Efficient Continuous Multi-Query Processing over Graph Streams

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ABSTRACT

Graphs are ubiquitous and ever-present data structures that have a wide range of applications involving social networks, knowledge bases and biological interactions. The evolution of a graph in such scenarios can yield important insights about the nature and activities of the underlying network, which can then be utilized for applications such as news dissemination, network monitoring, and content curation. Capturing the continuous evolution of a graph can be achieved by long-standing sub-graph queries. Although, for many applications this can only be achieved by a set of queries, state-of-the-art approaches focus on a single query scenario. In this paper, we therefore introduce the notion of continuous multi-query processing over graph streams and discuss its application to a number of use cases. To this end, we designed and developed a novel algorithmic solution for efficient multi-query evaluation against a stream of graph updates and experimentally demonstrated its applicability. Our results against two baseline approaches using real-world, as well as synthetic datasets, confirm a two orders of magnitude improvement of the proposed solution.

1 INTRODUCTION

In recent years, graphs have emerged as prevalent data structures to model information networks in several domains such as social networks, knowledge bases, communication networks, biological networks and the World Wide Web. These graphs are *massive* in scale and *evolve* constantly due to frequent updates. For example, according to its latest quarterly update, Facebook has over 1.52B daily active users who generate over 500K posts/comments and four million likes every minute resulting in massive updates to the Facebook social graph.

To gain meaningful and up-to-date insights in such frequently updated graphs, it is essential to be able to monitor and detect continuous patterns of interest. There are several applications from a variety of domains that may benefit from such monitoring. In social networks, such applications may involve targeted advertising, spam detection [3, 40], and fake news propagation monitoring based on specific patterns [34]. Similarly, other applications like (i) protein interaction patterns in biological networks [37, 45], (ii) traffic monitoring in transportation networks, (iii) attack detection (e.g., distributed denial of service attacks in computer networks), (iv) question answering in knowledge graphs [2], and (v) reasoning over RDF graphs may also benefit from such pattern detection.

For the applications mentioned above it is necessary to express the required patterns as *continuous sub-graph queries* over (one or many) streams of graph updates and appropriately *notify* the subscribed users for any patterns that match their subscription. Detecting these query patterns is fundamentally a sub-graph isomorphism problem which is known to be NP-complete due to the exponential search space resulting from all possible sub-graphs [18, 33]. The typical solution to address this issue is to pre-materialize the necessary sub-graph views for the queries and perform exploratory joins [36]; an expensive operation even for a single query in a static setting.

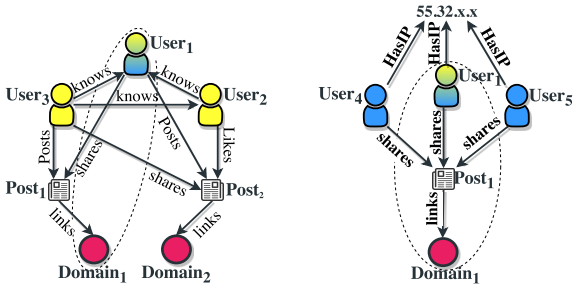


Figure 1: Spam detection: Users sharing and liking content with links to flagged domains. (a) A clique of users who know each other, and (b) Users sharing the same IP address.

These applications deal with graph streams in such a setup that is often essential to be able to support hundreds or thousands of continuous queries simultaneously. This leads to several challenges that require: (i) quickly detecting the affected queries for each update, (ii) maintaining a large number of materialized views, and (iii) avoiding the expensive join and explore approach for large sets of queries.

To better illustrate the remarks above, consider the application of spam detection in social networks. Fig. 1 shows an example of two graph patterns that may emerge from malicious user activities, i.e., users posting links to domains that have been flagged as fraudulent. Notice that malicious behavior could be caused either because a group of users that know each other share and like each other's posts containing content from a flagged domain (Fig. 1(a)), or because the group of users shared the same flagged post several times from the same IP (Fig. 1(b)). Even though these two queries are fundamentally different and produce different matching patterns, they share a common sub-graph pattern, i.e., "User1 $\xrightarrow{\text{shares}}$ Post1 $\xrightarrow{\text{links}}$ Domain1". If these two queries are evaluated independently, all the computations for processing the common pattern have to be executed twice. However, by identifying common patterns in query sets, we can amortize the costs of processing and answering them.

One simple approach to avoid processing all the (continuous) queries upon receiving a graph update is to index the query graphs using an inverted-index at the granularity of edges. While this

approach may help us quickly detect all the affected queries for a given graph update, we still need to perform several exploratory joins to answer the affected queries. For example, in Fig. 1, we would need to join and explore the edges matching the pattern "User1 $\xrightarrow{\text{Shares}}$ Post1 and Post1 $\xrightarrow{\text{Links}}$ Domain1" upon each update to process the two queries. On the contrary, if we first identify the maximal sub-graph patterns shared among the queries instead, we can minimize the number of operations necessary to answer the queries. Therefore, a solution which groups queries based on their shared patterns would be expected to deliver significant performance gains. To the best of our knowledge, none of the existing works provide a solution that exploits common patterns for continuous multi-query answering.

In this paper, we address this gap by proposing a novel *algorithmic solution*, coined TRIC (TRIe-based Clustering) to index and cluster continuous graph queries. In TRIC, we first decompose queries into a set of directed paths such that each vertex in the query graph pattern belongs to at least one path (path covering problem [11]). However, obtaining such paths leads to redundant query edges and vertices in the paths; this is undesirable since it affects the performance of the query processing. Therefore, we are interested in finding paths which are shared among different queries, with minimal duplication of vertices. The paths obtained are then indexed using 'tries' that allow us to minimize query answering time by (i) quickly identifying the affected queries, (ii) sharing materialized views between common patterns, and (iii) efficiently ordering the joins between materialized views affected from the update. To this end, our *contributions* are:

- We formalize the problem of continuous multi-query answering over graph streams (Section 3).
- We propose a novel query graph clustering algorithm that is able to efficiently handle large numbers of continuous graph queries by resorting on (i) the decomposition of continuous query graphs to minimum covering paths and (ii) the utilization of tries for capturing the common parts of those paths (Section 4).
- Since no prior work in the literature has considered continuous multi-query answering in the context of graph streams, we designed and developed two algorithmic solutions that utilize inverted indexes for the graph query answering. Additionally, we deploy and extend Neo4j [43], a well-established graph database solution, to support our proposed paradigm. To this end, the proposed solutions will serve as baselines approaches during the experimental evaluation (Section 5).
- We experimentally evaluate the proposed solution using three different datasets from social networks, transportation, and biology domains, and compare the performance against the three baselines. In this context, we show that our solution can achieve up to two orders of magnitude improvement in query processing time (Section 6).

2 RELATED WORK

Structural graph pattern search using graph isomorphism has been studied in the literature before [18, 33]. In [17], the authors propose a solution that aims at reducing the search space for a single query graph. The solution identifies candidate regions in the graph that can contain query embeddings, while it is coupled with a neighborhood equivalence locating strategy to generate enumerations. In the same spirit [30] aims at reducing the search space in the graph by exploiting syntactic similarities present on vertex relationships. [31] considers the sub-graph isomorphism problem when multiple queries are answered simultaneously. However, these techniques are designed for static graphs and are not suitable for processing continuous graph queries on evolving graphs.

Continuous sub-graph matching has been considered in [41] but the authors assume a static set of sub-graphs to be matched against update events, use approximate methods that yield false positives, and small (evolving) graphs. An extension to this work considers the problem of uncertain graph streams [7], over wireless sensor networks and PPIs. The work in [15] considers a setup of continuous graph pattern matching over knowledge graph streams. The proposed solution utilizes finite automatons to represent and answer the continuous queries. However, this approach can support a handful of queries, since, each query is evaluated separately, while, it generates false positives due to the adopted sliding window technique. These solutions are not suitable for answering large number of continuous queries on graphs with high update rates.

There are a few publish/subscribe solutions on ontology graphs proposed in [29, 42], but they are limited to the RDF data model. Distributed pub/sub middleware for graphs has recently been proposed in [5], however, the main focus is on node constraints (attributes) while ignoring the graph structure.

The work in [9] provides an exact subgraph search algorithm that exploits the *temporal* characteristics of representative queries for online news or social media exploration. The algorithm exploits the structural and semantic characteristics of the graph through a specialized data structure. Where the authors consider continuous query answering with graph patterns over dynamic multi-relation graphs. In [36] the authors perform subgraph matching over a billion node graph by proposing graph exploration methods based on cloud technologies. While the aforementioned works are similar to the query evaluation scenario, the emphasis is on efficient search mechanisms, rather than continuous answering over streaming graphs.

