuples (b_3, c_2) and (b_4, c_2), in T_{BC} are pruned because $\mathsf{out}(c_2) = \{c_2\}$ and $\mathsf{W}(C, D) = \{c_0, c_1, c_3\}$, and the intersection is empty (Eq. (6)). Fetch returns the final results, which are $\{(b_0, c_1, d_2), (b_0, c_1, d_3), (b_2, c_1, d_2), (b_2, c_1, d_3), (b_5, c_3, d_4), (b_5, c_3, d_5), (b_6, c_3, d_4), (b_6, c_3, d_5)\}$.

3.4 R-Semijoins

Reconsider *HPSJ+* (T_R, T_Y, $X\hookrightarrow Y$) for an *R*-join between a temporal table T_R and a base table T_Y. It can be simply rewritten as $\mathsf{Fetch}(\mathsf{Filter}(T_R, X\hookrightarrow Y), X\hookrightarrow Y)$ as given in Algorithm 2. Recall: the Filter prunes those T_R tuples that cannot join any T_Y using the W-table. The cost of pruning T_R tuples is small for the following reasons. First, W-table can be stored on disk with a B$^+$-tree, and accessed by a pair of labels, (X, Y), as a key. Second, the frequently used labels are small in size and the centers maintained in $W(X, Y)$ can be maintained in memory. Third, the number of centers in a $W(X, Y)$ on average is small. Fourth, the cost of getCenters (Eq. (6)) is small with caching and sharing (Remark 3.1). We consider Filter () as an *R*-semijoin Eq. (7).

$$T_R \underset{X\hookrightarrow Y}{\ltimes} T_Y = \pi_{T_R}(T_R \underset{X\hookrightarrow Y}{\bowtie} T_Y) \tag{7}$$

Here, label X appears in the temporal table T_R and label Y appears in the base table T_Y.

$$T_R \underset{X\hookrightarrow Y}{\ltimes} T_X = \pi_{T_R}(T_R \underset{X\hookrightarrow Y}{\bowtie} T_X) \tag{8}$$

Eq. (8) shows a similar case where label Y appears in the temporal table T_R and label X appears in the base table T_X.

The *R*-semijoin discussed in this work is different from the semijoin discussed in distributed database systems which is used to reduce the dominate data transmission cost over the network at the expense of the disk I/O access cost. In our problem, there is no such network cost involved. A unique feature of our *R*-semijoin is that it is the first of the two steps in an *R*-join algorithm. In other words, it must process *R*-semijoin to complete *R*-join. Below, we use $\ltimes$ denote $\mathsf{Filter}()$ as an *R*-semijoin and $\widetilde{\bowtie}$ denote $\mathsf{Fetch}()$. Then, we have

$$T_R \underset{X\hookrightarrow Y}{\bowtie} T_S \equiv (T_R \underset{X\hookrightarrow Y}{\ltimes} T_S) \underset{X\hookrightarrow Y}{\widetilde{\bowtie}} T_S \tag{9}$$

It is worth noting that the cost for both sides of Eq. (9) are almost the same.

Consider $((T_B \underset{B\hookrightarrow C}{\bowtie} T_C) \underset{C\hookrightarrow D}{\bowtie} T_D) \underset{C\hookrightarrow E}{\bowtie} T_E$. Suppose we process $T_B \underset{B\hookrightarrow C}{\bowtie} T_C$ first, and maintain the result in T_{BC}. It becomes $(T_{BC} \underset{C\hookrightarrow D}{\bowtie} T_D) \underset{C\hookrightarrow E}{\bowtie} T_E$. Then,

$$\begin{aligned}
(T_{BC} \underset{C\hookrightarrow D}{\bowtie} T_D) \underset{C\hookrightarrow E}{\bowtie} T_E &= ((T_{BC} \underset{C\hookrightarrow D}{\ltimes} T_D) \underset{C\hookrightarrow D}{\widetilde{\bowtie}} T_D) \underset{C\hookrightarrow E}{\bowtie} T_E \\
&= (((T_{BC} \underset{C\hookrightarrow D}{\ltimes} T_D) \underset{C\hookrightarrow D}{\widetilde{\bowtie}} T_D) \underset{C\hookrightarrow E}{\ltimes} T_E) \underset{C\hookrightarrow E}{\widetilde{\bowtie}} T_E \\
&= (((T_{BC} \underset{C\hookrightarrow D}{\ltimes} T_D) \underset{C\hookrightarrow E}{\ltimes} T_E) \underset{C\hookrightarrow D}{\widetilde{\bowtie}} T_D) \underset{C\hookrightarrow E}{\widetilde{\bowtie}} T_E
\end{aligned}$$

