Association Rules with Graph Patterns

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ABSTRACT

We propose graph-pattern association rules (GPARs) for social media marketing. Extending association rules for itemsets, GPARs help us discover regularities between entities in social graphs, and identify potential customers by exploring social influence. We study the problem of discovering top-k diversified GPARs. While this problem is NP-hard, we develop a parallel algorithm with accuracy bound. We also study the problem of identifying potential customers with GPARs. While it is also NP-hard, we provide a parallel scalable algorithm that guarantees a polynomial speedup over sequential algorithms with the increase of processors. Using real-life and synthetic graphs, we experimentally verify the scalability and effectiveness of the algorithms.

1. INTRODUCTION

Association rules have been well studied for discovering regularities between items in relational data, for promotional pricing and product placements [4, 45]. They have a traditional form $X \Rightarrow Y$, where X and Y are disjoint itemsets.

There have been recent interests in studying associations between entities in social graphs. Such associations are useful in social media marketing; indeed, "90% of customers trust peer recommendations versus 14% who trust advertising" [2], and "60% of users said Twitter plays an important role in their shopping" [43]. Nonetheless, association rules for social graphs are more involved than rules for itemsets.

Example 1: (1) Association rules for social graphs are defined on graphs rather on itemsets. Below is an example.

- *If (a) x and x' are friends living in the same city c, (b) there are at least 3 French restaurants in c that x and x' both like, and if (c) x' visits a newly opened French restaurant y in c, then x may also visit y.*

The antecedent of the rule can be represented as a graph pattern Q_1 (with solid edges) shown in Fig. 1(a), and the consequent is indicated by a dotted edge visit(x, y). A succinct presentation of Q_1 associates integer 3 with "French Restaurant" to indicate its 3 copies. As opposed to conventional association rules, Q_1 specifies conditions as topological constraints: edges between customers (the friend relation), customers and restaurants (like, visit), city and restaurants (in), and between city and customers (live_in).

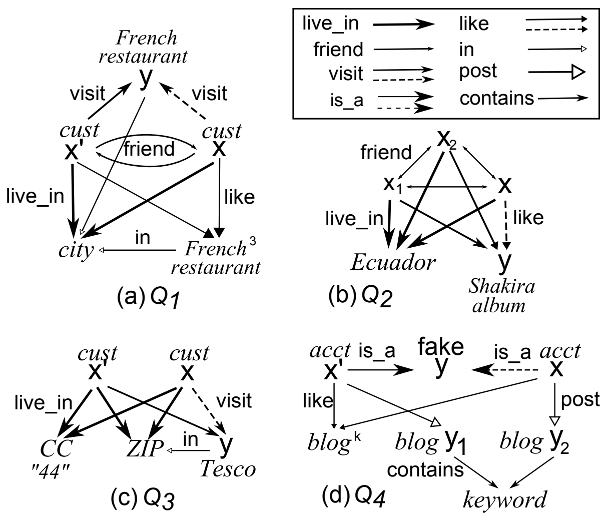

Figure 1: Associations as graph patterns

In a social graph G, for x and y satisfying the antecedent Q_1 via graph pattern matching, we can recommend y to x.

(2) As opposed to rules for itemsets, association rules for social graphs may target social groups with multiple entities:

- *If (a) x, x_1 and x_2 are friends, (b) they all live in Ecuador, and (c) if x_1, x_2 both like Shakira's album y (a Colombian singer), then x may also like y.*

This rule is depicted in Fig. 1(b), in which a graph pattern Q_2 (excluding the dotted edge) specifies conditions for (x, y) as antecedent, and dotted edge like(x, y) indicates its consequent. We can use the rule to identify potential customers x of y, characterized by a social group of three members.

(3) Association rules with graph patterns conveniently extend data dependencies such as conditional functional dependencies (CFDs) [14] in the context of social networks.

- *If the addresses of x and x' have the same country code "44" and same zip code, and if x' shops at a Tesco store y with the same zip, then x may also shop at y.*

Such a rule (Fig. 1(c)) embeds a corresponding CFD in its pattern Q_3, stating that if x and x' live in the UK with the same zip code, then they live on the same street. The rule is valid in the UK where zip code determines street.

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(4) The applications of association rules are not limited to marketing activities. They also help us detect scams. As an example, the rule below is used to identify fake accounts [9].

- *If (a) account x' is confirmed fake, (b) both x and x' like blogs $P_1, \ldots, P_k$, (c) x posts blog y_1, (d) x' posts y_2, and (e) if y_1 and y_2 contain the same particular content (keyword), then x is likely a fake account.*

As depicted in Fig. 1(d), its antecedent is given by graph pattern Q_4 (excluding the dotted edge), and its consequent is the dotted edge is_a(x, *fake*). In a social graph G, the rule is to identify suspects for fake accounts, *i.e.,* accounts x that satisfy the structural constraints of pattern Q_4. □

The need for graph-pattern association rules (GPARs) is evident in social media marketing, community structure analysis, social recommendation, knowledge extraction and link prediction [33]. Such rules, however, depart from association rules for itemsets, and introduce several challenges. (1) Conventional support and confidence metrics no longer work for GPARs. (2) Mining algorithms for traditional rules and frequent graph patterns cannot be used to discover practical diversified GPARs. (3) A major application of GPARs is to identify potential customers in social graphs. This is costly: graph pattern matching by subgraph isomorphism is intractable. Worse still, real-life social graphs are often big, *e.g.,* Facebook has 13.1 billion nodes and 1 trillion links [21].

Contributions. This paper proposes GPARs, and provide effective algorithms for discovering and applying GPARs.

(1) We introduce graph-pattern association rules (GPARs) for social media marketing (Section 2). GPARs differ from conventional rules for itemsets in both syntax and semantics. A GPAR defines its antecedent as a graph pattern, which specifies associations between entities in a social graph, and explores social links, influence and recommendations. It enforces conditions via both value bindings (*e.g.,* "44") and topological constraints by subgraph isomorphism.

(2) We define topological support and confidence metrics for GPARs (Section 3). Conventional support for itemsets is no longer anti-monotonic for GPARs. We define support in terms of distinct "potential customers" by revising a measure proposed by [7]. We propose a confidence measure for GPARs by revising Bayes Factor [31] to incorporate the local closed world assumption [11, 17]. This allows us to cope with (incomplete) social graphs, and to identify interesting GPARs with correlated antecedent and consequent.

(3) We study a new mining problem, referred to as the *diversified mining problem* and denoted by DMP (Section 4). It is a bi-criteria optimization problem to discover top-k GPARs. While useful, DMP is NP-hard. Nonetheless, we develop a parallel approximation algorithm with a *constant accuracy bound*. We also provide optimization methods to filter redundant or non-promising rules as early as possible.

(4) We also study how to identify potential customers by applying GPARs, referred to as *the entity identification problem* and denoted by EIP (Section 5). Given a social graph G and *a set* Σ of GPARs pertaining to an event $p(x, y)$, we identify potential customers x of y in G with confidence above a given bound η, by using GPARs in Σ. We show that it is NP-hard even to decide whether such x exists.

Despite this, we develop a *parallel scalable* algorithm for EIP such that its response time is in $O(t(|G|, |\Sigma|)/n)$, a polynomial reduction in the running time $t(|G|, |\Sigma|)$ of *sequential algorithms*, by using n processors. Hence given a big graph, we can identify potential customers in it by increasing n.

