Distributed Graph Pattern Matching

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ABSTRACT

Graph simulation has been adopted for pattern matching to reduce the complexity and capture the need of novel applications. With the rapid development of the Web and social networks, data is typically distributed over multiple machines. Hence a natural question raised is how to evaluate graph simulation on distributed data. To our knowledge, *no* such distributed algorithms are in place yet. This paper settles this question by providing evaluation algorithms and optimizations for graph simulation in a distributed setting. (1) We study the impacts of components and data locality on the evaluation of graph simulation. (2) We give an analysis of a large class of distributed algorithms, captured by a message-passing model, for graph simulation. We also identify three complexity measures: *visit times*, *makespan* and *data shipment*, for analyzing the distributed algorithms, and show that these measures are essentially *controversial* with each other. (3) We propose distributed algorithms and optimization techniques that exploit the properties of graph simulation and the analyses of distributed algorithms. (4) We experimentally verify the effectiveness and efficiency of these algorithms, using both real-life and synthetic data.

Categories and Subject Descriptors

H.2.8 [**Database Management**]: Database applications—*graph data, data mining*

Keywords

Graph querying, graph simulation, distributed algorithms

1. INTRODUCTION

Graph pattern matching is being increasingly used in various applications, *e.g.,* software plagiarism detection, protein interaction networks, social networks and intelligence analysis [18, 25, 26]. Graph matching is typically defined in terms of *subgraph isomorphism* (see, *e.g.,* [15] for a survey). Hence the problem is NP-complete [27]. Furthermore, subgraph isomorphism is often too restrictive to catch sensible matches in emerging applications such as social networks [5, 13].

To reduce the complexity and capture the need of novel applications, *graph simulation* [16] has been adopted for pattern matching [5, 13]. It is less restrictive than subgraph isomorphism, and can be determined in quadratic time [16]. We say that a graph G matches a pattern Q, via graph simulation, if there exists a binary *relation* $M \subseteq V_q \times V$, where V_q and V are the two sets of nodes in Q and G, respectively, such that (1) for each $(u, v) \in M$, u and v have the same label; and (2) for each node u in Q, there exists v in G such that (a) $(u, v) \in M$, and (b) for each edge (u, u') in Q, there exists an edge (v, v') in G having $(u', v') \in M$. Graph simulation (and its extensions) play a critical role for the analysis of social positions/roles in social networks [5, 13, 12].

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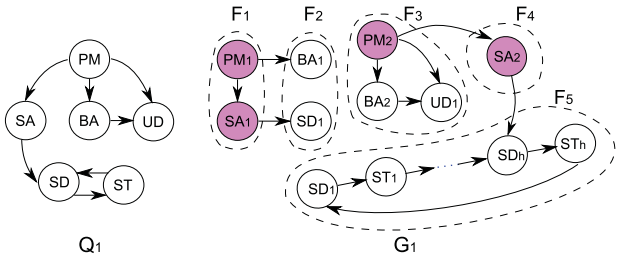


Figure 1: Pattern query and fragmented data graph

When evaluating a query on a large dataset, one wants to partition and distribute the data to multiple machines, so that the query can be efficiently evaluated in parallel, as advocated by, *e.g.,* MapReduce [11] and Pregel [21]. Moreover, it is common to find distributed real-life datasets, such as Facebook, Yahoo Flickr, Twitter, and Apple AppStore, that are stored at data centers, which typically host a cluster of tens to thousands of machines [1]. Hence, *a natural question* raised is how to evaluate graph pattern matching, in terms of graph simulation, on distributed data. To our knowledge, *no* such distributed algorithms are in place yet.

Example 1: Consider a real-life example for social matching, taken from [24], that recruits people from a social system to set up a team to develop a new software product.

Ideally such a team consists of members with the following roles: (1) project manager (PM), (2) business analyst (BA), (3) software architect (SA), (4) user interface designer (UD), (5) software developer (SD), and (6) software tester (ST). All candidates are stored in a social system in the form of data graph G_1 as shown in Fig. 1, where (1) a node is a person labeled with her expertise (with subscripts to distinguish one from another), and (2) an edge (A, B) indicates the relationship that B worked well under the supervision of A in previous projects. The relationships of team members are particularly important as the success of the software product heavily relies on their collaboration.

To identify the proper candidates from G_1, pattern query Q_1 is designed that requires (1) all SA, BA and UD worked well under the same PM, (2) UD worked well under BA such that the user interface could clearly reflect the idea of BA, (3) SD worked well under SA and ST, and (4) ST further worked well under SD as they are mostly related in the development.

Data graph G_1 is partitioned into five fragments: $F_1, \ldots, F_5$ (separated by dotted cycles), and it is distributed over a cluster of five machines, one fragment on each machine. Observe the following. (1) When graph simulation is used, a *sensible match* containing all nodes in F_3, F_4 and F_5 are identified. In contrast, when subgraph isomorphism is adopted, it imposes too strict constraints such that *no matches* can be found. (2) Furthermore, to build a well-organized team, one has to query over all these fragments over different machines to avoid missing any potential candidates.

This highlights the need for developing distributed algorithms for graph simulation. There are a few cheap solutions. (1) A naive one simply collects all parts of a data graph into one machine, and calls a centralized algorithm, *e.g.,* [16]. (2) Another one is to build a MapReduce [11] or Pregel [21] system, and to delegate most of the work to the system. There are, however, several problems for these two solutions. Obviously the first solution does not make use of the distributed facilities at all. Graph simulation needs recursive computations, as illustrated by its recursive definition given before. MapReduce is typically not fit for this kind of graph algorithms, which needs a series of chained MapReduce invocations [7, 21]. Pregel utilizes a message-passing model, which is typically fit for graph algorithms. However, if we simply delegate the computation tasks to Pregel, it may involve too many rounds of computations. As one knows, a good solution for graph simulation must exploit the nature of graph simulation itself.

As observed in [21], graph algorithms often exhibit poor data locality and hence, may incur prohibitive overhead on network traffic. One may verify that to make G_1 match Q_1, it essentially requires the complete information of the subgraph consisting of fragments F_3, F_4 and F_5 (, even the entire data graph in the worst case). That is, graph simulation has poor data locality (more sophisticated analyses are available in Section 3). This further brings challenge for developing distributed algorithms for graph simulation. □

Contributions & Roadmap. To this end, we develop algorithms and optimization techniques for evaluating graph simulation in a distributed setting.

Our contributions can be summarized as follows.

(1) We study fundamental properties of graph simulation (Section 3). We show that connected components in data graph can be treated separately, and the final matches are simply the union of those matches for all single components. We also show that graph simulation has poor data locality. Nevertheless, we identify cases when data locality could be exploited to facilitate the evaluation of graph simulation.

(2) We give an analysis of a large class of distributed algorithms for graph simulation (Section 4). These distributed algorithms are captured by a message-passing model, which is flexible enough to express a broad class of algorithms [19], and is typically fit for the evaluation of graph algorithms [21]. We also identify three complexity measures: *visit times*, *makespan* and *data shipment*, for the analyses of this class of distributed algorithms, and show that these measures are *controversial* with each other. As efficiency (makespan) remains the dominant factor, we make a decision to sacrifice visit times and data shipment for makespan when designing distributed algorithms.

(3) We propose distributed algorithms which exploit the properties of graph simulation and the analyses of distributed algorithms (Section 5). The algorithms guarantee the following. (a) The total computation cost at all machines is comparable to what is needed by the *best-known* centralized algorithm [16]. Moreover, the number of *rounds of computation* is bounded by a constant 4. (b) The total data shipment is at most $|G| + 4|\mathcal{B}| + |Q||G|+(k-1)|Q|$, where $|G|$ and $|Q|$ are the sizes of data graph and pattern graph, respectively, and $|\mathcal{B}|$ is the total number of nodes with edges across different fragments (boundary nodes), and k is the total number of machines. (c) Each machine except the coordinator is visited at most $g + 2$ times, where g is the maximum number of machines at which a connected component resides. The coordinator is visited with $2(k - 1)$ extra times due to the need for scheduling data shipment and assembling the final result. We also develop effective optimization techniques.