The conditions used in the two *R*-semijoins are $C\hookrightarrow D$ and $C\hookrightarrow E$. Both access C in table T_{BC}. If we process the two *R*-semijoins one followed by another, we need to scan the table T_{BC}, get another temporal table T'_{BC}, and then process the second *R*-semijoin against T'_{BC}. Instead, we can process the two *R*-semijoins together, which only requests to scan T_{BC} once. The Filter cost can also be shared. It can be done by simply modifying Filter. Due to space limit, we omit the details.

Remark 3.1: (**R-Semijoins Processing**) *In general, a sequence of R-semijoins,* $(((T_R \underset{C_1}{\ltimes} T_{X_1}) \cdots) \underset{C_k}{\ltimes} T_{X_k})$ *can be processed together by one-scan of the temporal table* T_R *under the following conditions. First, it is a sequence of R-semijoins, and there is no any R-join in the sequence. Second, let* C_i *be a reachability condition,* $X_i\hookrightarrow Y_i$. *Either all* X_i *or all* Y_i *are the same for a label appearing in* T_R. □

4 Order Selection

In this section, we focus ourselves on *R*-join/*R*-semijoin order selection. We maintain the join sizes and the processing costs for all *R*-joins between two base tables in a graph database. In order to find an optimized left-deep tree query plan, we estimate the cost for a self-*R*-join (Eq. (5)), which can be done as a selection, and a join between a temporal table and a base table. We adopt the similar techniques to estimate joins/semijoins used in relational database systems. Note: our approaches is not independent on a cost model. The cost parameters are listed in Table 1.

$$|T_{RS}| = |T_R| \cdot \frac{|T_X \underset{X\hookrightarrow Y}{\bowtie} T_Y|}{|T_X| \cdot |T_Y|} \tag{10}$$

$$|T_{RS}| = |T_R| \cdot \frac{|T_X \underset{X\hookrightarrow Y}{\bowtie} T_Y|}{|T_X|} \tag{11}$$

$$|T_{RS}| = |T_R| \cdot \frac{|T_X \underset{X\hookrightarrow Y}{\bowtie} T_Y|}{|T_Y|} \tag{12}$$

Eq. (10) estimates the size of a self-*R*-join (Eq. (5)), with condition $X\hookrightarrow Y$, using the join selectivity for the *R*-join $T_X \underset{X\hookrightarrow Y}{\bowtie} T_Y$ between two base tables T_X and T_Y (the second term on the right side). Eq. (11) and Eq. (12) estimate the join size for *R*-joins (Eq. (3) and Eq. (4)), respectively.

Symbol	Meanings
IO_H	Search cost over the B$^+$-tree (B_H).
IO_F	Disk access cost for one page scan in the F_H file.
IO^T_{XY}	Average cost of using *R*-join index to find an X-labeled node x, such that $x \in \pi_X(T_X \underset{X\hookrightarrow Y}{\ltimes} T_Y)$.
IO^F_{XY}	Average cost of using the *R*-join index to find a Y-labeled node y, such that $y \in \pi_Y(T_Y \underset{X\hookrightarrow Y}{\ltimes} T_X)$.

Table 1. I/O Cost Parameters

The second terms on the right in Eq. (11) and Eq. (12) estimate a ratio if it joins with an additional base table.

The cost for self-*R*-join (Eq. (10)) is $2 \cdot (IO_H + IO_F) \cdot |T_R|$, because it needs to access the graph codes for checking $x_i \leadsto y_j$. The cost for *R*-join between a temporal table and a base table (Eq. (11) and Eq. (12)) is $(IO_H + IO_F) \cdot |T_R| + IO^T_{XY} \cdot |T_{RS}|$. Here, the two terms are for $\mathsf{Filter}()$ and $\mathsf{Fetch}()$, the first term is the cost to retrieve graph codes using $\mathsf{getCenters}$ (Algorithm 2 line 7), and the second term is multiplication of the number of total nodes retrieved on *R*-join index by the average cost for finding out each node on *R*-join index.