(5) Using real-life and synthetic graphs, we experimentally verify the scalability and effectiveness of our algorithms (Section 6). We find the following. (a) Our algorithms for DMP and EIP scale well with the increase of processors (n): they are on average 3.2 and 3.53 times faster on real-world social networks, respectively, when n increases from 4 to 20. (b) They work reasonably well on large graphs: the one for DMP takes less than 9 minutes (533.2 seconds) on graphs with 30 million nodes and edges, and the one for EIP takes 45 seconds on graphs with 150 million nodes and edges for 24 GPARs, with 20 processors. (c) The DMP algorithm finds interesting GPARs from real-life social graphs. (d) Our optimization methods are effective: they speed up DMP and EIP processing by 1.52 and 1.27 times, respectively, on real-life graphs. Hence, despite their complexity, applying and discovering GPARs are feasible in practice via parallelization.

Related Work. We categorize related work as follows.

Association rules. Introduced in [4], association rules are defined on relations of transaction data. Prior work on association rules for social networks [41] and RDF knowledge bases resorts to mining conventional rules and Horn rules (as conjunctive binary predicates) [17] over tuples with extracted attributes from social graphs, instead of exploiting graph patterns. While [6] studies time-dependent rules via graph patterns, it focuses on evolving graphs and hence adopts different semantics for support and confidence.

GPARs extend association rules from relations to graphs. (a) It demands topological support and confidence metrics. Moreover, incomplete information is common in social graphs [11, 17] and has to be incorporated into the metrics. (b) GPARs are interpreted with isomorphic functions and hence, cannot be expressed as conjunctive queries, which do not support negation or inequality needed for functions. (c) Applying GPARs becomes an intractable problem of multi-pattern-query processing in big graphs. (d) Mining (diversified) GPARs is beyond rule mining from itemsets [46].

Graph pattern mining. There have been algorithms for pattern mining in graph databases [22,24] (see [25] for a survey). Large-scale mining techniques are also studied in a single graph [13], notably top-k algorithms [16, 27, 42, 44]. To reduce the cost, scalable subgraph isomorphism algorithms, *e.g.,* [38], can be adopted to generate pattern candidates. Diversity of graph patterns is not studied there.

However, (a) pattern mining over graph databases [24,27] cannot be used to mine GPARs, as their anti-monotonic property does not hold in a single graph [25]. (b) While mining single graphs is based only on isomorphic counting [13], DMP is bi-criteria optimization problem for confidence and diversity of GPARs, apart from [16,44]. We are not aware of prior work on discovering diversified graph patterns.

Graph pattern matching. Several parallel algorithms have been developed for subgraph isomorphism, *e.g.,* [28, 37, 38], and for multi-pattern optimization, *e.g.,* [23, 32]. Our algorithms for EIP differ from the prior work in the following. (a) Instead of enumerating isomorphic matches, EIP identifies a potential customer *once* one match is found, and moreover, computes its associated confidence. That is, EIP is beyond conventional subgraph isomorphism. (b) We provide parallel scalable algorithms for multi-pattern matching. To the best of our knowledge, these are among the first algorithms on big graphs that *guarantee a polynomial speedup over sequential algorithms* with the increase of processors [30]. (c) We propose optimization strategies that are not studied by previous work. This said, prior optimization techniques can be incorporated into GPAR-based entity identification; *e.g.,* the methods of [32] to extract common sub-patterns.

2. ASSOCIATION VIA GRAPH PATTERNS

In this section we define graph-pattern association rules.

2.1 Graphs, Patterns, and Pattern Matching

We start with notions of graphs and graph patterns.

Graphs. 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 set of edges, in which (v, v') denotes an edge from node v to v'; (3) each node v in V (resp. edge e) carries $L(v)$ (resp. $L(e)$), indicating its label or content *e.g.,* cust, French restaurant, 44 (resp. post, like), as found in social networks and property graphs.

Example 2: Two graphs G_1 and G_2 are shown in Fig. 2. (1) Graph G_1 depicts a restaurant recommendation network. For instance, cust_1 and cust_2 (labeled cust) live in New York; they share common interests in 3 French restaurants (marked with superscript 3 for simplicity); and they both visit a newly opened French restaurant "Le Bernadin" in New York. (2) Graph G_2 shows activities of social accounts. It contains (a) accounts $\text{acct}_1, \ldots, \text{acct}_4$ (labeled acct), (b) blogs $p_1, \ldots, p_7$; and (c) edges from accounts to blogs. For example, edge $\text{post}(\text{acct}_1, p_1)$ means that account acct_1 posts blog p_1, which contains keyword w_1 "claim a prize". □

Patterns. A *pattern query* Q is a graph (V_p, E_p, f, C), in which V_p and E_p are the set of pattern nodes and edges, respectively; each node u_p in V_p (resp. edge e_p in E_p) has a label $f(u_p)$ (resp. $f(e_p)$) specifying a search condition, *e.g.,* city, or "44" for *value binding* (Q_3 of Example 1). For succinct representation, a node u_p can be labeled with an integer $C(u_p) = k$, indicating k copies of u_p with the same label and associated links in the common neighborhood.

Graph pattern matching. We first review two notions of subgraphs. (1) A graph $G' = (V', E', L')$ is a *subgraph of* $G = (V, E, L)$, denoted by $G' \subseteq G$, if $V' \subseteq V$, $E' \subseteq E$, and moreover, for each edge $e \in E'$, $L'(e) = L(e)$, and for each $v \in V'$, $L'(v) = L(v)$. (2) We say that G' is *a subgraph induced by* a set V' of nodes if $G' \subseteq G$ and E' consists of all those edges in G whose endpoints are both in V'.

We adopt subgraph isomorphism for pattern matching. A *match* of pattern Q in graph G is a *bijective function* h from the nodes of Q to the nodes of a subgraph G' of G such that (a) for each node $u \in V_p$, $f(u) = L(h(u))$, and (b) (u, u') is an edge in Q if and only if $(h(u), h(u'))$ is an edge in G', and $f(u, u') = L(h(u), h(u'))$. We say that G' *matches* Q.

Note that *similarity predicates* can be used instead of equality "=" with no impact on our algorithms.

We denote by $Q(G)$ the set of all matches of Q in G. For each pattern node u, we use $Q(u, G)$ to denote the set of all *matches* of u in $Q(G)$, *i.e.,* $Q(u, G)$ consists of nodes v in G such that there exists a function h under which a subgraph $G' \in Q(G)$ is isomorphic to Q, $v \in G'$ and $h(u) = v$.