(4) Using both real-life data (Google and Amazon) and synthetic data, we conduct an extensive experimental study (Section 6). We find that our distributed algorithms for graph simulation scale well with large data graphs (*e.g.,* with 10^8 nodes). We also find that our optimization techniques are effective, reducing 1/5 of running time in average.

Related work. There has been a host of work on graph pattern matching, via subgraph isomorphism (*e.g.,* [18, 25, 26]; see [3, 15] for surveys) and via graph simulation [16] and its extensions [13, 12]. Nevertheless, none of these investigates the problem in a distributed fashion.

Distributed query processing has been studied for relational data [17] and XML [8]. There has also been recent work on distributed graph processing to manage large-scale graphs [11, 21]. However, to the best of our knowledge, no previous work has studied distributed computation of graph simulation [16] and its extensions[13, 12].

Close to this work is strong simulation [20], in which the locality property of strong simulation allows us to develop a simple yet effective algorithm to find matches in distributed graphs. In contrast, we show that graph simulation has poor locality, and hence the simple algorithm does not work here.

Message-passing model has been recently adopted for various famous distributed systems, *e.g.,* Pregel [21]. Our distributed algorithms follows this model, which is flexible enough to express a broad class of algorithms [19], and is typically fit for the evaluation of graph algorithms [21].

2. PRELIMINARIES

In this section, we first present basic graph notations. We then introduce the problems of graph pattern matching and its distributed counterpart, in terms of graph simulation.

2.1 Basic Graph Notations

We specify both pattern graphs and data graphs as follows. Let Σ be a (possibly infinite) set of labels.

Graphs. A *node-labeled directed graph* (or simply a *graph*) is defined as $G(V, E, l)$, where (1) V is a finite set of nodes; (2) $E \subseteq V \times V$ is a finite set of edges, in which (u, u') denotes an edge from nodes u to u'; and (3) l is a labeling total function that maps each node u in V to a label $l(u)$ in Σ. The size of G, denoted as $|G|$, is the total number of its nodes and edges, *i.e.,* $|V| + |E|$. We also denote G as (V, E) when it is clear from the context.

Intuitively, the function $l()$ specifies node attributes, *e.g.,* keywords, blogs, comments, ratings, names, emails, companies [4]; and the label set Σ denotes all such attributes.

Input: Pattern graph $Q(V_q, E_q)$ and data graph $G(V, E)$.
Output: The maximum match M in G for Q.

1. **for each** node $u \in V_q$ **do** $\mathsf{sim}(u) := \{w \mid w \in V, l_Q(w) = l_G(u)\}$;
2. **while** there exist $u \in Q$, $w \in \mathsf{sim}(u)$ **and** $v \in \mathsf{post}_Q(u)$ such that $\mathsf{post}_G(w) \cap \mathsf{sim}(u) = \emptyset$ **do**
3. $\quad \mathsf{sim}(v) := \mathsf{sim}(v) \setminus \{w\}$;
4. $M := \{(v, w) \mid v \in V_q, w \in \mathsf{sim}(v)\}$;
5. **return** M.

Figure 2: Centralized algorithm HHK

Subgraphs. Graph $H(V_s, E_s, l_H)$ is a *subgraph* of graph $G(V, E, l_G)$ if (1) for each node $u \in V_s$, $u \in V$ and $l_H(u) = l_G(u)$, and (2) for each edge $e \in E_s$, $e \in E$. That is, subgraph H only contains a subset of nodes and a subset of edges of G. We also denote subgraph H as $G[V_s]$ if E_s is exactly the edges that appear in G over V_s.

Descendants. We say that node v is a descendant of node u in G if v is reachable from u, *i.e.,* there is a directed path from u to v. We use $\mathsf{desc}(G, u)$ to denote the subgraph that contains the set of all descendants of u in G, including u itself, and the set of edges in G on those descendants exactly.

2.2 Graph Pattern Matching

We next review the notion of graph simulation [16]. Consider a pattern graph $Q(V_q, E_q)$ and a data graph $G(V, E)$.

A binary relation $R \subseteq V_q \times V$ is said to be a *match* if (1) for each $(u, v) \in R$, u and v have the same label, *i.e.,* $l_Q(u) = l_G(v)$; and (2) for each edge $(u, u') \in E_q$, there exists an edge (v, v') in E such that $(u', v') \in R$.

Note that an empty binary relation is a match.

Graph G matches pattern Q via *graph simulation*, denoted by $Q \prec G$, if there exists a *total* match relation M, *i.e.,* for each $u \in V_q$, there exists $v \in V$ such that $(u, v) \in M$.

Intuitively, simulation preserves the labels and the child relationship of a graph pattern in its match. Simulation was proposed for the analyses of programs [16], and studied for schema extraction from semi-structured data [2]. Simulation and its extensions were recently introduced for social networks [5] and for graph pattern matching [13, 12].

Graph pattern matching. The problem is to find, given any pattern graph Q and data graph G, the maximum match in G for Q if $P \prec G$. It was known that the following result holds [16, 13], by which the problem is well defined.

Proposition 1: *Given any pattern graph Q and data graph G, there exists a unique maximum match of G for Q no matter whether $Q \prec G$ or not [16, 13].* □

Algorithm HHK. We next present an algorithm for graph simulation in [16], denoted by HHK and shown in Fig. 2.

For each node u in Q, the set $\mathsf{sim}(u)$ contains candidate nodes in G, initially all nodes in G with the same label as u (line 1). By the definition, if $(u, v) \in E_q$ ($v \in \mathsf{post}_Q(u)$, successors of u), but there exist no nodes $w' \in \mathsf{sim}(v)$ such that $(w, w') \in E$ ($w' \in \mathsf{post}_G(v)$), then w cannot be matched to v, and hence is removed from $\mathsf{sim}(u)$. This process is repeated until there are no more changes (lines 2–3). Finally, the maximum match is assembled and returned (lines 4–5).

Example 2: Consider pattern graph Q_1 and data graph G_1 shown in Fig. 1. The maximum match computed by HHK is $\{(\mathsf{PM}, \mathsf{PM}_2), (\mathsf{SA}, \mathsf{SA}_2), (\mathsf{BA}, \mathsf{BA}_2), (\mathsf{UD}, \mathsf{UD}_1), (\mathsf{SD}, \mathsf{SD}_1), \ldots, (\mathsf{SD}, \mathsf{SD}_\mathsf{h}), (\mathsf{ST}, \mathsf{ST}_1), \ldots, (\mathsf{ST}, \mathsf{ST}_\mathsf{h})\}$. Note that here PM_1 cannot match PM since no child of PM_1 is labeled with UD, and it is similar for the other false matches. □

Remark. (1) Graph simulation is computable in quadratic time [16]. Algorithm HHK does not run in quadratic time, but it is simple and easy to be understood. Its further refinement leads to a quadratic algorithm [16], the best available algorithm as long as time complexity is concerned [23].
(2) Algorithm HHK correctly computes the maximum match M in data graph G for pattern graph Q, and $Q \prec G$ iff for each node v in Q, there exists a node u in G with $(v, u) \in M$. Hence we focus on computing the maximum match.

2.3 Distributed Graph Pattern Matching

We now introduce graph fragmentation, followed by the problem of distributed graph pattern matching.

We say $(G[V_1], \ldots, G[V_k])$ is a *partition* of graph $G(V, E)$ iff (1) $\bigcup_{i=1}^{k} V_i = V$; and (2) for any $i \neq j \in [1, k]$, $V_i \cap V_j = \emptyset$.