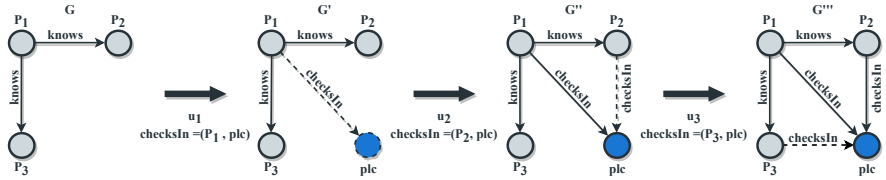
In the graph streams domain; [28] proposes algorithms to identify correlated graphs from a graph stream. This differs from our setup since a sliding window that covers a number of batches of data is used, and the main focus is set on identifying subgraphs with high Pearson correlation coefficients. In [14], the authors propose continuous pattern detection in graph streams with snapshot isolation. However, this solution considers only isolated queries (i.e., one query at a time) and the patterns detected are approximate. Finally, in [13] the authors propose a solution over a distributed computational environment, while the solution operates under the assumption of a static and limited query set.

Finally, some of the techniques used for increasing the efficiency of the proposed algorithm employ standard data indexing practices from a variety of domains, although the assumed setup and target applications differ significantly: (i) the representation of materialized views bears similarities with techniques from centralized RDF query processing [24, 32, 39] and statement/property tables as in Jena1 and Jena2 [44], (ii) the problem of maintaining the materialized views of (graph) queries relates to incremental view maintenance [4, 8, 25, 47] in database and warehousing environments, (iii) while query decomposition and tree-based clustering is typical in a variety of domains and applications [31, 38].

In general, solutions like the proposed one on continuous subgraph pattern matching can be applied in a wide range of domains such as social networks, protein-protein interactions (PPI), cyber-security, knowledge graphs, road network monitoring, and co-authorship graphs. Social network graphs emerge naturally

Update stream S
$u_1 = (checksIn = (P_1, \text{plc}))$
$u_2 = (checksIn = (P_2, \text{plc}))$
$u_3 = (checksIn = (P_3, \text{plc}))$

(a)



(b)

Figure 2: (a) An update stream S and (b) the evolution of graph G after inserting $u_i \in S$.

from the evolving interactions and activities of the users, while applications such as advertising, recommendation systems, and information discovery aim at exploiting these interactions. Social network applications may benefit from continuous pattern matching, and can leverage on already observed patterns in content propagation [21, 22, 46] and influential user discovery [6, 9]. PPIs are data repositories [35, 37] that index proteins (graph vertices) and the interactions (graph edges) between them. PPI graphs are constantly updated due to additions and invalidations of interactions, while scientists manually query PPIs to discover new patterns. In such scenarios, subgraph matching could enhance information discovery through appropriate graphical user interface tools. In cyber-security, subgraph matching could be applied for network motoring, denial of service, and exfiltration attacks [20], while subgraph matching over road networks could capture traffic events, and taxi route pricing. Finally, in the domain of co-authorship graphs, users may utilize continuous query evaluation in services similar to Google Scholar Alerts, when requesting to be notified about newly published content.

3 DATA MODEL AND PROBLEM DEFINITION

In this section we outline the data (Section 3.1) and query model (Section 3.2) that our approach builds upon.

3.1 Graph Model

In this paper, we use attribute graphs [10] (Definition 3.1), as our data model, as they are used natively in a wide variety of applications, such as social network graphs, traffic network graphs, and citation graphs. Datasets in other data models can be mapped to attribute graphs in a straightforward manner so that our approach can be applied to them as well.

Definition 3.1. An *attribute graph* G is defined as a directed labeled multigraph:

$$G = (V, E, l_V, l_E, \Sigma_V, \Sigma_E)$$

where V is the set of vertices and E the set of edges. An edge $e \in E$ is an ordered pair of vertices $e : (s, t)$, where $s, t \in V$ represent source and target vertices. $l_V : V \rightarrow \Sigma_V$ and $l_E : E \rightarrow \Sigma_E$ are labeling functions assigning labels to vertices and edges from the label sets Σ_V and Σ_E.

For ease of presentation, we denote an edge e as $e = (s, t)$, where e, s and t are the labels of the edge($l_E(e)$), source vertex ($l_V(s)$) and target vertex ($l_V(t)$) respectively.

As our goal is to facilitate efficient continuous multi-query processing over graph streams, we also provide formal definitions for updates and graph streams (Definitions 3.2 and 3.3).

Definition 3.2. An update u_t on graph G is defined as an *addition* (e) of an edge e at time t. An addition leads to new edges between vertices and possibly the creation of new vertices.

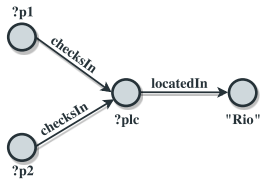


Figure 3: Example query graph pattern.

Definition 3.3. A *graph stream* $S = (u_1, u_2, \ldots, u_t)$ of graph G is an *ordered sequence* of updates.

Fig. 2(a) presents an update stream S consisting of three graph updates u_1, u_2, and u_3 generated from social network events. While, Fig. 2 (b) shows the initial state of graph G and its evolution after inserting sequentially the three updates.

3.2 Query Model

For our query model we assume that users (or services operating on their behalf) are interested to learn when certain patterns emerge in an evolving graph. Definition 3.4 formalizes *query graph patterns* that define structural and attribute constraints on graphs.

Definition 3.4. A *query graph pattern* Q_i is defined as a directed labeled multigraph:

$$Q_i = (V_{Q_i}, E_{Q_i}, vars, l_V, l_E, \Sigma_V, \Sigma_E)$$

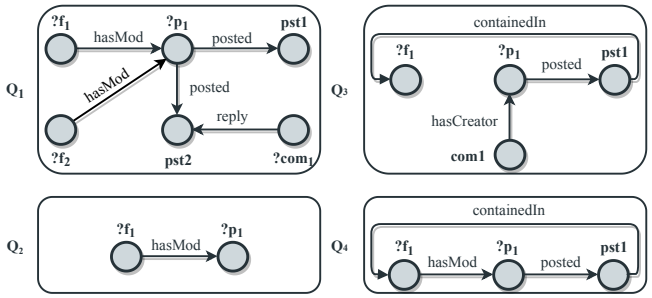
where V_{Q_i} is a set of vertices, E_{Q_i} a set of edges, and $vars$ a set of variables. $l_V : V \rightarrow \{\Sigma_V \cup vars\}$ and $l_E : E \rightarrow \Sigma_E$ are labeling functions assigning labels (and variables) to vertices and edges.

Let us consider an example where a user wants to be notified when his friends visit places nearby. Fig. 3 shows the corresponding query graph pattern that will result in a user notification when two people check in at the same place/location in Rio.

Based on the above definitions, let us now define the problem of *multi-query processing over graph streams*.

Problem Definition. Given a set of query graph patterns $Q_{DB} = \{Q_1, Q_2, \ldots, Q_k\}$, an initial attribute graph G, and a graph stream S with continuous updates $u_t \in S$, the problem of *multi-query processing over graph streams* consists of continuously identifying all satisfied query graph patterns $Q_i \in Q_{DB}$ when applying incoming updates.

Query Set and Graph Modifications. A set of query graph patterns Q_{DB} is subject to modifications (i.e., additions and deletions). In this work, we focus on streamlining the query indexing phase, while developing techniques that allow processing each incoming query graph pattern separately, thus supporting continuous additions in Q_{DB}. In the same manner, a graph G is subject to edge additions and deletions, our main objective is to efficiently determine the queries satisfied by an edge addition. The proposed model does not require indexing the entire graph G and retains solely the necessary parts of G for the query answering. To this



(a)

Query ID	Set of Covering Paths
Q_1	$P_1 = \{?var \xrightarrow{hasMod} ?var \xrightarrow{posted} \text{“}pst1\text{”}\}$ $P_2 = \{?var \xrightarrow{hasMod} ?var \xrightarrow{posted} \text{“}pst2\text{”}\}$ $P_3 = \{?var \xrightarrow{reply} \text{“}pst2\text{”}\}$
Q_2	$P_1 = \{?var \xrightarrow{hasMod} ?var\}$
Q_3	$P_1 = \{\text{“}com1\text{”} \xrightarrow{hasCreator} ?var \xrightarrow{posted}$ “$pst1$” $\xrightarrow{containedIn} ?var\}$
Q_4	$P_1 = \{?var \xrightarrow{hasMod} ?var \xrightarrow{posted} \text{“}pst1\text{”}$ $\xrightarrow{containedIn} ?var\}$

(b)

Figure 4: (a) Four query graph patterns that capture events generated inside a social network and (b) their covering paths.

end, we do not further discuss deletions on Q_{DB} and G, as we focus on providing high performance query answering algorithms.

4 TRIE-BASED CLUSTERING

To solve the problem defined in the previous section, we propose TRIC (TRIe-based Clustering). As motivated in Section 1, the *key idea* behind TRIC lies in the fact that query graph patterns overlap in their structural and attribute restrictions. After identifying and indexing these shared characteristics (Section 4.1), they can be exploited to batch-answer the indexed query set and in this way reduce query response time (Section 4.2).

4.1 Query Indexing Phase

TRIC indexes each query graph pattern Q_i by applying the following two steps:

1. Transforming the original query graph pattern Q_i into a set of path conjuncts, that cover all vertices and edges of Q_i, and when combined can effectively re-compose Q_i.
2. Indexing all paths in a trie-based structure along with unique query identifiers, while clustering all paths of all indexed queries by exploiting commonalities among them.