Example 3: For Q_1 of Fig. 1 and G_1 of Fig. 2, a match in $Q_1(G)$ is $x \mapsto \text{cust}_1$, $x' \mapsto \text{cust}_2$, *city* $\mapsto$ New York, $y \mapsto$ Le Bernardin, and French restaurant^3 to 3 French restaurants. Here $Q_1(x, G_1)$ includes cust_1–cust_3 and cust_5. □

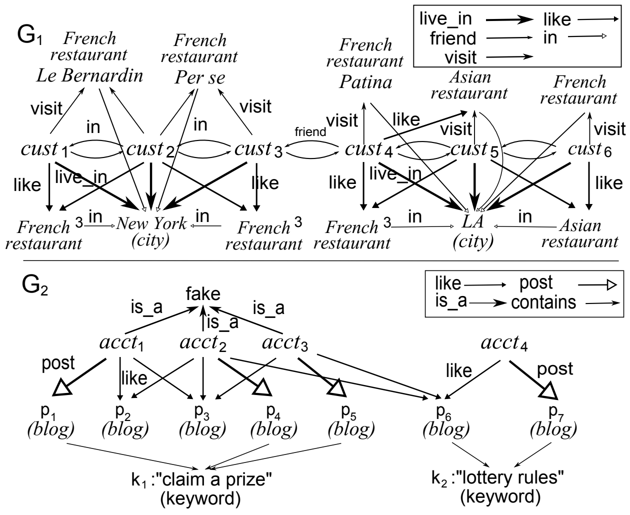


Figure 2: Labeled social graphs

A pattern $Q' = (V'_p, E'_p, f', C')$ is *subsumed by* another pattern $Q = (V_p, E_p, f, C)$, denoted by $Q' \sqsubseteq Q$, if (V'_p, E'_p) is a subgraph of (V_p, E_p), and functions f' and C' are restrictions of f and C in V, respectively. Observe that if $Q' \sqsubseteq Q$, then for any graph G' that matches Q, there exists a subgraph G'' of G' such that G'' matches Q'.

We will use the following notations. (1) For a pattern Q and a node x in Q, *the radius of* Q *at* x, denoted by $r(Q, x)$, is the longest distance from x to all nodes in Q when Q is treated as an *undirected* graph. (2) Pattern Q is *connected* if for each pair of nodes in Q, there exists an undirected path in Q between them. (3) For a node v_x in a graph G and a positive integer r, $N_r(v_x)$ denotes the set of all nodes in G within radius r of v_x. (4) The *size* $|G|$ of G is $|V| + |E|$, the number of nodes and edges in G. (5) Node v' is a *descendant* of v if there is a directed path from v to v' in G.

2.2 Graph Pattern Association Rules

We now define graph-pattern association rules.

GPARs. A *graph-pattern association rule* (GPAR) $R(x, y)$ is defined as $Q(x, y) \Rightarrow q(x, y)$, where $Q(x, y)$ is a graph pattern in which x and y are two *designated nodes*, and $q(x, y)$ is an edge labeled q from x to y, on which the same search conditions as in Q are imposed. We refer to Q and q as the *antecedent* and *consequent* of R, respectively.

The rule states that *for all nodes* v_x and v_y in a (social) graph G, if *there exists* a match $h \in Q(G)$ such that $h(x) = v_x$ and $h(y) = v_y$, *i.e.,* v_x and v_y match the designated nodes x and y in Q, respectively, then the consequent $q(v_x, v_y)$ will likely hold. Intuitively, v_x is a potential customer of v_y.

We model $R(x, y)$ as *a graph pattern* P_R, by extending Q with a (dotted) edge $q(x, y)$. We refer to pattern P_R as R when it is clear from the context. We treat $q(x, y)$ as pattern P_q, and $q(x, G)$ as the set of matches of x in G by P_q.

We consider practical and nontrivial GPARs by requiring that (1) P_R is connected; (2) Q is *nonempty*, *i.e.,* it has at least one edge; and (3) $q(x, y)$ does not appear in Q.

Example 4: Recall the first association rule described in Example 1. It can be expressed as a GPAR $R_1(x, y)$:

$Q_1(x, y) \Rightarrow \mathsf{visit}(x, y)$, where its antecedent is the pattern Q_1 given in Example 1, and its consequent is $\mathsf{visit}(x, y)$. The GPAR can be depicted as the graph pattern of Fig. 1(a), by extending $Q_1(x, y)$ with a dotted edge for $\mathsf{visit}(x, y)$.

The last rule of Example 1 is written as $R_4(x, y)$: $Q_4(x, y) \Rightarrow \mathsf{is\_a}(x, y)$, where in Q_4, $y = \mathit{fake}$ is a value binding. The GPAR is depicted as the pattern of Fig. 1(d). In $\mathsf{is\_a}(x, y)$, the same search condition $y = \mathit{fake}$ is imposed. □

Remark. (1) To simplify the discussion, we define the consequent of GPAR with a single predicate $q(x, y)$ following [4]. However, a consequent can be readily extended to *multiple* predicates and even to a *graph pattern*. (2) Conventional association rules [4] and a range of predication and classification rules [39] are a special case of GPARs, since their antecedents can be modeled as a graph pattern in which nodes denote items. Conditional functional dependencies [14] can also be represented by GPARs (see Q_3 of Fig. 1(c)).

3. SUPPORT AND CONFIDENCE

We next define support and confidence for GPARs.

Support. The support of a graph pattern Q in a graph G, denoted by $\mathsf{supp}(Q, G)$, indicates how often Q is applicable. As for association rules for itemsets, the support measure should be *anti-monotonic*, *i.e.,* for patterns Q and Q', if $Q' \sqsubseteq Q$, then in any graph G, $\mathsf{supp}(Q', G) \geq \mathsf{supp}(Q, G)$.

One may want to define $\mathsf{supp}(Q, G)$ as *the number* $\|Q(G)\|$ of matches of Q in $Q(G)$, following its counterpart for itemsets [46]. However, as observed in [7, 13, 25], this conventional notion is *not* anti-monotonic. For example, consider pattern Q' with a single node labeled cust, and Q with a single edge like(cust, French restaurant). When posed on G_1, $\|Q(G)\| = 18 > \|Q'(G)\| = 6$ (since French restaurant^3 denotes 3 nodes labeled French restaurant), although $Q' \sqsubseteq Q$.

To cope with this, we revise the support measure proposed in [7]. We define the support of the designated node x of Q as $\|Q(x, G)\|$, *i.e.,* the number of distinct matches of x in $Q(G)$. We define *the support of* Q *in* G as

$$\mathsf{supp}(Q, G) = \|Q(x, G)\|.$$

One can verify that this support measure is *anti-monotonic.*

For a GPAR $R(x, y)$: $Q(x, y) \Rightarrow q(x, y)$, we define

$$\mathsf{supp}(R, G) = \|P_R(x, G)\|,$$

by treating R as pattern $P_R(x, y)$ with designated nodes x, y.

Example 5: For GPAR $R_1(x, y)$: $Q_1(x, y) \Rightarrow \mathsf{visit}(x, y)$ of Example 4 and graph G_1 of Fig 2, (1) $\|Q_1(x, G_1)\| = 4$ (see Example 3); hence $\mathsf{supp}(Q_1, G_1)$ is 4; and (2) $\mathsf{supp}(R_1, G_1) = \|P_{R_1}(x, G_1)\| = 3$, where x has 3 matches cust_1–cust_3.

Similarly, consider $R_4(x, y)$: $Q_4(x, y) \Rightarrow \mathsf{is\_a}(x, y)$ of Example 4 and graph G_2 in Fig 2, where $y = \mathit{fake}$. When k=2, $\mathsf{supp}(R_4, G_2) = \mathsf{supp}(Q_4, G_2) = \|Q_4(x, G_2)\| = 3$, with matches acct_1–acct_3 for the designated node x in Q_4. □

Confidence. To find how likely $q(x, y)$ holds when x and y satisfy the constraints of $Q(x, y)$, we study the *confidence* of $R(x, y)$ in G, denoted as $\mathsf{conf}(R, G)$. One may want to adopt the conventional confidence for association rules, and define $\mathsf{conf}(R, G)$ as $\frac{\mathsf{supp}(R,G)}{\mathsf{supp}(Q,G)}$. That is, every match x in Q but not in R is considered as negative example for R. However, as observed in [11, 17], the standard confidence is blind to the distinction between "negative" and "unknown". This is particularly an overkill when G is incomplete [11, 34].