The size estimation of *R*-semijoins can be done in a similar way. We omit it due to space limit. In the following, we concentrate ourselves on *R*-join/*R*-semijoin order selection.

4.1 R-Join Order Selection

Join processing has been widely studied [20, 22, 18, 19, 9, 21, 29]. We use dynamic programming, as one of the main techniques, for join order selection. In this section, we discuss *R*-join order selection, and do not consider *R*-semijoins. We will discuss *R*-join/*R*-semijoin order selection in next subsection. The two basic components considered in dynamic programming are *statuses* and *moves*.

- A status, S_i, specifies a subquery, G_{s_i} $(\subseteq G_q)$, as an intermediate stage in generating a query plan. The intermediate result by evaluating the query graph G_s is represented as $\mathcal{R}(G_{s_i})$.
- A move from one status (subquery G_{s_i}) to another status (subquery G_{s_j}) considers an additional edge (*R*-join) in G_{s_j} that does not appear in G_{s_i}. 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.

The goal 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 determination of moves is based on a cost function. Such a cost function is associated with a status S, denoted $cost(S)$, which is the minimal accumulated estimated cost needed 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. Its search space is bounded by $O(2^m)$, where m is the number of edges in G_q.

4.2 Interleave R-Joins with R-Semijoins

Recall: $\bowtie$ is equivalent to $\ltimes$ ($\mathsf{Filter}()$) followed by $\tilde{\bowtie}$ ($\mathsf{Fetch}()$). In this section, we propose a new dynamic programming solution by interleaving *R*-joins with *R*-semijoins, or in precise, by interleaving $\ltimes$ and $\tilde{\bowtie}$.

Here, we define a status, $\mathcal{S}$, as a four element tuple, $(\mathcal{E}, \mathcal{L}, B^{in}, B^{out})$. A minimum-cost plan P is associated with a status which is a sequence of $\ltimes$ and $\tilde{\bowtie}$ being determined. We explain the four elements below. First, $\mathcal{E}$ is the set of edges (*R*-joins) in $E(G_q)$, that are already included in P associated with $\mathcal{S}$. Note: an edge $X \hookrightarrow Y$ is said to be included in $\mathcal{E}$, if its corresponding $\ltimes$ and $\tilde{\bowtie}$ are both included in P. Second, $\mathcal{L}$ is the set of labels that appear in the left-hand side of an *R*-semijoin or any side of an *R*-join. Third, B^{in} (B^{out}) is a set of labels, where each label $X \in B^{in}$ ($\in B^{out}$) indicates that the graph code in (out) in the base T_X is cached and can be used to process any remaining $\tilde{\bowtie}$, that has not been considered in the plan P yet. It is important to note that $\mathcal{E}$ is only related to $\bowtie$ (both $\ltimes$ and $\tilde{\bowtie}$), and the other two elements, B^{in} and B^{out}, are only related to $\tilde{\bowtie}$. There are three possible moves: a move by an additional $\ltimes$ (Filter), a move by an additional $\tilde{\bowtie}$ (Fetch), and a move by an additional *R*-join ($\bowtie$), We call them, Filter-move, Fetch-move, and *R*-join-move, respectively. Note: the *R*-join-move is designed to use *HPSJ* (Algorithm 1) to *R*-join the initial two base tables, and the other two moves are design to *HPSJ+* (Algorithm 2).

Filter-**move**: It corresponds to the addition of a new label, X, into B^{in} (or B^{out}) due to the inclusion of $\underset{X\hookrightarrow Y}{\ltimes}$ (or $\underset{Y\hookrightarrow X}{\ltimes}$), where X must be in $\mathcal{L}$, if $\mathcal{L} \neq \emptyset$, and $\underset{X\hookrightarrow Y}{\tilde{\bowtie}}$ (or $\underset{Y\hookrightarrow X}{\tilde{\bowtie}}$) has not been included yet. When moving to $(\mathcal{E}, B^{in} \cup \{X\}, B^{out})$ (or to $(\mathcal{E}, B^{in}, B^{out} \cup \{X\})$), it does not only append $T_R \underset{X\hookrightarrow Y}{\ltimes} T_S$ (or $T_R \underset{Y\hookrightarrow X}{\ltimes} T_S$), but also all other $\ltimes$ on X to maximize the cost sharing (Remark 3.1). All possible *R*-semijoins can be considered.