We also say node u in subgraph $G[V_i]$ ($1 \leq i \leq k$) is a *boundary* node if there exists an edge (u, v) in G from u to v in $G[V_j]$ such that $i \neq j$ and $1 \leq j \leq k$. To maintain the completeness of G, for each boundary node u in a partition $G[V_i]$, we maintain locally a set $\mathcal{B}_u$ of labeled nodes $v : j$ such that there exists an edge from u to v in subgraph $G[V_j]$.

Fragmented graph. A fragmented graph $\mathcal{F}$ of data graph G is denoted as $(F_1, \ldots, F_k)$, where (1) for each $i \in [1, k]$, $F_i = (G[V_i], \mathcal{B}_i)$ is a fragment of G placed at a separate machine S_i, (2) ($G[V_1]$, …, $G[V_k]$) is a partition of G, and (3) $\mathcal{B}_i$ ($i \in [1, k]$) is the union of the sets $\mathcal{B}_u$ of labeled nodes of all boundary nodes u in subgraph $G[V_i]$.

Example 3: Consider the fragmented data graph G_1 in Fig. 1 that consists of five fragments $F_1, \ldots, F_5$. Formally, $F_1 = (G[V_1], \{\mathcal{B}_{\mathsf{PM}_1}, \mathcal{B}_{\mathsf{SA}_1}\})$, $F_2 = (G[V_2], \emptyset)$, $F_3 = (G[V_3], \{\mathcal{B}_{\mathsf{PM}_2}\})$, $F_4 = (G[V_4], \{\mathcal{B}_{\mathsf{SA}_2}\})$, $F_5 = (G[V_5], \emptyset)$, where (1) $V_1 = \{\mathsf{PM}_1, \mathsf{BA}_1\}$, $V_2 = \{\mathsf{SA}_1, \mathsf{ST}_1\}$, $V_3 = \{\mathsf{PM}_2, \mathsf{BA}_2, \mathsf{UD}_1\}$, $V_4 = \{\mathsf{SA}_2\}$, and $V_5 = \{\mathsf{SD}_1, \mathsf{ST}_1, \ldots, \mathsf{SD}_\mathsf{h}, \mathsf{ST}_\mathsf{h}\}$, respectively; and (2) $\mathcal{B}_{\mathsf{PM}_1} = \{\mathsf{BA}_1 : 2\}$, $\mathcal{B}_{\mathsf{SA}_1} = \{\mathsf{SD}_1 : 2\}$, $\mathcal{B}_{\mathsf{PM}_2} = \{\mathsf{SA}_2 : 4\}$ and $\mathcal{B}_{\mathsf{SA}_2} = \{\mathsf{SD}_\mathsf{h} : 5\}$, respectively. □

Remark. (1) The fragmented graph has the same number of nodes and edges as the original graph except that the children of boundary nodes are labeled with IDs of the fragments in which they are located. (2) Graph partition is NP-complete in general [14], and is not the focus of this work. Here we allow arbitrary fragmentation of data graphs.

Distributed graph pattern matching. We now define the graph pattern matching problem in a distributed setting.

Given pattern graph Q, and fragmented graph $\mathcal{F} = (F_1, \ldots, F_k)$ of data graph G, in which each fragment $F_i = (G[V_i], \mathcal{B}_i)$ ($i \in [1, k]$) is placed at a separate machine S_i, the *distributed graph pattern matching problem* is to find the maximum match in G for Q, via graph simulation.

3. PROPERTY OF GRAPH SIMULATION

In this section, we study fundamental properties of graph simulation, which help us design distributed algorithms. We consider pattern graph $Q(V_q, E_q)$ and data graph $G(V, E)$.

3.1 Connected Components

We first show the impacts of connected components (CCs) on the evaluation of graph simulation.

Proposition 2: *Let pattern Q consist of h CCs $Q_1, \ldots, Q_h$. For any data graph G, if M_i is the maximum match in G for Q_i, then $\bigcup_{i=1}^{h} M_i$ is the maximum match in G for Q.* □

By Proposition 2, we assume *w.l.o.g.* that pattern graphs are always connected in the sequel.

Proposition 3: *Let data graph G consist of h CCs $G_1, \ldots, G_h$. For any pattern Q, if M_i is the maximum match in G_i for Q, then $\bigcup_{i=1}^{h} M_i$ is the maximum match in G for Q.* □

Proposition 3 implies that when a CC G_i ($i \in [1, h]$) is only located in a single fragment, we can simply compute the maximum match M_i in G_i for Q locally. However, this strategy does not work when a CC is across multiple fragments at different machines. We need a better solution.

To do this, we first introduce the following notions.

Consider a binary relation $R \subseteq V_q \times V$. We use $R(G)$ to denote the subgraph $H(V_s, E_s)$ of G, in which (1) $v \in V_s$ iff there exists $u \in V_q$ with $(u, v) \in R$, and (2) $(v, v') \in E_s$ iff (i) $(v, v') \in E$ and (ii) there exist $u, u' \in V_q$ with $(u, v) \in R$, $(u', v') \in R$ and $(u, u') \in E_q$. We also use $R(Q)$ to denote the subgraph $Q[V_{q,s}]$ of Q in which $u \in V_{q,s}$ iff there exists $v \in V$ with $(u, v) \in R$. Intuitively, $R(Q)$ and $R(G)$ are the subgraphs of Q and G, respectively, that play a role in R.

Theorem 4: *Consider any binary relation $R \subseteq V_q \times V$ on pattern graph $Q(V_q, E_q)$ and data graph $G(V, E)$ that contains the maximum match M in G for Q. If M_i is the maximum match in $R(G)_i$ for Q, then $\bigcup_{i=1}^{h} M_i$ is exactly M, where $R(G)$ consists of h CCs $R(G)_1, \ldots, R(G)_h$.* □

By Theorem 4, we can utilize subgraph $R(G)$, instead of the entire G, to compute the maximum match M if R is guaranteed to contain M. Note that even if G is connected, $R(G)$ might be highly disconnected, by removing useless nodes and edges from G. This enhances the possibility of treating each CC separately for evaluating graph simulation.

Remark. Note that finding all pairwise disconnected components is linear-time equivalent to finding strongly connected components, which is in linear time [9].

3.2 Data Locality

We then study the impacts of data locality on graph simulation. For distributed algorithms, one way to maximize parallelization is to explore "what can be computed locally" [22]. However, as observed in [21], graph algorithms often exhibit poor locality and hence, may incur prohibitive overhead on network traffic. This is indeed rather challenging for graph simulation, illustrated by an example below.

Example 4: Consider pattern Q_1 and data graph G_1 of Fig. 1. Let G_s be the CC of G_1 containing node PM_2. Then to decide whether $Q_1 \prec G_s$, we have to ship all subgraphs of G_s to a single site to re-assemble G_s. Indeed, (1) the match graph of Q_1 and G_s is the entire G_s; and (2) removing any node or edge from G_s makes $Q_1 \not\prec G_s$. This tells us that graph simulation has poor data locality. □

Theorem 5: *For any binary relation $R \subseteq V_q \times V$ on pattern graph $Q(V_q, E_q)$ and data graph $G(V, E)$ that contains the maximum match M in G for Q,*
(1) match $(u, v) \in R$ is in M iff it is in the maximum match in subgraph $\mathsf{desc}(R[G], v)$ for subgraph $\mathsf{desc}(R[Q], u)$; and
(2) if there exists a cycle in $\mathsf{desc}(R[Q], u)$, there must exist a cycle in $\mathsf{desc}(R[G], v)$ as well. □

By Theorem 5, whether node v in G can be mapped to node u in Q can be reduced to the sub-problem of checking whether it belongs to the maximum match in $\mathsf{desc}(R[G], v)$ for $\mathsf{desc}(R[Q], u)$, in which $\mathsf{desc}(R[G], v)$ and $\mathsf{desc}(R[Q], u)$ are connected subgraphs of G and Q, respectively. Moreover, a cycle in Q must match a cycle in G. Indeed, the poor data locality of simulation is caused by the cycles in Q.

Data locality. We next formally define *data locality* that may avoid unnecessary data shipment when evaluating pattern query Q on data graph G, via graph simulation.