Example 6: Consider pattern Q_2 in Fig. 1(b). Let $Q_2(x, G)$ contain three matches v_1, v_2, v_3 of x_1, x_2, x_3 in a social graph G, all living in Ecuador, where (1) v_1 has an edge like to Shakira album, (2) v_2 has only a single edge like to MJ's album, and (3) v_3 has no edge of type like. Conventional confidence treats v_2 and v_3 both as negative examples, with $\mathsf{conf}(R_2, G) = \frac{1}{3}$. However, G may be incomplete: v_3 has not entered any albums she likes. Thus we should treat v_3 as "unknown", not as a counterexample to R_2. □

Indeed, closed world assumption may not hold for social network [34]. To distinguish "unknown" cases from true negative for GPAR mining in incomplete social networks, we adopt the *local closed world assumption* [11, 17], as commonly used in mining incomplete knowledge bases.

Local closed world assumption (LCWA). Given a predicate $q(x, y)$, we introduce the following notations.

(1) $\mathsf{supp}(q, G) = \|P_q(x, G)\|$, the number of matches of x;
(2) $\mathsf{supp}(\bar{q}, G)$, the number of nodes u in G that (a) have the same label as x, (b) have at least one edge of type q, but (c) $u \notin P_q(x, G)$; and
(3) $\mathsf{supp}(Q\bar{q}, G)$, the number of nodes that satisfy conditions (a) to (c) of (2), and are also in $Q(x, G)$.

Given an (incomplete) social network G and a predicate $q(x, y)$, the local closed world assumption (LCWA) distinguishes the following three cases for a node u.

(1) "positive" case, if $u \in P_q(x, G)$;
(2) "negative" case, for every u counted in $\mathsf{supp}(\bar{q}, G)$; and
(3) "unknown" case, for every u that satisfies the search condition of x but has *no* edge labeled as q.

That is, G is assumed "locally complete": it either gives all correct local information of u in connection with predicate q, or knows nothing about q at node u (hence unknown cases).

Based on LCWA, we define conf (R, G) by revising Bayes Factor (BF) of association rules [31] as follows:

$$\mathsf{conf}(R, G) = \frac{\mathsf{supp}(R, G) \ * \ \mathsf{supp}(\bar{q}, G)}{\mathsf{supp}(Q\bar{q}, G) \ * \ \mathsf{supp}(q, G)}.$$

Intuitively, $\mathsf{conf}(R, G)$ measures the product of *completeness* and *discriminant.* A GPAR $R(x, y)$ has a better completeness if it holds on more matches x of $Q(x, y)$, and is more discriminant if it is less likely to hold on more nodes from $Q\bar{q}$. In addition, BF-based $\mathsf{conf}(R, G)$ is better justified than conventional confidence. As verified in [26, 31], BF satisfies a set of principles for reasonable interestingness measures, including fixed under independence ($\mathsf{conf}(R, G) = 1$ if Q and q are statistically independent), fixed under incompatibility ($\mathsf{conf}(R, G)$=0 if $\mathsf{supp}(R, G)$=0), and monotonicity (increases monotonically with $\mathsf{supp}(R, G)$ when $\mathsf{supp}(\bar{q}, G)$, $\mathsf{supp}(Q, G)$ and $\mathsf{supp}(q, G)$ are fixed). Hence we adapt BF by incorporating LCWA and topological support.

Example 7: Consider GPAR R_2 and $Q_2(x, G)$ described in Example 6. Under the LCWA, match v_1 accounts for "positive" for R_2, while v_2 and v_3 are "negative" and "unknown", respectively. Indeed, assuming that G provides complete local information for v_2, then v_2 is a counter-example to people who live in Ecuador but do not like Shakira album; in contrast, G knows nothing about what albums v_3 likes.

One can see that $\mathsf{supp}(R_2, G) = 1$ (match v_1), $\mathsf{supp}(\bar{q}, G) = 1$ (match v_2), $\mathsf{supp}(Q\bar{q}, G) = 1$ (match v_2), and $\mathsf{supp}(q, G) = 1$ (match v_1). The BF-based confidence $\mathsf{conf}(R_2, G)$ is 1, larger than its conventional counterpart ($\frac{1}{3}$) as the LCWA removes the impact of the unknown case v_3. □

symbols	notations
$Q(x, G)$	the set of distinct nodes that match x in $Q(G)$
$R(x, y)$	GPAR $Q(x, y) \Rightarrow q(x, y)$, represented as pattern P_R
$r(Q, x)$	the radius of Q at node x
$N_r(v_x)$	the set of nodes within radius r of v_x
$\mathsf{supp}(Q, G)$	the number $\|Q(x, G)\|$ of distinct matches of x in $Q(G)$
$\mathsf{conf}(Q, G)$	$(\mathsf{supp}(R, G) * \mathsf{supp}(\bar{q}, G))/(\mathsf{supp}(Q\bar{q}, G) * \mathsf{supp}(q, G))$
$\Sigma(x, G, \eta)$	$\{v_x \mid v_x \in Q(x, G), Q \Rightarrow q \in \Sigma, \mathsf{conf}(R, G) \geq \eta\}$

Table 1: Notations: graphs, queries and rules

There are other alternatives to define support and confidence for GPARs. (1) Following minimum image-based support [7], $\mathsf{supp}(R, G)$ can be defined as the the maximum number of matches for x in non-overlap matches (*i.e.,* no shared nodes and edges) of R. However, this excludes potential customers from matches that share even a single node (*e.g.,* only one of the three matches cust_1-cust_3 of Fig. 2 is counted), and thus underestimates the significance. (2) Similar to PCA confidence [17], $\mathsf{conf}(R, G)$ can be computed as $\frac{\mathsf{supp}(R,G)}{\mathsf{supp}(Q\bar{q},G)}$ under LCWA. However, this only considers the "coverage" of R instead of its interestingness in terms of completeness and discriminant [26, 31] (see Section 6).

Remark. We identify the following two "trivial" cases when $\mathsf{conf}(R, G) = \infty$: (1) $\mathsf{supp}(Q\bar{q}, G)$ is 0, which interprets R as a logic rule that holds on the entire G, *i.e.,* "if v is in $Q(x, G)$ then v is a match in $P_q(x, G)$ (hence $P_R(x, G)$)"; and (2) $\mathsf{supp}(q, G) = 0$, which means that $q(x, y)$ in R specifies no user in G; hence R should be discarded as uninteresting case. These two cases can be easily detected and distinguished in the GPAR discovery process (see Section 4).

The notations of this paper are summarized in Table 1.

4. DIVERSIFIED RULE DISCOVERY

We now study how to discover useful GPARs.

4.1 The Diversified Mining Problem

We are interested in GPARs for a particular event $q(x, y)$. However, this often generates an excessive number of rules, which often pertain to the same or similar people [5, 44].

This motivates us to study a diversified mining problem, to discover GPARs that are *both* interesting and diverse.

Objective function. To formalize the problem, we first define a function $\mathsf{diff}(,)$ to measure the difference of GPARs. Given two GPARs R_1 and R_2, $\mathsf{diff}(R_1, R_2)$ is defined as

$$\mathsf{diff}(R_1, R_2) = 1 - \frac{|P_{R_1}(x, G) \cap P_{R_2}(x, G)|}{|P_{R_1}(x, G) \cup P_{R_2}(x, G)|}$$

in terms of the Jaccard distance of their match set (as social groups). Such diversification has been adopted to battle against over-concentration in social recommender systems when the items recommended are too "homogeneous" [5].