In the following, we present each step of the query indexing phase of Algorithm TRIC, give details about the data structures utilized and provide its pseudocode (Fig. 5).

Step 1 : **Extracting the Covering Paths.** In the first step of the query indexing process, Algorithm TRIC decomposes a query graph pattern Q_i and extracts a set of paths $CP(Q_i)$ (Fig. 5, line 1). This set of paths, covers all vertices $V \in Q_i$ and edges $E \in Q_i$. At first, we give the definition of a path and subsequently define and discuss the covering path set problem.

Definition 4.1. A *path* $P_i \in Q_i$ is defined as a list of vertices $P_i = \{v_1 \xrightarrow{e_1} v_2 \xrightarrow{e_2} \dots v_k \xrightarrow{e_k} v_{k+1}\}$ where $v_i \in Q_i$, such that two sequential vertices $v_i, v_{i+1} \in P_i$ have exactly one edge $e_i \in Q_i$ connecting them, i.e., $e_k = (v_k, v_{k+1})$.

Definition 4.2. The *covering paths* [1] *CP* of a query graph Q_i is defined as a set of paths $CP(Q_i) = \{P_1, P_2, \dots, P_k\}$ that cover all *vertices* and *edges* of Q_i. In more detail, we are interested in the least number of paths while ensuring that for every vertex $v_i \in Q_i$ there is at least one path P_j that contains v_i, i.e., $\forall i \exists j : v_i \in P_j$, $v_i \in Q_i$. In the same manner, for every edge $e_i \in Q_i$ there is at least one path P_j that contains e_i, i.e., $\forall i \exists j : e_i \in P_j$.

Obtaining the Set of Covering Paths. The problem of obtaining a set of paths that covers all vertices and edges is a graph optimization problem that has been studied in literature [1, 27]. In our approach, we choose to solve the problem by applying a greedy

```
   Input: Query Q_i = (V_Qi, E_Qi, vars, l_V, l_E, Σ_V, Σ_E)
   Output: Q_DB ← Q_DB ∪ Q_i
Step 1
1  Paths ← CP(Q_i); // Obtain the set of covering paths
2  foreach P_i ∈ Paths do // For each covering path P_i of Q_i
3      foreach trie T_i with root(T_i) = e_1 : e_1 ∈ P_i do
4          depthFirstSearch(T_i); // Traverse trie in DFS
           // If there exists a trie that can store P_i
5          if ∃{n_0 → ... n_i → ... n_k} ⊆ P_i then
               // Store the trie path positions
6              positions ← {n_0 → ... n_i → ... n_k};
       // If all edges e_i ∈ P_i cannot be indexed, create
          additional trie nodes to index them
Step 2
7      if positions ∩ P_i ≠ ∅ then
8          create_nodes(P_i \ positions);
9      last(positions) ← id(Q_i); // Store the query id
       // Keep a reference to the last trie node
10     pathPositions → pathPositions ∪ last(positions);
       // Store tries T_i under which, edge e_i is indexed
11     foreach e_i ∈ P_i do
12         edgeInd[e_i] ← T_i;
   // Store the nodes that Q_i was indexed under
13 queryInd[id(Q_i)] ← pathPositions
```

Figure 5: Query indexing phase of Algorithm TRIC.

algorithm, as follows: For all vertices v_i in the query graph Q_i execute a depth-first walk until a leaf vertex (no outgoing edge) of the graph is reached, or there is no new vertex to visit. Subsequently, repeat this step until all vertices and edges of the query graph Q_i have been visited at least once and a list of paths has been obtained. Finally, for each path in the obtained list, check if it is a sub-path of an already discovered path, and remove it from the list of covering paths. The end result of this procedure yields the *set of covering paths*.

Example 4.3. In Fig. 4(a) we present four query graph patterns. These query graph patterns capture activities of users inside a social network. By applying Definition 4.2 on the four query graph patterns presented, Algorithm TRIC extracts four sets of covering paths, presented in Fig. 4(b).

Obtaining a set of paths serves two purposes: (a) it gives a less complex representation of the query graph that is easier to manage, index and cluster, as well as (b) it provides a streamlined approach on how to perform the materialization of the subgraphs that match a query graph pattern, i.e., the query answering during the evolution of the graph.

Materialization. Each edge e_i that is present in the query set has a materialized view that corresponds to its $matV[e_i]$. The materialized view of e_i stores all the updates u_i that contain e_i. In order to obtain the subgraphs that satisfy a query graph pattern Q_i all edges $e_i \in Q_i$ must have a non-empty materialized view (i.e., $matV \neq \emptyset$) and the materialized views should be joined as defined by the query graph pattern.

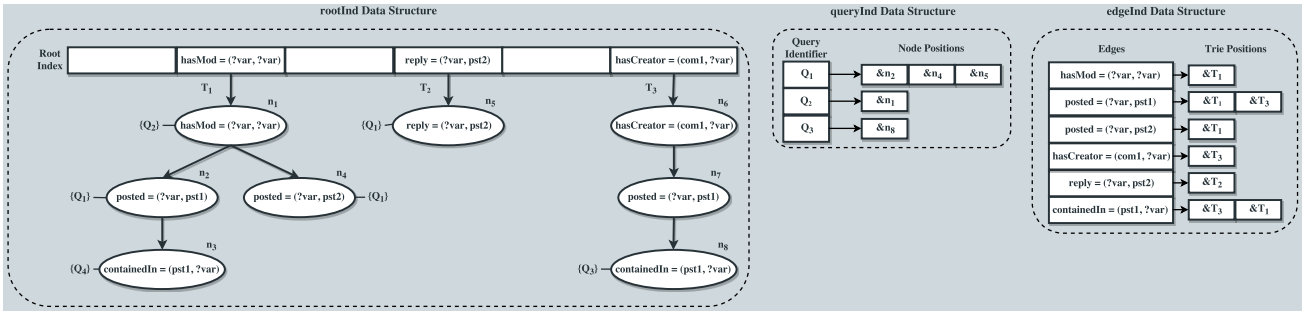


Figure 6: Data structures utilized by Algorithm TRIC to cluster query graph patterns.

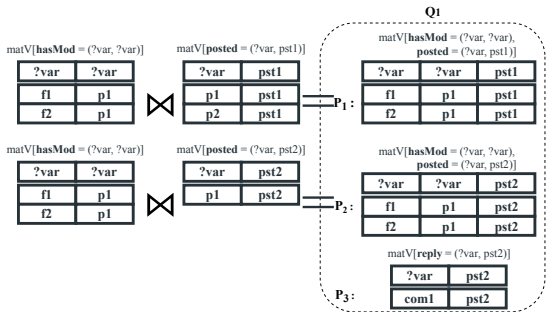


Figure 7: Materialized views of Q_1.

In essence, the query graph pattern determines the *execution plan* of the query. However, given that a query pattern in itself is a graph there is a high number of possible execution plans available. A path $P_i = \{v_1 \xrightarrow{e_1} v_2 \xrightarrow{e_2} \dots v_k\}$ serves as a model that defines the order in which the materialization should be performed. Thus, starting from the source vertex $v_1 \in P_i$ and joining all the materialized views from v_1 to the leaf vertex $v_k \in P_i : |P| = k$ yields all the subgraphs that satisfy the path P_i. After all paths P_i that belong in Q_i have been satisfied, a final join operation must be performed between all the paths. This join operation will produce the subgraphs that satisfy the query graph Q_i. To achieve this path joining set, additional information is kept about the intersection of the paths $P_i \in Q_i$. The intersection of two paths P_i and P_j are their common vertices.

Example 4.4. Fig. 7 presents some possible materialized views that correspond to the covering paths of query graph Q_1 (Fig. 4 (b)). In order to locate all subgraphs that satisfy the structural and attribute restrictions posed by paths P_1, P_2 and P_3 their materialized views should be calculated. More specifically, path $P_1 = \{?var \xrightarrow{hasMod} ?var \xrightarrow{posted} \text{“}pst1\text{”}\}$, is formulated by two edges, edges $hasMod = (?var, ?var)$ and $posted = (?var, pst1)$, thus, their materialized views $matV[hasMod = (?var, ?var)]$ and $matV[posted = (?var, pst1)]$ must be joined. These two views contains all updates u_i that correspond to them, while the result of their join operation will be a new materialized view $matV[hasMod = (?var, ?var), posted = (?var, pst1)]$ as shown in Fig. 7. In a similar manner, the subgraphs that satisfy path P_2 are calculated, while P_3 that is formulated by a single edge does not require any join operations. Finally, in order to calculate the subgraphs that match Q_1 all materialized views that correspond to paths P_1, P_2 and P_3 must be joined.