We say that a node v in data graph G can be determined *locally* if checking whether v matches any node u in Q involves only the nodes v' in G that have distance $\mathsf{dist}(v, v')$ bounded by a constant factor determined by Q only. Similarly, we say that data graph G can be determined *locally* if all nodes in G can be determined locally.

Theorem 6: *Checking whether node v in data graph G matches node u in pattern graph Q can be determined locally iff subgraph $\mathsf{desc}(Q, u)$ is a* DAG. □

Example 5: Consider again pattern graph Q_1 and data graph G_1 of Fig. 1. Observe that the cycle $\mathsf{SD}/\mathsf{ST}/\mathsf{SD}$ in Q_1 matches the cycle $\mathsf{SD}_1/\mathsf{ST}_1/\ldots/\mathsf{SD}_h/\mathsf{ST}_h$ in G_1. This makes G_1 impossible to be determined locally since h can be arbitrarily large and cannot be bounded by Q_1.

On the contrary, nodes BA and UD in G_1 can be determined locally since the involved nodes in G_1 have a distance bounded by the longest shortest distance in Q_1. □

Now let us consider a fragmented graph $\mathcal{F} = (F_1, \ldots, F_k)$ of data graph G, in which each fragment $F_i = (G[V_i], \mathcal{B}_i)$ ($i \in [1, k]$) is placed at a separate machine S_i.

Corollary 7: *A fragment F_i can be determined locally if all its boundary nodes can be determined locally.* □

Summary. (1) We can treat each connect component in a data graph separately when evaluating graph simulation.
(2) Theorem 6 tells us how to check whether a node in data graph G can be determined locally or not.
(3) Corollary 7 tells us that the key for distributed pattern matching is to determine the matches of boundary nodes.

4. ANALYSES OF DISTRIBUTED ALGORITHMS

In this section, we investigate the complexities of a large class of distributed algorithms for graph simulation, which guides us the design of distributed algorithms. We consider pattern graph $Q(V_q, E_q)$ and fragmented graph $\mathcal{F} = (F_1, \ldots, F_k)$ of data graph $G(V, E)$, where each fragment $F_i = (G[V_i], \mathcal{B}_i)$ ($i \in [1, k]$) is placed at a separate machine S_i.

4.1 Model of Computation

We first present the computational model for a large class of distributed algorithms for graph simulation.

We consider distributed algorithms in a pure message-passing (sharing nothing) model. The model consists of a cluster of identical machines, in which one machine can directly send arbitrary number of messages to another one, and those machines co-work with each other by local computations and message-passing. Note that this model is flexible enough to express a broad class of algorithms [19], and is typically fit for the evaluation of graph algorithms [21].

The class of distributed algorithms that we consider work in the following fashion. A user initiates a pattern query Q at an arbitrary machine, referred to as the *coordinator*, in the a cluster of k identical machines. Then query Q is

(possibly) broadcasted to all the rest machines in the cluster, after which those machines cooperate with each other, *through message passing*, to compute the maximum match M in data graph G for Q, via graph simulation. Finally, the maximum match M is collected and presented to the user at the coordinator. Here the fragmented graph of G is placed at k machines, one fragment at each machine, *i.e.,* the number of fragments is exactly the number of machines. Note that this should not be treated a restriction as an arbitrary number of fragments can be merged into a single fragment.

Complexity measures. There are a variety of complexity measures on the performance of distributed algorithms [19], closely related to their computation models. We consider three measures: (1) *visit times*, the maximum visiting times of a machine in the cluster which indicates the complexity of interactions, (2) *makespan*, the time cost measuring the completion time, from the time when the query is initiated to the time when the maximum match M is completely assembled, and (3) *data shipment*, the size of the total messages among distinct machines in the cluster during the computation. Intuitively, one wants to minimize visit times, makespan and data shipment in the same time. As will be seen shortly, these three measures, however, are controversial with each other, which advocates a *well-balanced strategy* when designing distributed algorithms.

Specifications. To help analyze the complexity of the class of distributed algorithms, we need to further specify the following: (1) the *local information* available at each machine, (2) the *messages* exchanged among machines, and (3) the *local computations* executed on single machines.

(1) The local information at each machine S_i ($i \in [1, k]$) consists of (a) pattern graph Q, (b) subgraph $G_{s,i}$ of data graph G and (c) a marked binary relation $R_i \subseteq V_q \times V$.

The pattern graph Q is broadcasted to all machines, and kept unchanged during the computation. The subgraph $G_{s,i}$ is initially the local fragment $F_i = (G[V_i], \mathcal{B}_i)$, and is updated once receiving messages containing subgraphs from other machines. For each node pair $(u, v) \in R_i$, it is marked as true, false or unknown, denoting that (u, v) is (a) in the maximum match M, (b) not in M, or (c) undetermined. Relation R_i can be updated by either messages or local computations.

(2) When machine S_i sends a message to another machine S_j, the message only consists of the local information (Q, $G_{s,i}$, R_i) available at machine S_i. Here we do not allow information coding [10] since it is orthogonal to the analysis of the data shipment of distributed algorithms.

(3) At each machine S_i, local algorithms that given the local information (Q, $G_{s,i}$, R_i), compute an updated R_i by utilizing the definition of graph simulation. We require that the local algorithms execute only local computations without involving message-passing during the computation, and they run in time of a *polynomial* of $|Q|$ and $|G_{s,i}|$. Note that this is to help analyze the makespan problem [28] of distributed algorithms, and should not be treated as a *restriction* at all.

Remark. Under the model and specifications, we can express a large class of distributed algorithms for graph simulation, including all the ones that come into our mind.

4.2 Complexities of Distributed Algorithms

We next present our findings on the class of distributed algorithms for evaluating graph simulation queries, which satisfy the computation model and specifications given above.

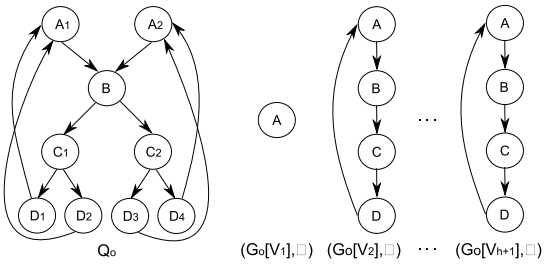


Figure 3: Example for complexity analyses

Our first set of findings are shown below.

Proposition 8: *The optimal data shipment of the class of distributed algorithms is* $|G| - 1$*, and the bound is tight.* □

Surprisingly, a simple distributed algorithm, referred to as naiveMatch$_{ds}$, can achieve the optimal data shipment. Given pattern graph Q and fragmented data graph G, the algorithm simply collects all fragments of the data graph to the coordinator, and then it calls a standard centralized algorithm of graph simulation, *e.g.,* HHK [16], to compute the maximum match in G for Q. Note that the total data shipment in the process is bounded by $|G|-1$ since the subgraph at the coordinator contains at least one node.

Proposition 9: *The optimal visit times of the class of distributed algorithms are* 1*, and the bound is tight.* □

Again a simple distributed algorithm, referred to as naiveMatch$_{vt}$, achieves the optimal visit times. Given pattern graph Q and fragmented data graph G, the algorithm visits k machines sequentially, where the last visited one is the coordinator. In the process, each time when the algorithm visits a machine, it collects the local fragment, and sends all the fragments collected so far to the next machine. Finally, all fragments of G reside at the coordinator, and it calls a centralized algorithm of graph simulation, *e.g.,* HHK [16], to compute the maximum match in G for Q. Note that each machine is visited one and only once in the process.

While there are efficient optimal algorithms for data shipment and visit times separately, the problem of finding a minimum makespan is much harder, as shown below.

Proposition 10: *The minimum makespan problem of the class of distributed algorithms is* NP*-complete [28].* □

We next present our second set of findings that these three complexity measures are *controversial with each other*. We illustrate this with the following example.