Given a set L_k of k GPARs that pertain to the same predicate $q(x, y)$, we define the objective function $F(L_k)$ again by following the practice of social recommender systems [19]:

$$(1 - \lambda) \sum_{R_i \in S} \frac{\mathsf{conf}(R_i)}{N} + \frac{2\lambda}{k - 1} \sum_{R_i, R_i \in S, i < j} \mathsf{diff}(R_i, R_j).$$

This, known as *max-sum diversification*, aims to strike a balance between interestingness (measured by revised Bayes Factor) and diversity (by distance $\mathsf{diff}(,)$) with a parameter λ controlled by users. We consider nontrivial GPARs (Section 3) with $\mathsf{conf}(R, G) \in [0, \mathsf{supp}(R, G) * \mathsf{supp}(\bar{q}, G)]$, and normalize (1) the confidence metric with $N = \mathsf{supp}(q, G) *$

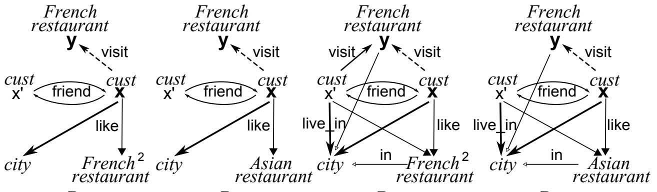


Figure 3: Diversified GPARs

$\mathsf{supp}(\bar{q}, G)$ (a constant for fixed $q(x, y)$), and (2) the diversity metric with $\frac{2\lambda}{k-1}$, since there are $\frac{k(k-1)}{2}$ numbers for the difference sum, while only k numbers for the confidence sum.

Example 8: Consider GPARs R_1 of Fig. 1, and R_7 and R_8 shown in Fig. 3, all pertaining to $\mathsf{visits}(x, \mathsf{French\ restaurant})$. Then in graph G_1 (Fig. 2), (1) $\mathsf{supp}(q, G_1) = 5$ (cust_1-cust_4, cust_6), $\mathsf{supp}(\bar{q}, G_1) = 1$ (cust_5); (2) $R_1(x, G_1) = R_7(x, G_1) = \{\mathsf{cust}_1, \mathsf{cust}_2, \mathsf{cust}_3\}$, $R_8(x, G_1) = \{\mathsf{cust}_6\}$; (3) $\mathsf{conf}(R_1, G_1) = \mathsf{conf}(R_7, G_1) = 0.6$, $\mathsf{conf}(R_8, G_1) = 0.2$; and (4) $\mathsf{diff}(R_1, R_7) = 0$, $\mathsf{diff}(R_1, R_8) = \mathsf{diff}(R_7, R_8) = 1$.

For $\lambda = 0.5$, a top-2 diversified set of these GPARs is $\{R_7, R_8\}$ with $F(R_7, R_8) = 0.5 * \frac{0.8}{5} + 1 * 1 = 1.08$ (similarly for $\{R_1, R_8\}$). Indeed, R_7 and R_8 find two disjoint customer groups sharing interests in French restaurant and Asian restaurant, respectively, with their friends. □

Problem. Based on the objective function, the *diversified* GPAR *mining problem* (DMP) is stated as follows.

- ○ *Input*: A graph G, a predicate $q(x, y)$, a support bound σ and positive integers k and d.
- ○ *Output*: A set L_k of k nontrivial GPARs pertaining to $q(x, y)$ such that (a) $F(L_k)$ is maximized; and (b) for each GPAR $R \in L_k$, $\mathsf{supp}(R, G) \geq \sigma$ and $r(P_R, x) \leq d$.

DMP is a bi-criteria optimization problem to discover GPARs for a particular event $q(x, y)$ with high support, bounded radius, and a balanced confidence and diversity. In practice, users can freely specify $q(x, y)$ of interests, while proper parameters (*e.g.,* support, confidence, diversity) can be estimated from query logs or recommended by domain experts.

The problem is nontrivial. Consider its decision problem to decide whether there exists a set L_k of k GPARs with $F(L_k) \geq B$ for a given bound B. One can show the following by reduction from the dispersion problem (cf. [19]).

Proposition 1: *The* DMP *decision problem is* NP*-hard.* □

4.2 Discovery Algorithm

One might want to follow a "discover and diversify" approach that (1) first finds all GPARs pertaining to $q(x, y)$ by frequent graph pattern mining [35], and then (2) selects top-k GPARs via result diversification [19]. However, this is costly: (a) an excessive number of GPARs are generated; and (b) for all GPARs R generated, it has to compute $\mathsf{conf}(R, G)$ and their pairwise distances, and moreover, pick a top-k set based on $F()$; the latter is an intractable process itself.

One can do it more efficiently, with accuracy guarantees.

Theorem 2: *There exists a parallel algorithm for* DMP *that finds a set L_k of top-k diversified* GPARs *such that (a) L_k has approximation ratio 2, and (b) L_k is discovered in d rounds by using n processors, and each round takes at most $t(|G|/n, k, |\Sigma|)$ time, where Σ is the set of* GPARs *$R(x, y)$ such that $\mathsf{supp}(R, G) \geq \sigma$ and $r(P_R, x) \leq d$.* □

Here $t(|G|/n, k, |\Sigma|)$ is a function that takes $|G|/n$, k and $|\Sigma|$ as parameters, *rather than* the size $|G|$ of the entire G.

As a proof, we give such an algorithm, denoted as DMine and shown in Fig. 4. It designates one processor as *coordinator* S_c and the rest as *workers* S_i. It works as follows.

(1) It divides G into $n-1$ fragments $(F_1, \ldots, F_{n-1})$ such that (a) for each "candidate" v_x that satisfies the search condition on x in $q(x,y)$, its *d-neighbor* $G_d(v_x)$, *i.e.,* the subgraph of G induced by $N_d(v_x)$, is in some fragment; and (b) the fragments have roughly even size. These are possible since 98% of real-life patterns have radius 1, 1.8% have radius 2 [18], and the average node degree is 14.3 in social graphs [8]; thus $G_d(v_x)$ is typically small compared with fragment size.

Fragment F_i is stored at worker S_i, for $i \in [1, n-1]$.

(2) DMine discovers GPARs *in parallel* by following bulk synchronous processing, in d rounds. The coordinator S_c maintains a list L_k of diversified top-k GPARs, initially empty. In each round, (a) S_c posts a set M of GPARs to all workers, initially $q(x,y)$ only; (b) each worker S_i generates GPARs *locally* at F_i in parallel, by extending those in M with new edges if possible; (c) these GPARs are collected and assembled by S_c in the barrier synchronization phase; moreover, S_c *incrementally* updates L_k: it filters GPARs that have low support or cannot make top-k *as early as possible*, and prepares a set M of GPARs for expansion in the next round.

As opposed to the "discover and diversify" method, DMine (a) combines diversifying into discovering to *terminate* the expansion of non-promising rules *early*, rather than to conduct diversifying after discovering; and (b) it *incrementally* computes top-k diversified matches, rather than recomputing the diversification function $F()$ starting from scratch.

We next present the details of algorithm DMine.