$\underline{Step\ 2}$: **Indexing the Paths.** Algorithm TRIC proceeds into indexing all the paths, extracted in $Step\ 1$, into a trie-based data structure. For each path $P_i \in CP(Q_i)$, TRIC examines the forest for trie roots that can index the first edge $e_1 \in P_i$ (Fig. 5, lines $3-6$). To access the trie roots, TRIC utilizes a hash table (namely *rootInd*) that indexes the values of the root-nodes (keys) and the references to the root nodes (values). If such trie T_i is located, T_i is traversed in a *DFS* manner to determine in which sub-trie path P_i can be indexed (Fig. 5, line 4). Thus, TRIC traverses the forest to locate an existing trie-path $\{n_1 \rightarrow \dots n_i \rightarrow \dots n_k\}$ that can index the ordered set of edges $\{e_1, \dots, e_k\} \in P_i$. If the discovered trie-path can index P_i partially (Fig. 5, line 7), TRIC proceeds into creating a set of new nodes under n_k that can index the remaining edges (Fig. 5, line 8). Finally, the algorithm stores the identifier of Q_i at the last node of the trie path (Fig. 5, line 9).

Algorithm TRIC makes use of two additional data structures, namely *edgeInd* and *queryInd*. The former data structure is a hash table that stores each edge $e_i \in P_i$ (key) and a collection of trie roots T_i which index e_i as the hash table's value (Fig. 5, lines $11-12$). Finally, TRIC utilizes a matrix *queryInd* that indexes the query identifier alongside the set of nodes under which its covering paths $P_i \in CP(Q_i)$ was indexed (Fig. 5, line 13).

Example 4.5. Fig. 6 presents an example of *rootInd*, *queryInd* and *edgeInd* of Algorithm TRIC when indexing the set of covering paths of Fig. 4 (b). Notice that TRIC indexes paths $P_1, P_2 \in Q_1$, path $P_1 \in Q_2$ and path $P_1 \in Q_4$ under the same trie T_1, thus, clustering together their common structural restrictions (all the aforementioned paths) and their attribute restrictions. Additionally, note that the *queryInd* data structure keeps references to the last node where each path $P_i \in Q_i$ is stored, e.g. for Q_1 it keeps a set of node positions $\{\&n_2, \&n_4, \&n_5\}$ that correspond to its original paths P_1, P_2 and P_3 respectively. Finally, *edgeInd* stores all the unique edges present in the path set of Fig. 4 (b), with references to the trie roots under which they are indexed, e.g. edge $posted = (?var, pst1)$ that is present in $P_1 \in Q_1$, $P_1 \in Q_3$ and $P_1 \in Q_4$, is indexed under both tries T_1 and T_3, thus this information is stored in set $\{\&T_1, \&T_3\}$.

The time complexity of Algorithm TRIC when indexing a path P_i, where $|P_i| = M$ edges and B the branching factor of the forest, is $\mathcal{O}(M * B)$, since TRIC uses a DFS strategy, with the maximum depth bound by the number of edges. Thus, for a new query graph pattern Q_i with N covering paths, the total time complexity is $\mathcal{O}(N * M * B)$. Finally, the space complexity of Algorithm TRIC when indexing a query Q_i is $\mathcal{O}(N * M)$, where M is the number of edges in a path and N the cardinality of Q_i's covering paths.

Variable Handling. A query graph pattern Q_i contains vertices that can either be literals (specific entities in the graph) identified by their label, or variables denoted as “?var”. This approach alleviates restrictions posed by naming conventions and thus leverages on the common structural constraints of paths.

However, by substituting the variable vertices with the generic “?var” requires to keep information about the joining order of each edge $e_i \in P_i$, as well as, how each $P_i \in CP(Q_i)$ intersects with the

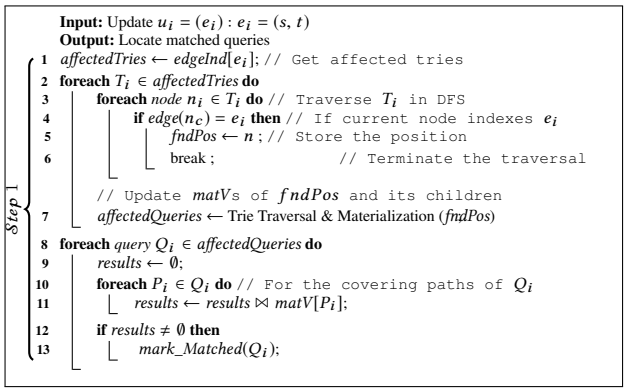


Figure 8: Query answering phase ($\mathcal{S}tep$ 1) of Algorithm TRIC.

rest of the paths in $CP(Q_i)$. In order to calculate the subgraphs that satisfy each covering path $P_i \in CP(Q_i)$, each $matV[e_i] : e_i \in P_i$ must be joined. Each path P_i that is indexed under a trie path $\{n_1 \rightarrow \ldots n_i \rightarrow \ldots n_k\}$ maintains the original ordering of its edges and vertices, while the order under which each edge of a node n_i is connected with its children nodes ($chn(n_i)$), is determined as follows: the target vertex $t \in e_i$ (where e_i is indexed under n_i) is connected with the source node $s \in e_{i+1} : e_{i+1} \in chn(n_i)$ of the parent node n_i. Finally, for each covering path $P_i \in CP(Q_i)$ TRIC maintains information about the vertices that intersected in the original query graph pattern Q_i, while this information is utilized during the query answering phase.

4.2 Query Answering Phase

During the evolution of the graph, a constant stream of updates $S = (u_1, u_2, \ldots, u_k)$ arrives at the system. For each update $u_i \in S$ Algorithm TRIC performs the following steps:

1. Determines which tries are affected by update u_i and proceeds in examining them.
2. While traversing the affected tries, performs the materialization and prunes sub-tries that are not affected by u_i.

In the following, we describe each step of the query answering phase of Algorithm TRIC. The pseudocode for each step is provided in Figs. 8 and 10.

$\underline{\mathcal{S}tep\ 1}$: **Locate and Traverse Affected Tries.** When an update u_i arrives at the system, Algorithm TRIC utilizes the edge $e_i \in u_i$ to locate the tries that are affected by u_i. To achieve this, TRIC uses the hash table *edgeInd* to obtain the list of tries that contain e_i in their children set. Thus, Algorithm TRIC receives a list (*affectedTries*) that contains all the tries that were affected by u_i and must be examined (Fig. 8, line 1). Subsequently, Algorithm TRIC proceeds into examining each trie $T_i \in$ *affectedTries* by traversing each T_i in order to locate the node n_i that indexes edge $e_i \in u_i$. When node n_i is located, the algorithm proceeds in $\mathcal{S}tep2$ of the query answering process described below (Fig. 8, lines 3 – 7).

Example 4.6. Let us consider the data structures presented in Fig. 6, the materialized views in Fig. 9, and an update $u_1 = (posted = (p2, pst1))$ that arrives into the evolving graph (Fig. 9(a)). Algorithm TRIC prompts hash table *edgeInd* and obtains list $\{\&T_1, \&T_3\}$. Subsequently, TRIC will traverse tries T_1 and T_3. When traversing trie T_1 TRIC locates node n_2 that matches update $e_1 \in u_1$ and proceeds in $\mathcal{S}tep2$ (described below). Finally, when traversing T_3 TRIC will stop the traversal at root

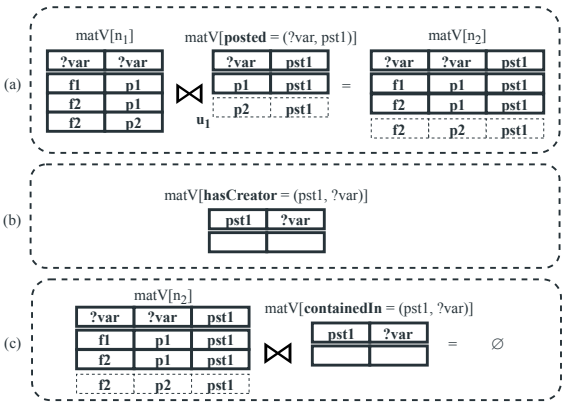


Figure 9: Updating materialized views.

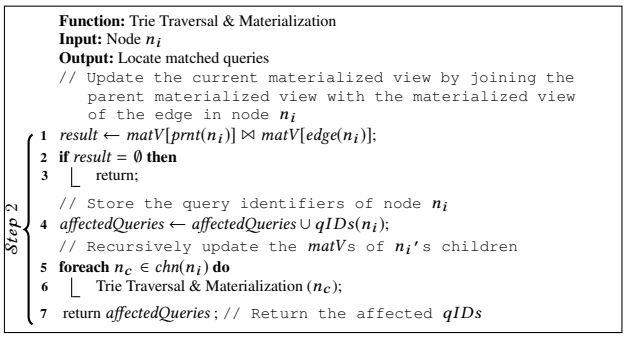


Figure 10: Query answering phase ($\mathcal{S}tep$ 2) of Algorithm TRIC.

node n_6 as its materialized view is empty $matV[hasCreator = (pst1, ?var)] = \emptyset$ (Fig. 9 (b)), thus all sub-tries will yield empty materialized views.