Fetch-**move**: Consider the status $\mathcal{S} = (\mathcal{E}, \mathcal{L}, B^{in}, B^{out})$, all unfinished Fetch are in $E(G_q) - \mathcal{E}$. Let $\underset{X\hookrightarrow Y}{\tilde{\bowtie}}$ be a unfinished Fetch, a move from $\mathcal{S}$ to $\mathcal{S}' = (\mathcal{E} \cup \{(X \hookrightarrow Y)\}, B^{in}, B^{out})$ appends P $\underset{X\hookrightarrow Y}{\tilde{\bowtie}}$, if its $\underset{X\hookrightarrow Y}{\ltimes}$ has been included. Note: $\underset{X\hookrightarrow Y}{\ltimes}$ is included if either X is in B^{out}, or Y is in B^{in}. As a special case, if both $X \in B^{out}$ and $Y \in B^{in}$, $\underset{X\hookrightarrow Y}{\bowtie}$ is a self *R*-join, which can be processed in this status together.

R-**join-move**: Consider the status $\mathcal{S} = (\mathcal{E}, \mathcal{L}, B^{in}, B^{out})$,

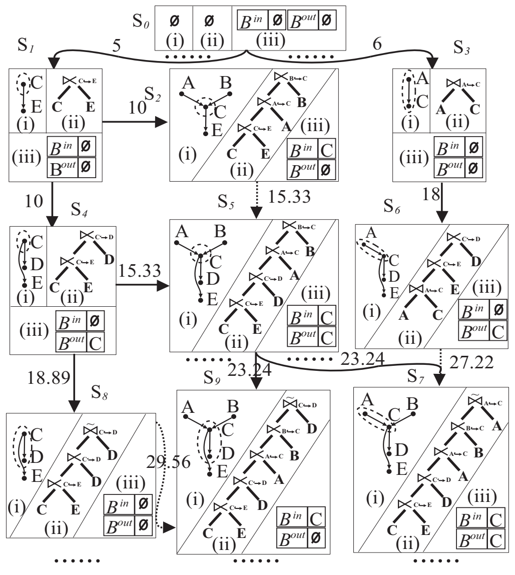


Figure 3. Order Selection

all unfinished Fetch are in $E(G_q) - \mathcal{E}$. Let $\underset{X \hookrightarrow Y}{\bowtie}$ be a unfinished *R*-join, a move from $\mathcal{S}$ to $\mathcal{S}' = (\mathcal{E} \cup \{(X \hookrightarrow Y)\}, B^{in}, B^{out})$ appends $\underset{X \hookrightarrow Y}{\bowtie}$ into P. Note: this *R*-join-move is only allowed to move from the initial status S_0 to another status.

Consider the query graph, G_q, in Figure 1. Figure 3 illustrates several moves for finding the minimum-cost *R*-join/*R*-semijoin plan from S_0. A status is shown in a block in Figure 3 with the following attributes: (i) subgraph of G_q being considered, (ii) a plan in the form of left-deep tree for (i), and (iii) B^{in} and B^{out}. Those subgraphs in a dot-circled in (i) shows $\mathcal{L}$. The edges appear in a dot-circled is $\mathcal{E}$. Initially, the start status $\mathcal{S}_0 = (\emptyset, \emptyset, \emptyset, \emptyset)$. From $\mathcal{S}_0$, there are 4 possible *R*-join-moves, because there are $n = 4$ edges in Figure 1, plus possible Filter-moves. In Figure 3, it shows two moves from $\mathcal{S}_0$: $\mathcal{S}_1$ (Filter-move) and $\mathcal{S}_3$ (*R*-join-move). In $\mathcal{S}_1$, $\mathcal{E} = \emptyset$, and $\mathcal{L} = \{C\}$, its plan P is shown in the part (ii), $T_C \underset{C \hookrightarrow E}{\ltimes} T_E$, and its B^{in} and B^{out} are shown in the part (iii). In $\mathcal{S}_3$, $\mathcal{E} = \{A \hookrightarrow C\}$, and $\mathcal{L} = \{A, C\}$, its plan P, $T_A \underset{A \hookrightarrow C}{\ltimes} T_C$, is shown in the part (ii), and its B^{in} and B^{out} are shown in the part (iii). From $\mathcal{S}_1$, there are two possible Filter-moves to either $\mathcal{S}_2$ or $\mathcal{S}_4$. Consider the Filter-move from $\mathcal{S}_1$ to $\mathcal{S}_2$. Because $C \in \mathcal{L}$ in $\mathcal{S}_2$, it adds C into B^{in} (getting C's graph code in) in $\mathcal{S}_2$. Let the resulting temporal table of $\mathcal{S}_1$ be T_R. In $\mathcal{S}_3$, it adds two new $\ltimes$ into the plan, $(T_R \underset{A \hookrightarrow C}{\ltimes} T_A) \underset{B \hookrightarrow C}{\ltimes} T_B$ to be processed together to share the processing cost (make use of C's graph code in).