Auxiliary structures. Algorithm DMine maintains the following: (a) at the coordinator S_c, a set L_k to store top k GPARs, and a set Σ to keep track of generated GPARs; and (b) at each worker S_i, a set C_i of candidates v_x for x at F_i.

Messages. In each round, coordinator S_c and workers S_i communicate via messages. (1) Each worker S_i generates a set M_i of messages. Each message is a triple $<R$, conf, flag$>$, where (a) R is a GPAR generated at S_i, (b) conf includes, *e.g.,* $\mathsf{supp}(R(x,y), F_i)$ and $\mathsf{supp}(Q\bar{q}(x,y), F_i)$, and (c) a Boolean flag to indicate whether R can be extended at S_i. (2) After receiving M_i, S_c generates a set M of messages, which are GPARs to be extended in the next round.

Algorithm. DMine initializes L_k and Σ as empty, and M as $\{q(x,y)\}$ (line 1). For r from 1 to d, it improves L_k by incorporating GPARs of radius r (lines 2-11), following a *levelwise* approach. In each round, it invokes localMine with M at all workers (line 4). Below we present the details.

<u>*Parallel* GPARs *generation*</u> (line 13). In the first round, procedure localMine receives $q(x,y)$ from S_c, and computes the following: (a) three sets: C_i, nodes v_x that satisfy the search condition of x in discovered GPARs, $P_q(x, F_i)$, matches of x in $q(x,y)$, and $\bar{q}(x, F_i)$, nodes v in F_i that account for $\mathsf{supp}(\bar{q}, F_i)$ (Section 2.2); and (b) $\mathsf{supp}(q, F_i) = \|P_q(x, F_i)\|$, $\mathsf{supp}(\bar{q}, F_i) = \|P_{\bar{q}}(x, F_i)\|$. Note that $\mathsf{supp}(q, F_i)$ and $\mathsf{supp}(\bar{q}, F_i)$ never change and hence are derived *once for all.* Each match $v_x \in q(x, F_i)$ is referred to as a *center node.*

In round r, upon receiving M from S_c, localMine does the following. For each GPAR $R(x,y) : Q(x,y) \Rightarrow q(x,y)$ in M, and each center node v_x, it expands Q by including *at least* one *new edge* that is at hop r from v_x, for all such edges.

```
Algorithm DMine
Input: A graph $G$, $q(x,y)$, bound $\sigma$, and positive integers $k$ and $d$.
Output: A set $L_k$ of top-$k$ diversified GPARs.

/* executed at coordinator */
1.  $L_k := \emptyset$; $\Sigma := \emptyset$; $r := 1$; $M := \{q(x,y)\}$;
2.  while $r \leq d$ do
3.     $r := r + 1$;
4.     post $M$ to all workers and invoke localMine ($M$) in parallel;
5.     collect in $\Delta E$ candidate GPARs in $M_i$ from all workers;
6.     check automorphism and assemble confidence for these GPARs;
7.     $\Delta E$ includes $R$ with supp$(R, G) \geq \sigma$; $\Sigma := \Sigma \cup \Delta E$; $M := \emptyset$;
8.     for each GPAR $R \in \Delta E$ do
9.        incDiv ($L_k, R, \Sigma$); /* incrementally update $L_k$, prune $\Sigma, \Delta E$ */
10.       if $R$ is "extendable"
11.        then $M := M \cup \{R\}$; /* next round */
12. return $L_k$;

/* executed at each worker $S_i$ in parallel, upon receiving $M$ */
13. $\Sigma_i :=$ localMine ($M$);
14. construct message set $M_i$ from $\Sigma_i$;
15. send $M_i$ to the coordinator;
```

Figure 4: Algorithm DMine

<u>*Message construction*</u> (lines 14–15). For each GPAR $R(x,y)$: $Q(x,y) \Rightarrow q(x,y)$, its *local confidence* conf is computed: (1) $\mathsf{supp}(R, F_i)$ and $\mathsf{supp}(Q, F_i)$ count nodes in $P_q(x, F_i)$ and C_i that match x in $R(x,y)$ and $Q(x,y)$, respectively; and (2) $\mathsf{supp}(Q\bar{q}, F_i) = \|Q(x, F_i) \cap P_{\bar{q}}(x, F_i)\|$. Then conf contains $\mathsf{supp}(R, F_i)$, $\mathsf{supp}(Q\bar{q}, F_i)$, $\mathsf{supp}(q, F_i)$ and $\mathsf{supp}(\bar{q}(x, F_i))$; where $\mathsf{supp}(q, F_i)$ and $\mathsf{supp}(\bar{q}, F_i)$ values are from the first round. A Boolean flag is also set to indicate whether R can be extended by checking whether there exists a center node v_x that has edges at $r+1$ hops from v_x. Message M_i includes $<R, \mathsf{conf}, \mathsf{flag}>$ for each R, and is sent to S_c.

<u>*Message assembling*</u> (lines 4-7). Upon receiving M_i from each S_i, coordinator S_c does the following. (1) It groups automorphic GPARs from all M_i. (2) For each group of $m_i = <R, \mathsf{conf}_i, \mathsf{flag}_i>$ that refers to the same (automorphic) R, it assembles $\mathsf{conf}(R)$ into a single $m = <R, \mathsf{conf}(R,G), \mathsf{flag}>$, where (a) $\mathsf{conf}(R,G) = \frac{\sum \mathsf{supp}(R,F_i) \sum \mathsf{supp}(\bar{q},F_i)}{\sum \mathsf{supp}(Q\bar{q},F_i) \sum \mathsf{supp}(q,F_i)}$; and (b) flag is the disjunction of all flag_i, for $i \in [1, n-1]$. This suffices since by the partitioning of graph G, nodes accounted for local support in F_i are disjoint from those in F_j if $i \neq j$; hence $\mathsf{conf}(R)$ can be directly assembled from local conf from F_i. Similarly, $\mathsf{supp}(R, G) = \sum_{i \in [1, n-1]} \mathsf{supp}(R, F_i)$. For each GPAR R, if $\mathsf{supp}(R, G) \geq \sigma$, it is added to ΔE and Σ.

<u>*Incremental diversification*</u> (lines 8-9). Next, DMine incrementally updates L_k by invoking procedure incDiv. It uses a max priority Queue of size $\lceil \frac{k}{2} \rceil$, where (1) each element in Queue is a pair of GPARs, and (2) all GPAR pairs in Queue are pairwise disjoint. In round r, starting from Queue of top-k diversified GPARs with radius at most $r-1$, DMine improves Queue by incorporating pairs of GPARs from ΔE, with radius r. (1) If Queue contains less than $\lceil \frac{k}{2} \rceil$ GPARs pairs, incDiv iteratively selects two distinct GPARs R and R' from ΔE that maximize a revised diversification function:

$$F'(R, R') = \frac{1-\lambda}{N(k-1)}(\mathsf{conf}(R) + \mathsf{conf}(R')) + \frac{2\lambda}{k-1}\mathsf{diff}(R, R').$$

and insert (R, R') into Queue, until $|\mathsf{Queue}| = \lceil \frac{k}{2} \rceil$. It bookkeeps each pair (R, R') and $F'(R, R')$. (2) If $|\mathsf{Queue}| = \lceil \frac{k}{2} \rceil$, for each new GPAR $R \in \Delta E$ (not in any pair of Queue) and $R' \in \Sigma$, it incrementally computes and adds a new pair $(R, R') \in \Delta E \times \Sigma$ that maximizes $F'(R, R')$ to Queue. This ensures that a pair (R_1, R_2) with minimum $F'(R_1, R_2)$ is replaced by (R, R'), if $F'(R_1, R_2) < F'(R, R')$.