$\underline{\mathcal{S}tep\ 2}$: **Trie Traversal and Materialization.** Intuitively, a trie path $\{n_0 \rightarrow \ldots n_i \rightarrow \ldots n_k\}$ represents a series of joined materialized views $matVs = \{matV_1, matV_2, \ldots, matV_k\}$. Each materialized view $matV_i \in matVs$ corresponds to a node n_i that stores edge e_i and the materialized view $matV_i$. The materialized view contains the results of the join operation between the $matV[e_i]$ and the materialized view of the parent node n_i ($matV(prnt(n_i))$), i.e., $matV_i = matV[prnt(n_i)] \bowtie matV[e_i]$. Thus, when an update u_i affects a node n_i in this "chain" of joins, n_i's and its children's ($chn(n_i)$) materialized views must be updated with u_i. Based on this TRIC searches for and locates node n_i inside T_i that is affected by u_i and updates n_i's sub-trie.

After locating node $n_i \in T_i$ that is affected by u_i, Algorithm TRIC continues the traversal of n_i's sub-trie and prunes the remaining sub-tries of T_i (Fig. 8, line 7). Subsequently, TRIC updates the materialized view of n_i by performing a join operation between its parent's node materialized view $matV[prnt(n_i)]$ and the update u_i, i.e., $results = matV[prnt(n_i)] \bowtie u_i$. Notice that Algorithm TRIC calculates the subgraphs formulated by the current update solely based on the update u_1 and does not perform a full join operation between $matV[prnt(n_i)]$ and $matV[edge(n_i)]$, the updated results are then stored in the corresponding $matV[n_i]$.

For each child node $n_j \in chn(n_i)$, TRIC updates its corresponding materialized view by joining its view $matV[n_j]$ that corresponds to the edge that it stores (given by $matV[edge(n_j)]$) with its parent node materialized view $matV[n_i]$ (Fig. 10, lines 1 – 7). If at any point the process of joining the materialized views returns an empty result set the specific sub-trie is pruned, while,

the traversal continues in a different sub-trie of T_i (Fig. 10, lines 5−6). Subsequently, for each trie node n_j in the trie traversal when there is a successful join operation among $matV[e_j] : e_j \in n_j$ and $matV[n_i]$, the query identifiers indexed under n_j are stored in *affectedQueries* list (Fig. 10, lines 4 and 7). Note that similarly to before, only the updated part of a materialized view is utilized as the parent's materialized view, an approach applied on database-management system [16].

Example 4.7. Let us consider the data structures presented in Fig. 6, Fig. 9, and an update $u_1 = (posted = (p2, pst1))$ that arrives into the evolving graph. After locating the affected trie node n_2 (described in Example 4.6) TRIC proceeds in updating the materialized view of n_2, i.e., $matV[n_2]$, by calculating the join operation between its parents materialized view, i.e., $matV[n_1]$ and the update u_1. Fig. 9, demonstrates the operations of joining $matV[n_2]$ with update u_1, the result of the operation is tuple $(f2, p2, pst1)$, which is added into $matV[n2]$, presented in Fig. 9(a). While the query identifiers of n_2 (i.e., Q_1) are indexed in *affectedQueries*. Finally, TRIC proceeds in updating the sub-trie of n_2, node n_3, where the updated tuple $(f2, p2, pst1)$ is joined with $matV[edge(n_3)]$ (i.e., $matV[containedIn = (pst1, ?var)]$). This operation yields an empty result (Fig. 9(c)), thus terminating the traversal.

Finally, to complete the filtering phase Algorithm TRIC iterates through the affected list of queries and performs the join operations among the paths that form a query, thus, yielding the final answer (Fig. 8, lines 8 − 13).

The time complexity, of Algorithm TRIC when filtering an update u_i, is calculated as follows: The traversal complexity is $\mathcal{O}(T * (P_m * B))$, where T denotes the number of tries that contain $e_i \in u_i$, P_m denotes the size of the longest trie path, and B the branching factor. The time complexity of joining two materialized views $matV_1$ and $matV_2$, where $|matV_1| = N$ and $|matV_2| = M$, is $\mathcal{O}(N * M)$. Finally, the total time complexity is calculated as $\mathcal{O}((T * (P_m * B)) * (N * M))$.

Caching. During $\mathcal{S}tep$ 2, two materialized views are joined using a typical hash join operation with a build and a probe phase. In the build phase, a hash table for the smallest (in the number of tuples) table is constructed, while in the probe phase the largest table is scanned and the hash table is probed to perform the join. TRIC discards all the data structures and intermediate results after the join operation commences. In order to enhance this resource intensive operation, we cache and reuse the data structures generated during the build and probe phases as well as the intermediate results whenever possible. This approach constitutes an extension of our proposed solution (TRIC) and it is coined TRIC+.

4.3 Supporting richer models and languages

The proposed algorithm is easily extensible to more sophisticated data models and query languages; in this section, we briefly outline the necessary modifications to support graph deletions and updates, as well as more general types of graphs (e.g., property graphs).

Edge deletions may be handled by algorithms TRIC and TRIC+ by locating the affected paths, and traversing each path to locate the deleted edges; while visiting each edge, the materialized view that corresponds to that edge should be accessed and all affected tuples should be removed. Updates on the graph (e.g., on the label of an edge) may be modeled as an edge deletion followed by an edge addition operation. Finally, extending our solution

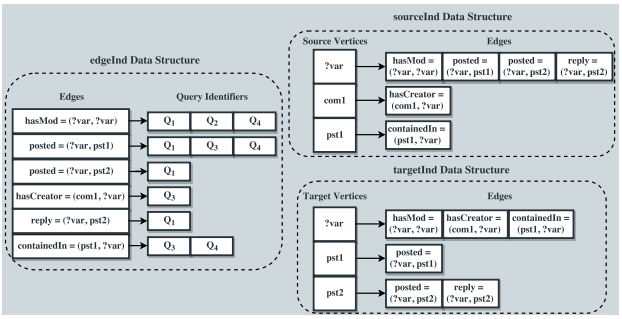


Figure 11: Index structures utilized by Algorithm INV.

for more general graph types, like property graphs, entails the addition of extra constraints within the nodes of the tries and the usage of a separate data structure to appropriately index these constraints. Then, query answering would include an extra phase for the determining the satisfaction of the additional constraints. Efficient execution of such extensions is an interesting topic for future research (see Section 7).

5 ADVANCED BASELINES

Since no prior work in the literature considers the problem of continuous multi-query evaluation, we designed and implemented Algorithms INV and INC, two advanced baselines that utilize inverted index data structures. Finally, we provide a third baseline that is based on the well-established graph database Neo4j [43].

5.1 Algorithm INV

Algorithm INV (INVerted Index), utilizes inverted index data structures to index the query graph patterns. The inverted index data structure is able to capture and index common elements of the graph patterns at the edge level during indexing time. Subsequently, the inverted index is utilized during filtering time to determine which queries have been satisfied. In the following, we describe the query indexing and answering phase of INV.

The Query Indexing Phase of Algorithm INV, for each query graph pattern Q_i, is performed in two steps: (1) Transforming the original query graph pattern Q_i into a set of path conjuncts, that cover all vertices and edges of Q_i, and when combined can effectively re-compose Q_i, and finally, indexing those covering paths in a matrix along the unique query identifier, (2) Indexing all edges $e_i \in Q_i$ into an inverted index structure. In the following, we present each step of the query indexing phase of INV and give details about the data structures utilized.

$\mathcal{S}tep$ 1 : **Extracting the Covering Paths.** In the first step of the query indexing phase, Algorithm INV decomposes a query graph Q_i into a set of paths *CP*, a process described in detail in Section 4.1. Thus, given the query set presented in Fig. 4 (a), INV yields the same set of covering paths *CP* (Fig. 4 (b)). Finally, the covering path set *CP* is indexed into an array (*queryInd*) with the query identifier of Q_i.

$\mathcal{S}tep$ 2 : **Indexing the Query Graph.** Algorithm INV builds three inverted indexes, where it stores the structural and attribute constrains of the query graph pattern Q_i. Hash table *edgeInd* indexes all edges $e_i \in Q_{DB}$ (keys), and the respective query identifiers as values, hash table *sourceInd* indexes the source vertices of each edge (key), where the edges are indexed as values , and hash table *targetInd* that indexes the target vertices of each edge (key), where the edges are indexed as values. In Fig. 4(a) we present four query graph patterns, and in Fig. 11 the data structures of

INV when indexing those queries. Finally, INV applies the same techniques of handling variables as Algorithm TRIC (Section 4.1).

The Query Answering Phase of Algorithm INV, when a constant stream of updates $S = (u_1, u_2, \ldots, u_k)$ arrives at the system, is performed in three steps: (1) Determines which queries are affected by update u_i, (2) Prompts the inverted index data structure and determines which paths have been affected by update u_i, (3) Performs the materialization while querying the inverted index data structures. In the following, we describe each step of the query answering phase:

$\mathit{Step}\ 1$: **Locate the Affected Queries.** When a new update u_i arrives at the system, Algorithm INV utilizes the edge $e_i \in u_i$ to locate the queries that are affected, by querying the hash table *edgeInd* to obtain the query identifier *qIDs* that contain e_i. Subsequently, the algorithm iterates through the list of *affectedQueries* and checks each query $Q_i \in qIDs$. For each query Q_i the algorithm checks $\forall e_i \in Q_i$ if $matV[e_i] \neq \emptyset$, i.e., each e_i should have a *non empty* materialized view. The check is performed by iterating through the edge list that is provided by *queryInd* and a hash table that keeps all materialized views present in the system. Intuitively, a query Q_i is candidate to match, as long as, all materialized views that correspond to its edges can be used in the query answering process.