Time/Space Complexity: Consider the number of statuses, $(\mathcal{E}, \mathcal{L}, B^{in}, B^{out})$. Because $\mathcal{L}$ contains all labels appeared in the previous statuses, provided the initial n *R*-join-moves, where $n = |V(G_q)|$, $\mathcal{L}$ fully determines $\mathcal{E}$. Furthermore, consider the number of combinations for $(\mathcal{L}, B^{in}, B^{out})$, which determine the number of statuses. Note that $B^{in} \cup B^{out} \subseteq \mathcal{L}$. Thus regarding a node $v_q \in V(G_q)$, there are 5 possible cases: 1) $v_q \notin \mathcal{L}$; 2) $v_q \in \mathcal{L}$, $v_q \notin B^{in}$, $v_q \notin B^{out}$; 3) $v_q \in \mathcal{L}$, $v_q \in B^{in}$, $v_q \notin B^{out}$; 4) $v_q \in \mathcal{L}$, $v_q \notin B^{in}$, $v_q \in B^{out}$; 5) $v_q \in \mathcal{L}$, $v_q \in B^{in}$, $v_q \in B^{out}$. There are in total 5^n combinations. Therefore, the total number of statuses is $n \cdot 5^n$. The space complexity is $O(n \cdot 5^n)$. There are m possible moves from each status, hence the total time complexity is $O(mn \cdot 5^n)$. The time complexity becomes $O(mn \cdot 3^n)$, if B^{in} and B^{out} is replaced by a single set as $B^{in} \cup B^{out}$, where our previous discussions of moves fit as well with the implication that the X_{in} and X_{out} columns of a base table T_X are accessed with the other each time.

As a closely related issue of this problem, Wu et al. in [29] studied a tree-structured query graph for accessing *XML* data which is tree structured. The time complexity of their algorithm is $O(n^2 \cdot 2^n)$. In this paper, we study graph pattern matching over a large data graph. The time complexity of our solution is reasonable comparing the time complexity of $O(n^2 \cdot 2^n)$ for accessing a large *XML* tree.

5 Two Existing Approaches

In this section, we discuss two existing approaches for graph pattern matching. One is a holistic based approach for a graph pattern against a subclass of directed graphs, directed acyclic graphs (*DAG*) [11]. The other is sort-merge based multi-join approach to process a graph pattern against a directed graph [28].

5.1 A Holistic Based Approach

Chen et al. in [11] studied graph pattern matching over a directed acyclic graph (*DAG*) instead of a directed graph that we are studying in this paper. Both graph patterns and data graphs are *DAG*s in [11]. As an approach along the line of *Twig-Join* [8], Chen et al. used the interval-based encoding scheme, which 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, v_i and v_j in an *XML* tree, v_i is an ancestor of v_j, $v_i \rightsquigarrow v_j$, if $v_i.s < v_j.s$ and $v_i.e > v_j.e$ or simply v_j's interval contains v_i's.

The test of a reachability condition between two data nodes used in [11] is broken into two phases. In the first phase, like the existing interval-based techniques for processing graph pattern matching over an *XML* tree, they first check if the reachability condition can be identified over a spanning tree generated by depth-first traversal of *DAG*. In the second phase, in order to find the reachability conditions that can not be referred in the spanning tree, they keep all non-tree edges (named remaining edges) in [11] and all nodes being incident with any such non-tree edges in a data structure called *SSPI* (Surrogate and Surplus Predecessor Index). Thus, all predecessor/successor relationships that can not be identified by the intervals alone can be found with the help of *SSPI*.