Example 6: Consider pattern graph Q_o and the fragmented data graph G_o in Fig. 3, in which each fragment is a CC without any boundary nodes. Here nodes in Q_o are only allowed to match nodes in G_o with the same labels by ignoring their subscripts. We also assume *w.l.o.g.* that $F_1 = (G[V_1], \emptyset)$ lies at the coordinator.

One can verify the following:

(1) For algorithm naiveMatch$_{ds}$, the (optimal) data shipment is $|G| - 1 = 8h$, while the visit times are h.

(2) For algorithm naiveMatch$_{vt}$, the (optimal) visit times are 1, while the data shipment is $4h(h + 1)$.

Observe that all the computational workload in these algorithms is mostly laid at a single machine, the coordinator. Essentially, no computing power is used *in parallel* at all.

(3) Ideally, a distributed algorithm would work as follows.

(i) After receiving Q on each machine, a local algorithm is called to compute the local match in the fragment.

Input: Pattern graph Q and fragmented data graph $\mathcal{F} = (F_1, \ldots, F_k)$ with $F_i = (G[V_i], \mathcal{B}_i)$ placed at machine S_i $(i \in [1, k])$.
Output: The maximum match M in G for Q.

Coordinator S_Q.
1. **send** pattern graph Q to all k participating machines;

case (1): **upon** receiving M_is and CCs from all k machines **do**
1. $M := M_1 \cup \ldots \cup M_k$;
2. **call** dSchedule to find an assignment of those CCs;
3. **send** the assignment to all k participating machines;

case (2): **upon** receiving $M_{b,i}$s from all k machines **do**
1. $M := M \cup M_{b,1} \cup \ldots \cup M_{b,k}$;
2. **return** M.

Machine S_i.
case (3): **upon** receiving pattern graph Q **do**
1. $PM_i :=$ localHHK(Q, F_i);
2. **let** $\mathcal{C}_{b,i}$ be the CCs in $PM_i(G)$ containing nodes in $\mathcal{B}_i$;
3. **let** M_i be the matches in PM_i containing no nodes in $\mathcal{C}_{b,i}$;
4. **send** M_i and the sizes and boundary nodes of CCs in $\mathcal{C}_{b,i}$ to S_Q;

case (4): **upon** receiving the assignment of data shipment **do**
1. **send** CCs in $\mathcal{C}_{b,i}$ to their corresponding machines;

case (5) **upon** receiving all the assigned CCs $\mathcal{C}_i$ **do**
1. $M_{b,i} :=$ refineHHK$(Q, \mathcal{C}_i)$;
2. **send** $M_{b,i}$ to coordinator S_Q;

Figure 4: Distributed algorithm disHHK

(ii) Here since each fragment is a CC, all local match results are simply sent to and assembled at the coordinator. Recall Proposition 3 in Section 3.

In this way, the computation is maximally *parallelized*, and the makespan is minimized, accordingly. However, one may verify that the data shipment is $30h$, and the visit times are h. In contrast, the optimal data shipment and visit times are $8h$ and 1, respectively. □

Summary. We find that data shipment, visit times and makespan of a large class of distributed algorithms for graph simulation are controversial with each other. As efficiency remains the dominant factor, there needs a well-balanced strategy between makespan and the other two measures.

5. DISTRIBUTED EVALUATION

In this section, we present the distributed algorithms that exploit the properties of graph simulation (Section 3) and the analyses of distributed algorithms (Section 4). We consider pattern graph $Q(V_q, E_q)$ and fragmented graph $\mathcal{F} = (F_1, \ldots, F_k)$ of data graph $G(V, E)$, where each fragment $F_i = (G[V_i], \mathcal{B}_i)$ $(i \in [1, k])$ is placed at a separate machine S_i.

The distributed algorithm, referred to as disHHK, follows the computation model and specifications given in Section 4. It is initiated at the coordinator S_Q where the query Q is issued, and it consists of five stages (shown in Fig. 4).

Stage 1: Coordinator S_Q simply broadcasts pattern query Q to all the k participating machines.

Stage 2: The main objective is to (partially) evaluate Q in each fragment at local machines in parallel (**case** (3)). As a by-product, the local evaluation filters out useless nodes and edges in the fragment, and hence reduces the data shipment. It also breaks a large fragment into smaller CCs, which further reduces the sizes of CCs across different machines.

Stage 3: The objective is to ship those CCs across different machines to single machines (**case** (1) and **case** (4)). This involves two important, but controversial, issues: minimizing data shipment and makespan. We provide a solution that (a) both minimizes the makespan with performance guarantees and (b) minimizes the data shipment with heuristics in the same time.

Stage 4: The objective is to compute the maximum matches in those CCs originally across different machines in parallel, by making use of those partial matches on these components computed locally at Stage 1 (**case** (5)).

Stage 5: Finally, the match results on all machines are sent to and assembled at the coordinator (**case** (5) and **case** (2)).

Correctness. The correctness of disHHK can be easily verified by the analyses of graph simulation in Section 3.

Proposition 11: *Given any pattern graph Q and fragmented graph $\mathcal{F}$ of data graph G, algorithm* disHHK *computes the maximum match in G for Q.* □

Performance. The algorithm guarantees the following.
(1) The total computation cost is comparable to the one of the *best-known* centralized algorithm [16]. And it invokes four rounds of message-passing and local evaluation only.
(2) The total data shipment is at most $|G| + 4|\mathcal{B}| + |Q||G| + (k-1)|Q|$, where $|\mathcal{B}|$ is the total number of boundary nodes.
(3) Each machine except coordinator S_Q is visited at most $g+2$ times, where g is the maximum number of machines at which a CC resides at the end of Stage 2. Coordinator S_Q is visited with $2(k-1)$ extra times since it needs to schedule the data shipment and assemble the final result.

Remark. (1) We have decided to sacrifice the visit times and data shipment for the benefits of the makespan, a decision based on the analyses of Section 4.
(2) As one may notice, most stages are run in parallel except for **case** (1) at Stage 3. As will be seen soon, its computation cost is really low, and would not cause a bottleneck.

In what follows, we describe each stage in more detail.

5.1 Local Evaluation of Partial Match

As shown by the analyses of Section 3, special care needs to be paid on boundary nodes. To do this, we introduce a notion of *partial match relation*. We consider a fragment $F_i = (G[V_i], \mathcal{B}_i)$ at machine S_i $(i \in [1, k])$.

Partial match. A binary relation $R \subseteq V_q \times V_i$ is said to be a *partial match* if (1) for each $(u, v) \in R$, u and v have the same label; and (2) for each edge (u, u') in E_q, (a) there exists a node $v' \in \mathcal{B}_v$ in $\mathcal{B}_i$ having the same label as u' if v is a boundary node, or (b) there exists an edge (v, v') in $G[V_i]$ such that $(u', v') \in R$, otherwise.

The difference between a partial match and a match given in Section 2 is the latter deals with boundary nodes. When there are no boundary nodes involved, they are equivalent. Note that (u, v) in a partial match might not appear in the maximum match in G for Q since the matches on boundary nodes are checked partially only with their directed neighbors. We illustrate this with an example below.

Example 7: Consider pattern graph Q_1 and data graph G_1 in Example 1. Pair $(\mathsf{SA}, \mathsf{SA}_1)$ is in the maximum partial match PM_1 in fragment F_1 for Q. However, it does not belong to the maximum match M in G for Q. □

Algorithm localHHK. To compute the partial match, we propose algorithm localHHK, a revision of algorithm HHK that further deals with boundary nodes. Given pattern graph Q and fragment $F_i = (G[V_i], \mathcal{B}_i)$ $(i \in [1, k])$, it computes the maximum *partial match* in the fragment for Q. Due to space limitations, its detail is omitted here.

It is easy to get the following result, along the same lines as Proposition 1 and algorithm HHK in Section 2.2.