$\mathit{Step}\ 2$: **Locate the Affected Paths.** Algorithm INV proceeds to examine the inverted index structures *sourceInd* and *targetInd* by making use of $e_i \in u_i$. INV queries *sourceInd* and *targetInd* to determine which edges are affected by the update, by utilizing the source and target vertices of update u_i. INV examines each current edge e_c of the affected edge set and recursively visits all edges connected to e_c, which are determined by querying the *sourceInd* and *targetInd*. While examining the current edge e_c, INV checks if e_c is part of *affectedQueries*, if not, the examination of the specific path is pruned. For efficiency reasons, the examination is bound by the maximum length of a path present in *affectedQueries* which is calculated by utilizing the *queryInd* data structure.

$\mathit{Step}\ 3$: **Path Examination and Materialization.** While INV examines the paths affected by update u_i ($\mathit{Step}\ 2$), it performs the materialization on the currently examined path. INV searches through the paths formulated by the visits of edge sets determined by *targetInd* and *sourceInd*, and maintains a path $P_c = \{v_1 \xrightarrow{e_1} v_2 \xrightarrow{e_2} \ldots v_k \xrightarrow{e_k} v_{k+1}\}$ that corresponds to the edges already visited.

While, visiting each edge e_c, INV accesses the materialized view that corresponds to it (i.e., $matV[e_c]$) and updates the set of materialized views $matVs = \{matV_1, matV_2, \ldots, matV_k\}$ that correspond to the current path. For example, given an already visited path $P = \{v_1 \xrightarrow{e_1} v_2 \xrightarrow{e_2} v_3\}$ its materialized view $matV[P]$ will be generated, by $matV[P] = matV[e_1] \bowtie matV[e_2]$. When visiting the next edge e_n, a new path P' is generated and its materialized view $matV[P'] = matV[P] \bowtie matV[e_n]$ will be generated. If at any point, the process of joining the materialized views yields an empty result set the examination of the edge is terminated (pruning). This allows us to prune paths that are not going to satisfy any $Q_i \in$ *affectedQueries*. If a path P_i yields a successful series of join operations (i.e., $matV[P_i] \neq \emptyset$), it is marked as matched.

Finally, to produce the final answer subgraphs Algorithm INV iterates through the affected list of queries $qIDs \in$ *affectedQueries* and performs the final join operation among all the paths that comprise the query.

Caching. In the spirit of TRIC+ (Section 4.2), we developed an extension of INV, namely INV+, that caches and reuses the calculated data structures of the hash join phase.

5.2 Algorithm INC

Based on Algorithm INV we developed an algorithmic extension, namely Algorithm INC. Algorithm INC utilizes the same inverted index data structures to index the covering paths, edges, source and target vertices as Algorithm INV, while the examination of a path affected during query answering remains similar. The key difference lies in executing the joining operations between the materialized views that correspond to edges belonging to a path. More specifically, when Algorithm INV executes a series of joins between the materialized views (that formulate a path) to determine which subgraphs match a path; it utilizes all tuples of each materialized view that participate in the joining process. On the other hand, Algorithm INC makes use of only the update u_i and thus reduces the number of tuples examined through out the joining process of the paths.

Caching. In the spirit of TRIC+ (Section 4.2), we developed an extension of INC, namely INC+, that caches and reuses the calculated data structures of the hash join phase.

5.3 Neo4j

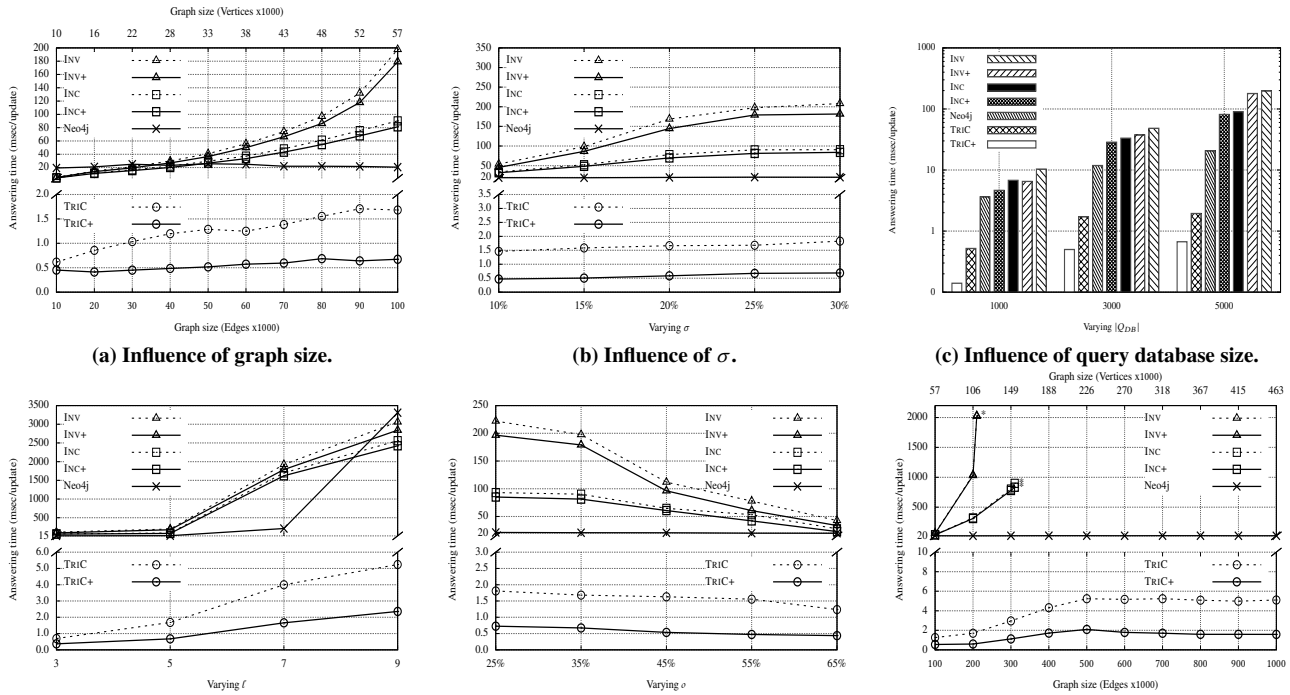
To evaluate the efficiency of the proposed algorithm against a real-world approach, we implemented a solution based on the well-established graph database Neo4j [43]. In this approach, we extend Neo4j's native functionality with auxiliary data structures to efficiently store the query set. They are used during the answering phase to located affected queries and execute them on Neo4j.

The Query Indexing Phase. To address the continuous multi-query evaluation scenario, we designed main-memory data structures to facilitate indexing of query graph patterns. Initially, in the preprocessing phase, we convert each incoming query Q_i into Neo4j's native query language Cypher[1]. Subsequently, the query indexing phase of Neo4j commences as follows: (1) indexing each Cypher query in the *queryInd* data structure, and (2) indexing all edges $e_i \in Q_i$ in the *edgeInd* data structure where e_i is used as key, and a collection of query identifiers as values. The *queryInd* structure is defined as matrix, while the *edgeInd* is an inverted index, similarly to the data structures described in Section 5.1.

The Query Answering Phase. Each update that is received as part of an incoming stream of updates $S = (u_1, u_2, \ldots, u_k)$ is processed in the following steps: (1) an incoming update u_i is applied to Neo4j (2) the inverted index *edgeInd* is queried with $e_i \in u_i$, to determine which queries are affected, (3) all affected queries are retrieved from matrix *queryInd*, (4) the affected queries are executed.

To enhance performance, the following configurations are applied: (1) the graph database builds indexes on all labels of the schema allowing for faster look up times of nodes, (2) the execution of Cypher queries employs the *parameters syntax*[2] as it enables the execution planner of Neo4j to cache the query plans for future use, (3) the number of writes per transaction[3] in the database and the allocated memory were optimized based on the hardware configuration (see Section 6.1).

[1] https://neo4j.com/developer/cypher-query-language/
[2] https://neo4j.com/docs/cypher-manual/current/syntax/parameters/
[3] https://neo4j.com/docs/cypher-manual/current/introduction/transactions/



(a) Influence of graph size. **(b) Influence of σ.** **(c) Influence of query database size.**

(d) Influence of ℓ. **(e) Influence of o.** **(f) Influence of graph size.**

Figure 12: Query answering time for the SNB dataset.

6 EXPERIMENTAL EVALUATION

In this section, we present a series of experiments that compare the performance of the presented algorithms.

6.1 Experimental Setup

Data and Query Sets. For the experimental evaluation we used a synthetic and two real-world datasets.