The algorithm proposed in [11] is a stack-based algorithm, called *TwigStackD*. For the first phase, it uses *Twig-Join* algorithm in [8] to find all *DAG* graph patterns found in the spanning tree. For the second phase, for each node popped out from stacks used in *Twig-Join* algorithm, *TwigStackD* buffers all nodes which at least match a reachability condition in a bottom-up fashion, and maintains all the corresponding links among those nodes. When a top-most node that matches a reachability condition, *TwigStackD* enumerates the buffer pool and outputs all fully matched patterns. *TwigStackD* performs well for very sparse *DAG*s. But, its performance degrades noticeably when the *DAG* becomes dense, due to the high overhead of accessing edge transitive closures.

5.2 Sort-Merge Based Multi Join

Wang et al. studied processing $T_X \underset{X \hookrightarrow Y}{\bowtie} T_Y$ over a directed graph [28] and proposed a join algorithm, called *IGMJ*. First, it constructs a *DAG* G' by condensing a maximal strongly connected component in G_D as a node in G'. Second, it generates a multi-interval code for a node in G' based on the approach given in [2]. As its name implies, the multi-interval-based code for encoding *DAG* [2] is to assign a set of intervals and a postorder number to each node in *DAG* G'. Let $I_v = \{[s_1, e_1], [s_2, e_2], \cdots, [s_n, e_n]\}$ be a set of intervals assigned to a node v, there is a path from v_i to v_j, $v_i \rightsquigarrow v_j$, if the postorder number of v_j is contained in an interval, $[s_k, e_k]$ in I_{v_i}. Note: nodes in a strongly connected component in G share the same code assigned to the corresponding representative node condensed in *DAG* G'.

In the *IGMJ* algorithm, given $T_X \underset{X \hookrightarrow Y}{\bowtie} T_Y$, two lists $Xlist$ and $Ylist$ are formed respectively. Here, in $Xlist$, every node x_i has n entries, if it has n intervals in I_{x_i}. In $Ylist$, every node y_j is encoded by the postorder number po_{y_j}. Note: $Xlist$ is sorted on the intervals $[s, e]$ by the ascending order of s and then the descending order of e, and $Ylist$ is sorted by the postorder number in ascending order. Then, *IGMJ* evaluates $T_X \underset{X \hookrightarrow Y}{\bowtie} T_Y$ against *DAG* G' by a single scan on the $Xlist$ and $Ylist$. If $x_i \rightsquigarrow y_j$ is satisfied, then every node that is contracted to v_i can reach every node that is contracted to v_j in the data graph G_D.

It needs extra cost to use the *IGMJ* algorithm to process multi *R*-joins, because it requests that both T_X ($\mathsf{ext}(X)$) and T_Y ($\mathsf{ext}(Y)$) must be sorted. Otherwise, it needs to scan two input tables multiple times to process an *R*-join. Consider an example. For processing $T_A \underset{A \hookrightarrow D}{\bowtie} T_D$, $Dlist$ needs to be sorted based on the postnumbers, because D-labeled nodes are the nodes to be reached. Let the temporal table T_R keep the result of $(T_A \underset{A \hookrightarrow D}{\bowtie} T_D)$. Then, for processing $(T_R \underset{D \hookrightarrow E}{\bowtie} T_E)$, it needs to sort all D-labeled nodes in T_R, based on their intervals, $[s, e]$, because D-labeled nodes now become the nodes to reach others. The main extra cost is the sorting cost.

6 Performance Evaluation

We conducted extensive experimental studies to study the performance of our two *R*-join/*R*-semijoin approaches, namely DP and DPS. Both use the *HPSJ* and *HPSJ*+ algorithms to process *R*-joins. Here, DP performs *R*-join order selection only (Section 4.1). DPS performs the optimal order selection by interleaving *R*-joins with *R*-semijoins (Section 4.2).

We compare DP and DPS with the holistic-based approach discussed in Section 5.1, denoted as TSD, and the multi *R*-joins approach discussed in Section 5.2 using a multi-interval code, denoted as INT-DP. The TSD is based on the *TwigStackD* algorithm [11], and can be only used to find graph matching over a special class of directed graphs, namely, directed acyclic graph (*DAG*). The INT-DP is based on the *IGMJ* algorithm [28] to process *R*-joins. We use dynamic programming for *R*-join order selection with INT-DP, as discussed in Section 4.1. We have implemented all the algorithms using C++ on top of the `minibase` database system developed at Univ. of Wisconsin-Madison.