After all GPAR pairs are processed, incDiv inserts R and R' into L_k, for each GPARs pairs $(R, R') \in$ Queue.

Message generation at S_c (lines 10-11). DMine next selects promising GPARs for further parallel extension at the workers. These include $R \in \Delta E$ that satisfy two conditions: (1) $\mathsf{supp}(R, G) \geq \sigma$, since by the anti-monotonic property of support, if $\mathsf{supp}(R, G) < \sigma$, then any extension of R cannot have support no less than σ; and (2) R is "Extendable", *i.e.,* flag = true in <R, conf, flag>. It includes such R in M, and posts M to all workers in the next round.

Example 9: Suppose that graph G_1 in Fig. 2 is distributed to two workers S_1 and S_2, where S_1 (resp. S_2) contains subgraphs induced by cust_1-cust_3 (resp. cust_4-cust_6) and their 2-hop neighborhoods in G_1. Let predicate q be visits(x, French restaurant), λ=0.5, d=2 and k=2. We demonstrate algorithm DMine using example GPARs R_5-R_8 (Fig. 3).

(1) Coordinator S_c sends q to all workers, and computes $\mathsf{supp}(q, G_1) = 5$ (cust_1-cust_4, cust_6), $\mathsf{supp}(\bar{q}, G_1) = 1$ (cust_5).

(2) In round 1, R_5 (among others) is generated at S_1 from 1-hop neighbors of cust_1-cust_3, which are matches in $q(x, G_1)$ (Fig. 3). At S_2, R_5 and R_6 are generated by expanding cust_4 and cust_6. Local messages M_i from S_i include the following:

site	message	GPAR	$R(x, G_1)$	$Q\bar{q}(x, y)$	flag
S_1	M_1	R_5	cust_1-cust_3	$\emptyset$	T
S2	M_2	R_5	cust_4	cust_5	T
		R_6	cust_4,cust_6	cust_5	T
S_c	M	R_5	cust_1-cust_4	cust_5	T
	M	R_6	cust_4,cust_6	cust_5	T

(3) Coordinator S_c assembles M_1 and M_2, and builds ΔE including $\{R_5, R_6\}$. It computes $\mathsf{conf}(R_5) = 0.8$, $\mathsf{conf}(R_6) = 0.4$, $\mathsf{diff}(R_5, R_6) = 0.8$. It updates $L_k = \{R_5, R_6\}$, with $F'(R_5, R_6) = 0.5 * \frac{1.2}{5} + 1 * 0.8 = 0.92$. It includes R_5 and R_6 in message M (the table above), and posts it to S_1 and S_2.

(4) In round 2, R_5 is extended to R_7 and R_1 at S_1 and S_2, and R_6 to R_8 at S_2 (Fig. 3); the messages include:

site	message	GPAR	$R(x, G_1)$	$Q\bar{q}(x, y)$	flag
S_1	M_1	R_7, R_1	cust_1-cust_3	$\emptyset$	F
S2	M_2	R_7	$\emptyset$	cust_5	F
		R_8	cust_6	cust_5	F

(5) Given these, coordinator S_c assembles the messages and computes $\mathsf{conf}(R_7)$=0.6, $\mathsf{conf}(R_8)$=0.2 and $\mathsf{diff}(R_7, R_8)$=1. DMine computes $F'(R_7, R_8) = 0.5 * \frac{0.8}{5} + 1 * 1 = 1.08 > F'(R_5, R_6) = 0.92$. Hence, it replaces (R_5, R_6) with (R_7, R_8) and updates L_k to be $\{R_7, R_8\}$. As R_7 and R_8 are marked as "not extendable" at radius 2 (since d=2), DMine returns $\{R_7, R_8\}$ as top-2 diversified GPARs, in total 2 rounds. $\square$

Message reduction. By maintaining additional information, DMine reduces the sizes of Σ, M and M_i. The idea is to test whether an upper bound of marginal benefit for any GPAR pairs can improve the minimum F'-value of L_k.

In each round r, incDiv filters non-promising GPARs from Σ and ΔE that cannot make top-k even after new GPARs are discovered. It keeps track of (1) a value F'_m=min $F'(R_1, R_2)$ for all pairs (R_1, R_2) in L_k, (2) for each GPAR R_j in ΔE, an estimated maximum confidence $\mathsf{Uconf}^+(R_j, G)$ for all the possible GPARs extended from R_j, and (3) $\mathsf{conf}(R, G)$ for each GPAR R in Σ. Here $\mathsf{Uconf}^+(R_j, G)$ is estimated as follows. (a) Each S_i computes $\mathsf{Usupp}_i(R_j, F_i)$ as the number of matches of x in $R_j(x, F_i)$ that connect to a center node in F_i at hop $r + 1$ ($r \leq d - 1$). (b) Then $\mathsf{Uconf}^+(R_j)$ is assembled at S_c as $\frac{\sum \mathsf{Usupp}_i(R_j, F_i)\mathsf{supp}(\bar{q}, G)}{1 * \mathsf{supp}(q, G)}$. Denote the maximum $\mathsf{Uconf}^+(R_j, G)$ for $R_j \in \Delta E$ as $\max \mathsf{Uconf}^+(\Delta E)$, and the maximum $\mathsf{conf}(R, G)$ for $R \in \Sigma$ as $\max \mathsf{conf}(\Sigma)$. Then incDiv reduces Σ and M based on the reduction rules below.

Lemma 3: ***[Reduction rules]****: (1) A* GPAR $R \in \Sigma$ *cannot contribute to* L_k *if* $\frac{1-\lambda}{N(k-1)}(\mathsf{conf}(R, G) + \max \mathsf{Uconf}^+(\Delta E)) + \frac{2\lambda}{k-1} \leq F'_m$. *(2) Extending a* GPAR $R_j \in \Delta E$ *does not contribute to* L_k *if either (a)* R_j *is not extendable, or (b)* $\frac{1-\lambda}{N(k-1)}(\mathsf{Uconf}^+(R_j, G) + \max \mathsf{conf}(\Sigma)) + \frac{2\lambda}{k-1} \leq F'_m$. $\square$

For the correctness of the rules, observe the following. (1) For each $R \in \Sigma$, $\mathsf{conf}(R) + \max \mathsf{Uconf}^+(\Delta E) + 1$ is an upper bound for its maximum possible increment to the F'-value of L_k; similarly for any R_j from ΔE. (2) If GPAR R does not contribute to L_k, then any GPARs extended from R do not contribute to L_k. Indeed, (a) upper bounds $\mathsf{Uconf}(R)$, $\mathsf{Usupp}_i(R)$, and $\mathsf{Uconf}^+(R)$ are *anti-monotonic* with any R' expanded of R, and (b) $\max \mathsf{Uconf}^+(\Delta E)$ and $\max \mathsf{conf}(\Sigma)$ are *monotonically decreasing*, while F'_m is *monotonically increasing* with the increase of rounds. Hence R can be safely removed from Σ, ΔE or M_i. Note that the removal of GPARs from Σ benefit the reduction of ΔE with smaller $\max \mathsf{conf}(\Sigma)$), and vice versa. DMine repeatedly applies the rules until no GPARs can be reduced from Σ and ΔE.