Corollary 12: *For any pattern graph Q and fragment F_i, (1) there is a unique maximum partial match; and (2) algorithm* localHHK *computes the maximum partial match.* □

We next illustrate with an example how local evaluation also filters out useless nodes and edges in data graphs, which reduces data shipment and computations.

Example 8: Consider again pattern graph Q_1 and fragments F_1 and F_2 in data graph G_1 in Example 1. Recall that the maximum partial matches $PM_1 = \{(\mathsf{SA}, \mathsf{SA}_1)\}$ and $PM_2 = \emptyset$. Hence, instead of the connected component consisting of fragments F_1 and F_2, only node SA_1 in F_1 will be considered in the following stages. Thus a plenty of unnecessary nodes and edges are filtered out at this stage. □

5.2 Scheduling Data Shipment

After the local evaluation of partial match is done, we have a partial match PM_i on each machine S_i ($i \in [1, k]$). Let PM be $\bigcup_{i=1}^{k} PM_i$, and M be the maximum match in G for Q. It is easy to verify that $M \subseteq PM$.

Now let us consider subgraph $PM(G)$ consisting of nodes and edges of G that play a role in PM, as defined in Section 3.1. Theorem 4 tells us that those matches in PM involved with those CCs residing at single machines must belong to the maximum match M. Due to the poor data quality of graph simulation, those CCs of PM residing at multiple machines need to be gathered into single machines.

A challenging task here is how to schedule the data shipment such that both the data shipment and the makespan are minimized. Note that the visit times have been fixed in the algorithm, and hence are not involved.

To do this, we introduce the following problem.

The scheduling problem. Consider subgraph $PM_i(G)$ at machine S_i. Each CC of $PM_i(G)$ is identified by its boundary nodes, its size (*e.g.,* the number of nodes and edges) and its location S_i. These information of all the CCs involved with boundary nodes are sent to the coordinator, at which those CCs of $PM(G)$ across different machines are merged. Hence, we have a set $\{C_1, \ldots, C_l\}$ of CCs of $PM(G)$. For each $j \in [1, l]$, C_j is associated with $k+1$ costs: (1) for each $i \in [1, k]$, the data shipment $C_j.d_i$ if C_j is shipped to S_i; and (2) the computation cost $C_j.c$. Recall that the computation cost of C_j is a polynomial of $|Q|$ and $|C_j|$.

Formally, *the scheduling problem* is defined as follows. Given l CCs $C_1, \ldots, C_l$, and an integer k, find an assignment of the CC to k identical machines, so that both the makespan and the total data shipment are minimized.

Approximation hardness. To minimize the makespan, the key is to distribute those connected components evenly on those k machines. As the minimum makespan problem is NP-complete (Proposition 10), we focus on approximate solutions here. We first look for chances that minimize both the makespan and the data shipment.

We say that the scheduling problem is approximatable within (α, β) if there exists a PTIME algorithm such that given any instance of the problem, the algorithm produces a scheduling solution such that the data shipment is bounded by α times of the optimal data shipment and the makespan is bounded by β times of the optimal makespan.

Input: Connected components $C_1, \ldots, C_l$ and an integer k.
Output: An assignment of $C_1, \ldots, C_l$ to k identical machines.
1. **let** $avg_c := (C_1.c + \ldots + C_l.c)/k$;
2. **for** each connected component C_i ($i \in [1, l]$) **do**
3. **if** the total load of C_i and its optimal machine $\leq avg_c$ **then**
4. Assign C_i to its optimal machine;
5. **for** each of the rest connected components C_j **do**
6. Assign C_j to the machine that has the least amount of load.

Figure 5: Scheduling algorithm dSchedule

The result is, however, negative due to the controversial nature of these two measures as shown in Section 4.2.

Theorem 13: *The scheduling problem is not approximable within $(\xi, \mathsf{max}(k-1, 2))$ for any $\xi > 1$.* □

Approximation algorithm. This motivates us to look for solutions that have performance guarantees for the makespan only. We propose an approximation algorithm dSchedule that has a heuristic for minimizing the data shipment, and a performance guarantee for the makespan.

Theorem 14: *Algorithm* dSchedule *produces an assignment of the scheduling problem such that the makespan is within a factor $(2 - 1/k)$ of the optimal one.* □

We now present the details of dSchedule, shown in Fig. 5. Given connected components $C_1, \ldots, C_l$ and an integer k as inputs, the algorithm finds an assignment for these CCs. It first computes the average computation avg_c cost of all CCs (line 1). Given a CC C_j, the optimal machine S_{j_o} to which C_j is assigned is the one on which the largest part of C_j resides, *i.e.,* $C_j.d_{j_o}$ is the largest among $\{C_j.1, \ldots, C_j.k\}$. If the total load of C_i and its optimal assigned machine together is equal or less than the average computation cost avg_c, then C_i is assigned to its optimal machine (lines 2-4). For the rest CCs C_j, schedule C_j to the machine that has the least amount of load (lines 5-6).

Remark. (1) A heuristic is used to minimize the data shipment, by shipping CCs to their corresponding optimal machines *w.r.t.* the data shipment (lines 1-4).
(2) A greedy approach (lines 5-6) is adopted to guarantee the performance of the makesapn, along the same lines as the one for the standard makespan problem [28].
(3) The algorithm runs in $O(kl)$, and is very efficient. Hence, its evaluation could not cause a bottleneck.

Example 9: Consider again pattern graph Q_1 and data graph G_1 in Example 1. Algorithm dSchedule finds an assignment for the two connected components C_1 consisting of a single node SA_1, and C_2 consisting of the entire fragments F_3, F_4 and F_5. In this case, (1) C_1 is simply assigned to S_1, and (2) C_2 is assigned to S_5. That is, these CCs are assigned to the machines with optimal data shipment. □

5.3 Refining Partial Match

Similar to algorithm localHHK, algorithm refineHHK is also a revision of algorithm HHK. The key differences between refineHHK and HHK lie in that (1) partial matches evaluated at stage 1 are treated as initial candidate matches, and (2) we process the matches of boundary nodes first, in which way the total computation cost of refineHHK and localHHK is comparative to the one of HHK.

5.4 Optimization Techniques

We next present optimization techniques for algorithm disHHK, by means of data locality and query minimization.

Determining boundary matches using data locality. For each partial match PM_i ($i \in [1, k]$) in fragment F_i for Q, we further determine whether those matches in PM_i with boundary nodes, computed by localHHK, belong to the maximum match M in the entire data graph G for Q. It is based on an application of Theorems 5 and 6 in Section 3. This reduces both computations and data shipments. Consider the matches (u, v) for a boundary node v in a partial match PM_i in fragment $F_i = (G[V_i], \mathcal{B}_i)$ for Q.

To determine whether (u, v) belongs to the maximum match M in G for Q, it suffices to determine whether for each child u' of u in Q, there is a child v' of v such that (u', v') is in M. For each child node $j : v'$ in $\mathcal{B}_v$ of $\mathcal{B}_i$, if v' matches a child u' of u in PM_i, match (v', u') is further checked by *lazy evaluation* at machine S_j as follows.

Let $C_{v'}$ be the connected component of PM_j such that v' is in C_j, and let $PM_{i,v'}$ be the set of matches in PM_j that involve nodes in C_j. We have two cases to consider:

Case 1: when there are no boundary nodes in G_j.

For this case, we simply check whether node u' belongs to subgraph $PM_{i,v'}(Q)$. If the answer is 'yes', then match (v', u') is a *true* match, *i.e.,* (v', u') belongs to the maximum match M in G for Q. Otherwise, it is a *false* match. The correctness of this approach is guaranteed by Theorem 5.

Case 2: when there are boundary nodes in C_j, but subgraph desc(Q, u') of pattern graph Q is a DAG.

For this case, we need to check whether all nodes in desc(Q, u'), including u' itself, matches no boundary nodes in C_j. If the answer is 'yes', then match (v', u') is a *true* match, *i.e.,* (v', u') belongs to the maximum match M in G for Q. Otherwise, it is an *unknown* match. The correctness of this approach is guaranteed by Theorems 5 and 6.