We generated five large graphs based on *XMark* benchmark [25]. First, we generate five *XML* datasets using five factors, 0.2, 0.4, 0.6, 0.8, and 1.0, and name them as `20M`, `40M`, `60M`, `80M`, and `100M`, respectively. Here, `nM` means the dataset is n megabyte in size. Second, for each dataset, we generate a large graph by treating both document-internal links (parent-child) and cross-document links (ID/IDREF) as edges in the same manner. The details of the five databases are given in Table 2. In Table 2, the first column is the dataset name, the second and third columns are the numbers of nodes and edges, in the corresponding graphs, respectively. The forth column is the 2-hop cover size, while the last column shows the average size of graph codes using 2-hop cover.

We tested a large number of graph patterns as illustrated in Figure 4. We conducted our testing on a PC with a 3.4GHz Pentium processor, and 120GB hard disk running Windows XP. Note: the buffer size we used in our testing is 1MB for I/O access where the PC has 2GB memory. In the following, the reported elapse time includes both query optimization time and query processing time.

Dataset	$\|V\|$	$\|E\|$	$\|H\|$	$\|H\|/\|V\|$
20M	336,244	397,713	1,165,683	3.467
40M	667,242	789,538	2,324,539	3.483
60M	1,003,441	1,187,349	3,501,044	3.489
80M	1,337,383	1,581,682	4,672,991	3.494
100M	1,666,315	1,970,909	5,836,824	3.503

Table 2. Datasets Statistics

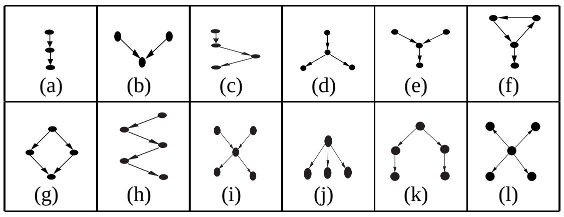


Figure 4. Graph-Patterns

6.1 R-Join vs Holistic over DAG

We first compare the two basic *R*-join order selection approaches, INT-DP and DP, with the holistic-based approach TSD. We used nine path-patterns and nine tree-patterns. A path-pattern has a linear structure (Figure 4(a), 4(c), and 4(h)). For the nine path-patterns, the 3-node path-patterns are P1, P2, and P3; the 4-node path-patterns are P4, P5, P6; and the 5-node path-patterns are P7, P8, P9. For tree-patterns, Figure 4(d) shows the shape of T1 to T3. Figure 4(j) shows the shape of T4 to T6. Figure 4(k) shows the shape of T7 to T8. Figure 4(l) shows the shape of T9.

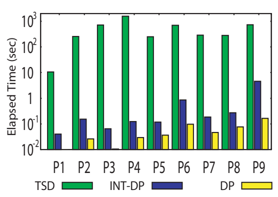
We tested these graph patterns using a small *XMark* dataset with a factor 0.01 (16K nodes), because TSD has difficult to answer graph patterns over a large graph [11]. For comparing with TSD, we process the directed acyclic graphs (*DAG*s) obtained from the *XMark* dataset, because *TwigStackD* can only support *DAG*. Its *XMark* data has $15,733$ nodes, $18,102$ edges. The 2-hop cover size is $55,158$.

As shown in Figure 5, both *R*-join based approaches, INT-DP and DP, significantly outperform TSD, in terms of elapsed time. For example, TSD spends $1,668$ and $9,709$ times of elapsed time as the amount that INT-DP and DP used to process P2, respectively. It is because that *TwigStackD* needs to buffer every node that can possibly be in one final solution. DP outperforms INT-DP for all patterns because DP needs less I/O cost. INT-DP needs to sort for *R*-joins, and therefore needs extra I/O cost.

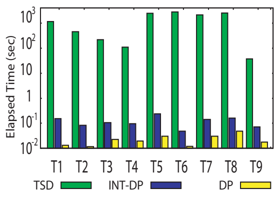
In the following, we focus on our *R*-join approaches, DP and DPS, over directed graphs.