The SNB Dataset. The first dataset we utilized is the LDBC Social Network Benchmark (*SNB*) [12]. *SNB* is a synthetic benchmark designed to accurately simulate the evolution of a social network through time (i.e, vertex and edge sets labels, event distribution etc). This evolution is modeled using activities that occur inside a social network (i.e. user account creation, friendship linking, content creation, user interactions etc). Based on the *SNB* generator we simulated the evolution of a graph consisting of user activities over a time period of 2 years. From this dataset we derived 3 query loads and configurations: (i) a set with a graph size of $|G_E| = 100K$ edges and $|G_V| = 57K$ vertices, (ii) a set with a graph size of $|G_E| = 1M$ edges and $|G_V| = 463K$ vertices, and (iii) a set with a graph size of $|G_E| = 10M$ edges and $|G_V| = 3.5M$.

The NYC Dataset. The second dataset we utilized is a real world set of taxi rides performed in New York City[4] (*TAXI*) in 2013 utilized in *DEBS 2015 Grand Challenge* [19]. *TAXI* contains more that $160M$ entries of taxi rides with information about the license, pickup and drop-off location, the trip distance, the date and duration of the trip, and the fare. We utilized the available data to generate a stream of updates that result in a graph of $|G_E| = 1M$ edges and $|G_V| = 280K$, accompanied by a set of $5K$ query graph patterns.

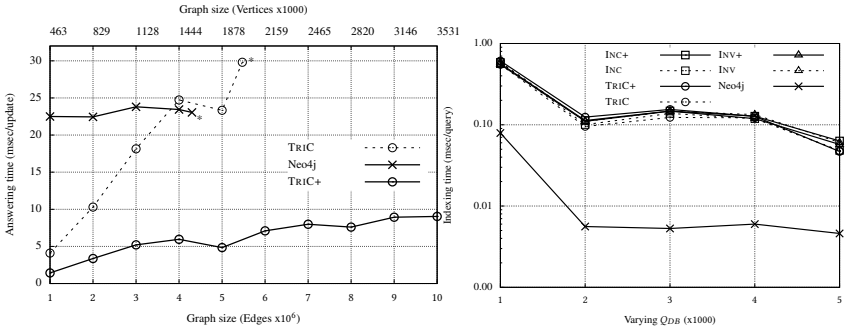
The BioGRID Dataset. The third dataset we utilized is BioGRID [35], a real world dataset that represents protein to protein interactions. This dataset is used as a stress test for our algorithms since it contains one type of edge (interacts) and vertex (protein), and thus every update affects the whole query database. We used BioGRID to generate a stream of updates that result in a graph size of $|G_E| = 1M$ edges and $|G_V| = 63K$ vertices, with a set of $5K$ query graph patterns.

Query Set Configuration. In order to construct the set of query graph patterns Q_{DB} we identified three distinct query classes that are typical in the relevant literature: chains, stars, and cycles [15, 26]. Each type of query graph pattern was chosen equiprobably during the generation of the query set. The baseline values for the query set are: (i) an average size ℓ of 5 edges/query graph pattern, a value derived from the query workloads presented in *SNB* [12], (ii) a query database $|Q_{DB}|$ size of $5K$ graph patterns, (iii) a factor that denotes the percentage of the query set Q_{DB} that will ultimately be satisfied, denoted as selectivity $\sigma = 25\%$, and (iv) a factor that denotes the percentage of overlap between the queries in the set, $o = 35\%$.

Metrics. In our evaluation, we present and discuss the filtering and indexing time of each algorithm, along with the total memory requirements.

Technical Configuration. All algorithms were implemented in Java 8 while for the materialization implementation the Stream API was employed. The Neo4j-based approach was implemented using the embedded version of Neo4j 3.4.7. Extensive experimentation evaluation concluded that a transactionsection 5.3 can perform up to $20K$ writes in the database without degrading Neo4j's performance, while in order to guarantee indexes are cached in main memory $55GB$ of main memory were allocated. A machine with Intel(R) Xeon(R) Processor E5-2650 at $2.00GHz$, $64GB$ RAM, and Ubuntu Linux 14.04 was used. The time shown in the graphs is wall-clock time and the results of each experiment are averaged over 10 runs to eliminate fluctuations in measurements.

[4] https://chriswhong.com/open-data/foil_nyc_taxi/



(a) Query answering time.

(b) Query insertion time.

Algorithm	Dataset		
	SNB	*NYC*	*BioGRID*
TRIC	201*MB*	257*MB*	233*MB*
TRIC+	248*MB*	273*MB*	262*MB*
INV	205*MB*	273*MB*	271MB^{50K}
INV+	228*MB*	381*MB*	301MB^{50K}
INC	206*MB*	273*MB*	270MB^{50K}
INC+	228*MB*	378*MB*	310MB^{60K}
Neo4j	443*MB*	590*MB*	314*MB*

(c) Memory requirements.

Figure 13: Results for (a) & (b) the *SNB* dataset, and (c) the *SNB*, *TAXI*, *BioGRID* datasets.

6.2 Results for the SNB Dataset

In this section, we present the evaluation for the *SNB* benchmark and highlight the most significant findings.

Query Answering Time. Fig. 12(a) presents the results regarding the query answering time, i.e., the average time in milliseconds needed to determine which queries are satisfied by an incoming update, against a query set of $Q_{DB} = 5K$. Please notice that the y-axis is split due to the high differences in the performance of TRIC/TRIC+and its competitors. We observe that the answering time increases for all algorithms as the graph size increases. Algorithms TRIC/TRIC+ achieve the lowest answering times, suggesting better performance. Contrary, the competitors are more sensitive in graph size changes, with Algorithm INV performing the worst (highest query answering time). When comparing Algorithm TRIC to INV, INC and Neo4j the query answering time is improved by 99.15%, 98.14% and 91.86% respectively, while the improvement between INC and INV is 54.33%. Finally, comparing Algorithm TRIC+ to INV+, INC+ and Neo4j demonstrates a performance improvement of 99.62%, 99.17% and 96.74% respectively, while the difference of INC+ and INV+ is 54.6%.

The results (Fig. 12(a)) suggest that all solutions that implement caching are faster compared to the versions without it. In more detail, Algorithms TRIC+/INV+/INC+ are consistently faster than their non-caching counterparts, by 59.95%, 9.36% and 9.91% respectively. This is attributed to the fact that Algorithms TRIC/INV/INC, have to recalculate the probe and build structures required for the joining process, in contrast to Algorithms TRIC+/INV+/INC+ that store these structures and incrementally update them, thus providing better performance.

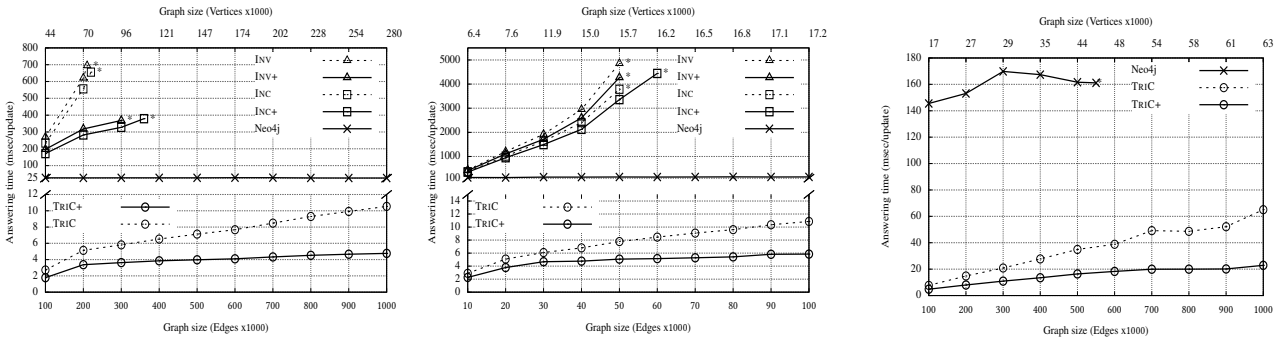
In Fig. 12(b) we present the results when varying the parameter σ, for 10%, 15%, 20%, 25% and 30% of a query set for $|Q_{DB}| = 5K$ and $|G_E| = 100K$. In this setup the algorithms are evaluated for a varying percentage of queries that match. A higher number of queries satisfied, increases the number of calculations performed by each algorithm. The results show that all algorithms behave in a similar manner as previously described. In more detail, Algorithm TRIC+ is the most efficient of all, and thus the fastest among the extensions that utilize caching, while TRIC is the most efficient solution among the solutions that do not employ a caching strategy. Finally, the percentage differences, between the algorithmic solutions remain the same as before in most cases.

Fig. 12(c) presents the results of the experimental evaluation when varying the size of the query database $|Q_{DB}|$. More specifically, we present the answering time per triple when $|Q_{DB}| = 1K$, $3K$ and $5K$, and $|G_E| = 100K$. Please notice the y-axis is in logarithmic scale. The results demonstrate that all algorithm's behavior is aligned with our previous observations. More specifically, Algorithms TRIC+ and TRIC exhibit the highest performance (i.e., lowest answering time), throughout the increase of $|Q_{DB}|$, and thus determine faster which queries of $|Q_{DB}|$ have matched given an update u_i. Similarly to the previous setups, the competitors have the lowest performance, while Algorithms INC and INC+ perform better compared to INV and INV+.