We next illustrate the benefits of this optimization technique with the following example.

Example 10: Consider pattern graph Q_1 and data graph G_1 in Fig. 1, and the partial match results in Example 7. One can verify that (1) boundary nodes SA_1 and SA_2 can be determined by this optimization technique, while nothing can be done for boundary node PM_2.

(1) For node SA_1, its only child SD_1 is located in fragment F_2. The partial match PM_2 is empty. Hence, a false match decision is sent back to machine S_1, and this further helps determine that (SA, SA_1) is a false match.

(2) For node SA_2, its only child SD_1 is located in fragment F_5. The subgraph $PM_5(G)$ contains no boundary nodes, and SD belongs to $PM_5(Q)$. Hence, a true match decision is sent back to machine S_4, and this further helps determine that (SA, SA_2) is a true match.

After these are done, fragment F_3 is the only part of G that needs to be further evaluated. To check the matches in F_3, we simply ship fragment F_4 to machine S_3, instead of shipping F_3 and F_4 to machine S_5 as shown in Example 9. That is, our approach could potentially save a large amount of unnecessary data shipments and computations. □

Remark. (1) This approach exploits the partial match results at other machines, and the checking is simple and efficient. (2) Only a *small* amount of data shipment is incurred. The only involved data shipment is the triggers of the lazy evaluation and the decisions (true, false, or unknown). Note that the evaluation is done at machine S_j, not S_i. This is why the data shipment incurred is small.

Minimizing pattern graphs. Given pattern graph Q, we compute a minimized pattern graph Q_m such that for any data graph G, G matches Q iff G matches Q_m, via graph simulation. The algorithm runs in quadratic time, and is taken from [6]. Note that Q is typically small.

We next illustrate the benefits of minimizing pattern graphs with an example below.

Example 11: Consider pattern graph Q_o in Fig.3. The minimized equivalent pattern graph Q_{m_o} of Q_o is a compact representation of Q_o, by merging (1) nodes A_1, A_2, (2) nodes C_1, C_2, and (3) nodes D_1, D_2, D_3, D_4. It only consists of four nodes and four edges. Hence, Q_{m_o} is much smaller than Q_o. It is easy to see that both the data shipment and computation cost of evaluating Q_{m_o} on G_o are much smaller that those of evaluating Q_o on G_o. □

We have implemented a version of disHHK that supports these optimizations, referred to as disHHK$^+$. As will be seen in Section 6, disHHK$^+$ significantly outperforms disHHK.

6. EXPERIMENTAL STUDY

We next present an experimental study of our algorithms disHHK and disHHK$^+$. Using both real-life and synthetic data, we conducted four sets of tests to evaluate: (1) the makespan, (2) the data shipment, (3) the visit times of our algorithms, and (4) the effectiveness of algorithm localHHK.

Experimental setting. We use the following datasets.

Real-life data. We used two real-life datasets[1]. (a) *Google* records a Web graph with 875,713 nodes and 5,105,039 edges where nodes are URLs and an edge from URLs x to y indicates that there exists a hyperlink from x to y. (b) *Amazon* contains a product co-purchasing network with 548,552 nodes and 1,788,725 edges in which nodes are products and an edge from products x to y represents that people buy y with high probability when they buy x.

Synthetic graph generator. We adopted the graph-tool library[2] to produce both pattern and data graphs. It is controlled by three parameters: the number n of nodes, the number n^α of edges, and the number l of node labels. Given n, α and l, the generator produces a graph with n nodes, n^α edges, and the nodes are labeled from a set of l labels.

Algorithms. We implemented the following algorithms, all in Python: (1) algorithms disHHK and disHHK$^+$, and (2) optimal algorithms naiveMatch$_{ds}$ and naiveMatch$_{vt}$ (Section 4).

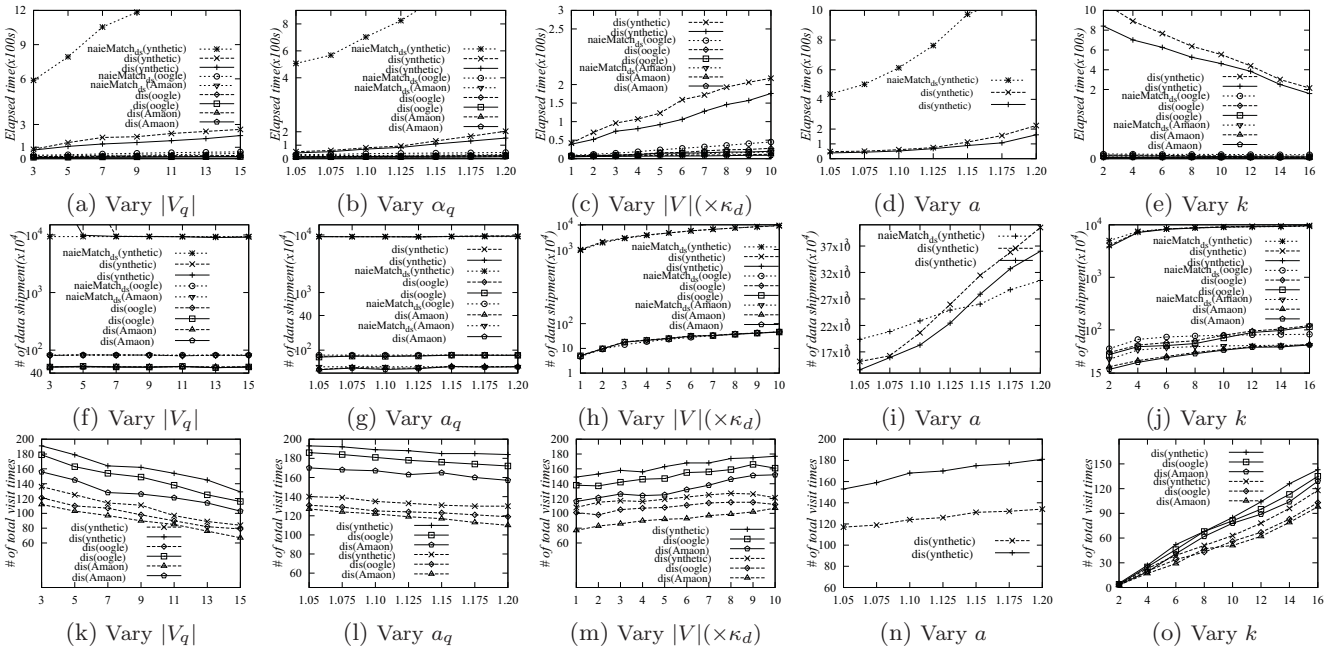
The experiments were run on a cluster of 16 machines, all with 2 Intel Xeon E5620 CPUs and 64GB memory, that are connected by kilomega network. Each test was repeated over 5 times and the average is reported here.

Experimental results. In all the experiments, we fixed $l = 200$, $k = 16$, and set α (α_q) = 1.20 by default. All datasets are partitioned with a hashing function hash(ID) mod k, and distributed over all participating machines. This partition approach has been commonly used in large-scale data process systems, such as MapReduce [11] and Pregel [21].

Exp-1: Makespan. In the first set of tests, we evaluated the performance of disHHK, disHHK$^+$, naiveMatch$_{ds}$ and naiveMatch$_{vt}$. We did not report naiveMatch$_{vt}$ here as it is always *much slower* than naiveMatch$_{ds}$.