6.2 R-Join/Semijoin over Directed Graphs

We tested DP and DPS using query structures listed through Figure 4(a) to Figure 4(h) by enumerating all possible patterns with different labels. For most queries, DP spends over five times of I/O cost than what DPS spends.

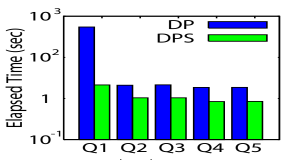


(a) 9 Path Patterns

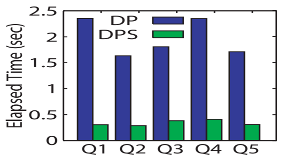


(b) 9 Tree Patterns

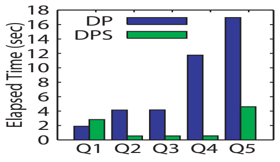
Figure 5. TSD **vs** INT-DP **vs** DP



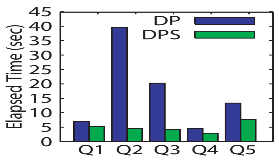
(a) $|V_q| = 4$



(b) $|V_q| = 4$



(c) $|V_q| = 5$



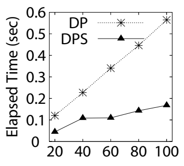
(d) $|V_q| = 5$

Figure 6. DP **vs** DPS

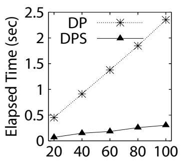
We report several results below.

We compare DP and DPS using the 100M data set. Figure 6(a) and Figure 6(b) show the elapsed time with 4-node graph patterns (Figure 4(e) and Figure 4(d)), respectively. Figure 6(c) and Figure 6(d) show the elapsed time for 4-node graph patterns (Figure 4(h) and Figure 4(i)), respectively. DPS significantly outperforms DP.

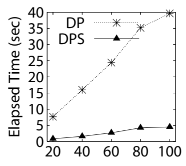
We also tested the scalability for DP and DPS using the five large graphs: 20M, 40M, 60M, 80M, and 100M (Table 2). Figure 7(a), Figure 7(b), and Figure 7(c), show the elapsed time for graph patterns given in Figure 4(a), Figure 4(d), and Figure 4(i), respectively. DPS significantly outperforms DP by at least one order of magnitude. One of the main reasons is that when the scale of the data sets increases the I/O cost of DP increases much faster than DPS does.



(a)



(b)



(c)

Figure 7. Scalability Test

7 Related Work

Query optimization has been studied for decades, dynamic programming is still used as the major technique

[26, 20, 22, 19, 10]. The optimization of a single select-project-join query in a centralized relational DBMS is outlined in [19]. Optimization for join processing are surveyed in [22]. [29] studied optimizing multiple structural join for XML tree-structured data.

Semijoins has also been studied in distributed database systems [6], which reduces the dominate data transmission cost over the network at the expense of the disk I/O access cost. Semijoin full reduction is discussed in [5]. A two-step approach to optimize queries using join and semijoin is discussed [12], by adding semijoins to a join sequence. An approach that considers both semijoins and joins in query optimization is reported in [13], however, the overall complexity can be as high as $O(3|E|)^{|V|-1})$ in [13]. In this paper, we propose dynamic programming strategies to deal with both *R*-joins/*R*-semijoins together with the overhead manageable.

Surveys on recursive query processing strategies can be found in [4]. In this paper, we show how to use graph coding and a join-index to process graph matching that avoids recursive query processing.

8 Conclusion

We proposed new *R*-join/*R*-semijoin processing and optimization techniques for the graph pattern matching problem. Given a graph pattern, G_q, where an edge represents a reachability condition that can be processed by an *R*-join, we proposed a new filter/fetch *R*-join algorithm, based on a new cluster-based join-index. By taking the first step as an *R*-semijoin, we optimize such a query by optimizing the *R*-joins/*R*-semijoins sequence. A unique feature of our *R*-semijoin/*R*-join approach is that *R*-semijoin is the first step of *R*-join so that there is a minimal overhead to process *R*-semijoins. We proposed a new optimization approach by interleaving *R*-joins with *R*-semijoins. We conducted extensive performance studies using large data graphs, and confirmed the effectiveness and efficiency of our approach.

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