In Fig. 12(d) we give the results of the experimental evaluation when varying the average query size ℓ. More specifically, we present the answering time per triple when $\ell = 3$, 5, 7 and 9 of a query set for $|Q_{DB}| = 5K$ and $|G_E| = 100K$. We observe that the answering time increases for all algorithms as the average query length increases. More specifically, Algorithms TRIC+ and TRIC exhibit the highest performance (i.e., lowest answering time), throughout the increase of ℓs, and thus determine faster which queries have been satisfied. Similarly to the previous evaluation setups, the Algorithms INV/INV+/INC/INC+/Neo4j have the lowest performance, and increase significantly their answering time when ℓ increases, while Algorithms INC and INC+ perform better compared to INV, INV+ and Neo4j when $\ell = 9$.

Fig. 12(e) gives the results of the experimental evaluation when varying the parameter o, for 25%, 35%, 45%, 55% and 65% of a query set for $|Q_{DB}| = 5K$ and $|G_E| = 100K$. In this setup the algorithms are evaluated for varying percentage of query overlap. A higher number of query overlap, should decrease the number of calculations performed by algorithms designed to exploit commonalities among the query set. The results show that all algorithm behave in a similar manner as previously described, while AlgorithmsINV/INV+/INC/INC+ observe higher performance gains. Algorithm TRIC+ is the most efficient of all, and thus the fastest among the extensions that utilize caching techniques, while TRIC is the most efficient solution among the solutions that do not employ caching.

Fig. 12(f) presents the results regarding the query answering time, for all algorithms when indexing a query set of $|Q_{DB}| = 5K$ and a final graph of $|G_E| = 1M$ and $|G_V| = 463K$. Given the extremely slow performance of some algorithms we have set an *execution time threshold* of 24 hours, for all algorithms under evaluation, thus, when the threshold was crossed the evaluation was terminated. Algorithms TRIC/TRIC+ achieve the lowest answering times, suggesting better performance, while Algorithms INV/INV+/INC/INC+ are more sensitive in graph size changes and thus fail to terminate within the time threshold. More specifically, Algorithms INV/INV+ *time out* at $|G_E| = 210K$, while INC/INC+ *time out* at $|G_E| = 310K$ as denoted by the asterisks



(a) Influence of graph size. **(b) Influence of graph size.** **(c) Influence of graph size.**

Figure 14: Query answering time for (a) the *TAXI* dataset, and (b) & (c) the *BioGRID* dataset.

in the plot. When comparing TRIC/TRIC+ to Neo4j the query answering is improved by 77.01% and 92.86% respectively.

Fig. 13(a) presents the results regarding the query answering time, for Algorithms TRIC, TRIC+ and Neo4j when indexing a query set of $Q_{DB} = 5K$ and a final graph size of $|G_E| = 10M$ and $|G_V| = 3.5M$. Again, we have set an *execution time threshold* of 24 hours, for all the algorithms under evaluation. Algorithm TRIC+ achieves the lowest answering times, suggesting better performance, while Algorithms TRIC and Neo4j fail to terminate within the given time threshold. More specifically, Algorithm TRIC *times out* at $|G_E| = 5.47M$, while Algorithm Neo4j times out at $|G_E| = 4.3M$ as denoted by the asterisks in the plot.

Overall, Algorithms TRIC+ and TRIC, the two solutions that utilize trie structures to capture and index the common structural and attribute restrictions of query graphs achieve the lowest query answering times, compared to Algorithms INV/INV+/INC/INC+ that employ no clustering techniques, as well as when compared with commercial solutions such as Neo4j. Adopting the incremental joining techniques (found in Algorithm TRIC) into Algorithm INC does not seem to significantly improve its performance when compared to Algorithm INV. While, adopting caching techniques that store the data structures generated during the join operations, changes significantly the performance of Algorithm TRIC+. Taking all the above into consideration, we conclude that the algorithms that utilize trie-based indexing achieve low query answering times compared to their competitors.

Indexing Time. Fig. 13(b) presents the indexing time in milliseconds required to insert $1K$ query graph patterns when the query database size increases. We observe that the time required to go from an empty query database to a query database of size $1K$ is higher compared to the time required for the next iterations. Please notice the y-axis is in logarithmic scale. This can be explained as follows, all algorithms utilize data structures that need to be initialized during the initial stages of query indexing phase, i.e. when inserting queries in an empty database, while as the queries share common restrictions less time is required for creating new entries in the data structures. Additionally, the time required to index a query graph pattern in the database does not vary significantly for all algorithms. Notice that query indexing time is not a critical performance parameter in the proposed paradigm, since the most important dimension is query answering time.

6.3 Results for the NYC and BioGRID Dataset

In this section, we present the evaluation for the *NYC* and *BioGRID* dataset and highlight the most significant findings.

The *NYC* Dataset. Fig. 14(a) presents the results from the evaluation of the algorithms for the *NYC* dataset. More specifically, we present the results regarding the query answering performance of all algorithms when $Q_{DB} = 5K$, $\ell = 5$, $o = 35\%$, $\sigma = 25\%$ and an execution time threshold of 24 hours. Please notice that the y-axis is split due to high differences in the performance of the algorithms. Algorithms INV and INV+ fail to terminate within the time threshold and *time out* at $|G_E| = 210K$ and $|G_E| = 300K$ respectively. Similarly, Algorithms INC and INC+ *time out* at $|G_E| = 220K$ and $360K$ respectively. When comparing Algorithms TRIC and TRIC+ to Neo4j the query answering is improved by 59.68% and 81.76% respectively. These results indicate that again an algorithmic solution that exploits and indexes together the common parts of query graphs (i.e., Algorithms TRIC/TRIC+) achieves significantly lower query answering time compared to approaches that do not apply any clustering techniques (i.e., AlgorithmsINV/INV+INC/INC+/Neo4j).

The *BioGRID* Dataset. Figs. 14(b) and 14(c) present the results from the evaluation of the algorithms for the *BioGRID* dataset. In Fig. 14(b) we present the results regarding the query answering performance of the algorithms, when $Q_{DB} = 5K$, $\sigma = 25\%$ for a final graph size of $|G_E| = 100K$ and $|G_V| = 17.2K$. Additionally, we set an execution time threshold of 24 hours due to the high differences in the performance of the algorithms. The *BioGRID* dataset serves as a stress test for our algorithms, since it contains only one type of edge and vertex, thus each incoming update will affect (but not necessarily satisfy) the entire query database. To this end, Algorithms INV/INV+/INC exceed the time threshold and time out at $|G_E| = 50K$, while INC+ times out at $|G_E| = 60K$ as denoted by the asterisks in the plot. Finally, Fig. 14(c) presents the results for the *BioGRID* dataset for a final graph size of $|G_E| = 1M$ and $|G_V| = 63K$. We again observe that Algorithms TRIC and TRIC+ achieve the lowest answering time, while Neo4j exceeds the time threshold and times out at $|G_E| = 550K$. As it is demonstrated from the results yielded by the evaluation, Algorithms TRIC and TRIC+ are the most efficient of all; this is attributed to the fact that both algorithms create a combined representation of the query graph patterns that can efficiently be utilized during query answering time.

Comparing Memory Requirements. Fig. 13(c) presents the memory requirements of each algorithm, for the *SNB*, *NYC* and *BioGRID* datasets when indexing $|Q_{DB} = 5K|$ and a graph of $|G_E| = 100K$. We observe, that across all datasets, Algorithms TRIC, INV and INC have the lowest main memory requirements, while, Algorithms TRIC+, INV+, INC+ and Neo4j exhibit higher memory requirements. The marginally higher memory requirements of algorithms that employ a caching strategy,

(i.e., Algorithms TRIC+/INV+/INC+) is attributed to the fact that all structures calculated during the materialization phase are kept in memory for future usage; this results in slightly higher memory requirements compared to algorithms that do not apply this caching technique (i.e., Algorithms TRIC/INV/INC). To this end, employing a caching strategy for all algorithms yields significant performance gains with minimal impact on main memory. Finally, Neo4j is a full fledged database management system, thus it occupies more memory to support the required specifications.

7 OUTLOOK

In this work, we proposed a new paradigm to efficiently capture the evolving nature of graphs through query graph patterns. We proposed a novel method that indexes and continuously evaluates queries over graph streams, by leveraging on the shared restrictions present in query sets. We also evaluated our solution using three different datasets from social networks, transportation and biological interactions domains, and demonstrated that our approach is up to two orders of magnitude faster when compared to typical join-and-explore inverted index solutions, and the well-established graph database Neo4j.

Our future research plans involve (i) further improving the algorithm performance by storing materializations within the trie to minimize trie traversal at query answering time and exploiting workload-driven statistics in the spirit of [23] and (ii) increasing the model expressiveness by implementing graph deletions, supporting more general graph types (e.g., property graphs), and introducing query classes that aim at clustering coefficient, shortest path, and betweenness centrality.

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