[1] http://snap.stanford.edu/data/index.html

[2] http://projects.skewed.de/graph-tool/



(a) Vary $|V_q|$ (b) Vary α_q (c) Vary $|V|(\times\kappa_d)$ (d) Vary a (e) Vary k

(f) Vary $|V_q|$ (g) Vary a_q (h) Vary $|V|(\times\kappa_d)$ (i) Vary a (j) Vary k

(k) Vary $|V_q|$ (l) Vary a_q (m) Vary $|V|(\times\kappa_d)$ (n) Vary a (o) Vary k

Figure 6: Evaluation on makespan, data shipment and visit times

(1) To evaluate the impacts of pattern graphs Q, we fixed data graphs G, *e.g.,* Google with 875,713 nodes, Amazon with 548,552 nodes and synthetic data with 10^8 nodes, while varying (a) the number $|V_q|$ of nodes in Q from 3 to 15 and (b) the density α_q of Q from 1.05 to 1.20, respectively. The results are reported in Figures 6(a) and 6(b), respectively.

One can find the following. (a) All these algorithms scale well with V_q and α_q on large data graphs, except $\mathsf{naiveMatch}_{ds}$. While it took disHHK and disHHK^+ less than 300s in all cases, it took $\mathsf{naiveMatch}_{ds}$ over 500s in all cases, and was much slower than disHHK and disHHK^+. (b) disHHK^+ is faster than disHHK. Indeed, the running time of disHHK^+ is consistently about [3/4, 4/5] of the time taken by disHHK, a significant reduction. (c) Finally, the elapsed time of all algorithms increases when $|V_q|$ or α_q increases.

(2) To evaluate the impacts of data graphs G, we fixed pattern graphs Q with $|V_q| = 9$, while varying the number $|V|$ of nodes of G (Google from 5×10^4 to 5×10^5, Amazon from 10^3 to 10^4 and synthetic data from 10^7 to 10^8), and the density α of G on synthetic data from 1.05 to 1.20, respectively. The results are reported in Figures 6(c) and 6(d), respectively, where κ_d is a constant such that it is 5×10^4, 10^3 and 10^7 for Google, Amazon and synthetic data, respectively.

One can find the following. (a) All algorithms scale well on the large data graphs except $\mathsf{naiveMatch}_{ds}$, which took over 300s even on the smallest synthetic graphs with 10^7 nodes. Hence we did not report its running time on synthetic data graphs in Figure 6(c). (b) disHHK^+ is consistently faster than disHHK, *e.g.,* it took disHHK 217s on synthetic data graphs with $|V| = 10^8$ while it was only 176s for disHHK^+. Indeed, the running time of disHHK^+ is consistently about [3/4, 4/5] of the time taken by disHHK, the same as the case above when varying pattern graphs. (c) Finally, the elapsed time of all algorithms increases when $|V|$ or α increases.

(3) To evaluate the impacts of the number k of participating machines, we fixed both data graphs G (with the same setting for data graphs as (1)) and pattern graphs Q (with the setting for pattern graphs as (2)), while varying k from 2 to 16. The results are shown in Figure 6(e).

We find the following. (a) The elapsed time of all algorithms decreases when k increases. (b) The elapsed time of disHHK and disHHK^+ decreases faster than the one of $\mathsf{naiveMatch}_{ds}$ when k increases. The elapsed time of disHHK on synthetic data was reduced from 1081s with $k = 2$ to 215s with $k = 16$, while the one of $\mathsf{naiveMatch}_{ds}$ was only reduced from 1603s with $k = 2$ to 1521s with $k = 16$. And (c) the running time of disHHK^+ is consistently about [3/4, 4/5] of the time taken by disHHK, the same as the cases when varying pattern or data graphs.

Exp-2: Data shipments. In the second set of tests, using the same setting as Exp-1, we evaluated the total data shipments of disHHK, disHHK^+, $\mathsf{naiveMatch}_{ds}$ and $\mathsf{naiveMatch}_{vt}$. We did not report $\mathsf{naiveMatch}_{vt}$ here since it always triggered much more data shipments than $\mathsf{naiveMatch}_{ds}$.

(1) We tested the impacts of Q using the same setting as Exp-1(1). The results are reported in Figs. 6(f) and 6(g).
(a) The total data shipments of all algorithms are *not* sensitive to the size of pattern graphs, (b) although $\mathsf{naiveMatch}_{ds}$ achieves the theoretical optimal data shipment, disHHK and disHHK^+ trigger similar amount of data shipments as $\mathsf{naiveMatch}_{ds}$, and (c) they even trigger less data shipments than $\mathsf{naiveMatch}_{ds}$ on large and sparse data graphs, *e.g.,* when $|V_q| > 11$ on synthetic data or $\alpha_q \leq 1.125$ on Amazon.
(2) We tested the impacts of G using the same setting as Exp-1(2). The results are reported in Figs. 6(h) and 6(i).
(a) It is obvious that the total data shipments of all algorithms increase while $|V|$ or α increases. (b) disHHK and disHHK^+ shipped less data than $\mathsf{naiveMatch}_{ds}$ on large and sparse data graphs, *e.g.,* when $\alpha \leq 1.125$ on synthetic data. And (c) disHHK^+ always shipped less data than disHHK.
(3) We tested the impacts of k using the same setting as Exp-1(3). The results are reported in Figure 6(j).
(a) The total data shipments of all algorithms increase when k increases. This is obvious since there are more boundary nodes when k increases when fixing data graphs. And (b)

disHHK and disHHK$^+$ again trigger similar amount of data shipments as naiveMatch$_{ds}$.

Exp-3: Visit times. In the third set of tests, using the same setting as Exp-1, we evaluated total visits times of all algorithms. We did not report naiveMatch$_{vt}$ here as it is always equal to the number k of participating machines. The impacts of Q, G and k are reported in Figs. 6(k) and 6(l), Figs. 6(m) and 6(n), and Figure 6(o), respectively.
(a) The total visit times of all algorithms decrease when $|V_q|$ or α_q increases. This is because when the size of pattern graphs increases, there are less matches in data graphs. (b) The visit times of all algorithms obviously increase when $|V|$, α or k increases. (c) disHHK and disHHK$^+$ have more visit times than naiveMatch$_{ds}$, and disHHK$^+$ has [30%, 53%] more visit times than disHHK, as expected. Indeed, this is a price that has to be paid in exchange for efficiency.

Exp-4: Effectiveness of localHHK. Adopting the same setting as Exp-1, we also evaluated the effectiveness of localHHK, measured by the number of boundary nodes that are filtered out by localHHK. The results are shown below:

	Google	Amazon	Synthetic
# of total boundary nodes	4287	2418	1343952
# of filtered boundary nodes	1916	1305	446192

It shows that localHHK eliminates a large portion of boundary nodes for disHHK and disHHK$^+$, *e.g.,* it cuts off 44%, 54% and 33% boundary nodes on Google, Amazon and synthetic data, respectively. This means that localHHK indeed plays a considerable role in our algorithms.

Summary. From these experiments, we find the following. (1) disHHK and disHHK$^+$ are efficient and scale well on large and dense data graphs, and considerably outperform naiveMatch$_{ds}$ (optimal data shipment alone) and naiveMatch$_{vt}$ (optimal visit times alone). (2) Our optimization techniques are effective, reducing the running time by 20% to 25%. (3) We have intensionally sacrificed data shipment and visit times for makespan. However, disHHK and disHHK$^+$ even ship less data than naiveMatch$_{ds}$ when data graphs are large and sparse. Recall that real-life graphs are often large and sparse. disHHK and disHHK$^+$ indeed have more visit times than naiveMatch$_{vs}$, a price that has to be paid in exchange for improving efficiency and minimizing data shipments. (4) localHHK effectively filters out [33%, 54%] unnecessary boundary nodes for disHHK and disHHK$^+$.

7. CONCLUSION

We have proposed evaluation algorithms for graph simulation in a distributed setting. To our knowledge, we are among the first to settle this problem. We have also verified, both analytically and experimentally, the effectiveness of our algorithms and optimization techniques.

Several topics are targeted for future work. First, we are to extend our algorithms to deal with skewed graph partitions. Second, we are experimentally verifying our algorithms using MapReduce and Pregel platforms [11, 21]). Finally, we are to explore indexing techniques and distributed incremental methods to speed up the computation, in response to the dynamic changes of real-life data graphs.

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