Automorphism checking. To reduce redundant GPARs, DMine checks whether GPARs in ΔE are automorphic at coordinator S_c (line 6) and locally at each S_i (localMine). It is costly to conduct pairwise automorphism tests on all GPARs in ΔE, since it is equivalent to graph isomorphism.

To reduce the cost, we use *bisimulation* [12]. A graph pattern P_{R_1} is *bisimilar* to P_{R_2} if there exists a binary relation O_b on nodes of P_{R_1} and P_{R_2} such that (a) for all nodes u_1 in P_{R_1}, there exists a node u_2 in P_{R_2} with the same label such that $(u_1, u_2) \in O_b$, and vice versa for all nodes in P_{R_2}; and (b) for all edges (u_1, u_1') in P_{R_1}, there exists an edge (u_2, u_2') in P_{R_2} with the same label such that $(u_1', u_2') \in O_b$; and vice versa for all edges in P_{R_2}. The connection between bisimulation and automorphism is stated as follows.

Lemma 4: *If graph pattern* P_{R_1} *is not bisimilar to* P_{R_2}*, then* R_1 *is not an automorphism of* R_2*,* $\square$

Hence, for a pair R_1 and R_2 of GPARs, DMine first checks whether P_{R_1} is bisimilar to P_{R_2}. It checks automorphism between R_1 and R_2 *only if* so. It takes $O(|\Delta E|^2)$ time to check pairwise bisimilarity O_b for all GPARs in ΔE [12]. Moreover, O_b can be incrementally maintained when new GPARs are added [40]. These allow us to use efficient (incremental) bisimulation tests instead of automorphism tests.

Trivial GPARs. DMine detects trivial GPARs $R(x, y)$: $Q(x, y) \Rightarrow q(x, y)$ at S_c as follows: (1) if $\mathsf{supp}(q, G)$ is 0, it returns $\emptyset$ to indicate that no interesting GPARs exist; and (2) if an extension leads to $\mathsf{supp}(Q\bar{q}) = 0$, *i.e.,* no match in $Q(x, G)$ violates $q(x, y)$, S_c removes R from ΔE and Σ.

Analyses. DMine returns a set L_k of k diversified GPARs with approximation ratio 2 (line 12), for the following reasons. (1) Parallel generation of GPARs finds all candidate GPARs within radius d. This is due to the *data locality* of subgraph isomorphism: for any node v_x in G, $v_x \in P_R(x, G)$ iff $v_x \in P_R(x, G_d(v_x))$ for any GPAR R of radius at most d at x. That is, we can decide whether v_x matches x via R by checking the d-neighbor of v_x locally at a fragment F_i. (2) Procedure incDiv updates L_k following the greedy strategy of [19], with approximation ratio 2. This is verified by approximation-preserving reduction to the max-sum dispersion problem, which maximizes the sum of pairwise distance for a set of data points and has approximation ratio 2 [19]. The reduction maps each GPAR to a data point, and sets the distance between two GPARs R and R' as $F'(R, R')$.

For time complexity, observe that in each round, the cost consists of (a) local parallel generation time T_1 of candidate GPARs, determined by $|F_i|$, M and M_i; and (b) total assembling and incremental maintenance cost T_2 of L_k at S_c, dominated by $|\Sigma|$, k and $|M_i|$. The cost of message reduction (by applying Lemma 3) takes in total $O(d|\Sigma|)$ time, where in each round, it takes a linear scan of ΔE and Σ to identify redundant GPARs. Note that $\sum_{i\in[1,n-1]} |M_i| \leq |\Delta E| \leq |\Sigma|$, $|M| \leq |\Sigma|$, and $|F_i|$ is roughly $|G|/n$ by our partitioning strategy. Hence T_1 and T_2 are functions of $|G|/n$, k and $|\Sigma|$.

This completes the proof of Theorem 2.

Remarks. Algorithm DMine can be easily adapted to the following two cases. (1) When a set of predicates instead of a single $q(x, y)$ is given, it groups the predicates and iteratively mines GPARs for each distinct $q(x, y)$. (2) When no specific $q(x, y)$ is given, it first collects a set of predicates of interests (*e.g.,* most frequent edges, or with user specified label q), and then mines GPARs for the predicate set as in (1).

5. IDENTIFYING CUSTOMERS

We study how to identify potential customers with GPARs.

5.1 The Entity Identification Problem

Consider a set Σ of GPARs *pertaining to the same* $q(x, y)$, *i.e.,* their consequents are the same event $q(x, y)$. We define *the set of entities* identified by Σ in a (social) graph G with confidence η, denoted by $\Sigma(x, G, \eta)$, as follows:

$$\{v_x \mid v_x \in Q(x, G), Q(x, y) \Rightarrow q(x, y) \in \Sigma, \mathsf{conf}(R, G) \geq \eta\}$$

Problem. We study the *entity identification problem* (EIP):

- *Input*: A set Σ of GPARs pertaining to the same $q(x, y)$, a confidence bound $\eta > 0$, and a graph G.
- *Output*: $\Sigma(x, G, \eta)$.

It is to find potential customers x of y in G identified by *at least one* GPAR in Σ, with confidence of at least η.

Intractability. The decision problem of EIP is to determine, given Σ, G and η, whether $\Sigma(x, G, \eta) \neq \emptyset$. It is equivalent to decide whether there exists a GPAR $R \in \Sigma$ such that $\mathsf{conf}(R, G) \geq \eta$. The problem is nontrivial, as it embeds the subgraph isomorphism problem, which is NP-hard.

Proposition 5: *The decision problem for* EIP *is* NP*-hard, even when* Σ *consists of a single* GPAR. □

A naive way to compute $\Sigma(x, G, \eta)$ is as follows. For each $R(x, y)$: $Q(x, y) \Rightarrow q(x, y)$ in Σ, (a) enumerate all matches of $Q\bar{q}$ and P_R in G by using an algorithm for subgraph isomorphism, *e.g.,* VF2 [10]; (b) compute $\mathsf{supp}(q, G)$ and $\mathsf{supp}(\bar{q}, G)$ once in G; then based on the findings, (c) identify those R with $\mathsf{conf}(R, G) \geq \eta$, and return matches of x by these GPARs. This is cost-prohibitive (*e.g.,* takes $O(|G|!|G||\Sigma|)$ time using VF2 [10]) in real-life social graphs G, which often have billions of nodes and edges [21]. It is thus not practical to simply apply graph pattern matching algorithms to EIP over large G.

One might think that parallelization would solve the problem. However, parallelization is *not always effective*.

Parallel scalability. To characterize the effectiveness of parallelization, we formalize parallel scalability following [30]. Consider a problem A posed on a graph G. We denote by $t(|A|, |G|)$ the worst-case running time of a *sequential algorithm* for solving A on G. For a parallel algorithm, we denote by $T(|A|, |G|, n)$ the time taken by the algorithm for solving A on G by using n processors. Here we assume $n \ll |G|$, *i.e.,* the number of processors does not exceed the size of the graph; this typically holds in practice since G has billions of nodes and edges, much larger than n.

We say that the algorithm is *parallel scalable* if

$$T(|A|, |G|, n) = O(t(|A|, |G|)/n) + (n|A|)^{O(1)}.$$

That is, the parallel algorithm achieves a polynomial reduction in sequential running time, plus a "bookkeeping" cost $O((n|A|)^l)$ for a constant l that is *independent of* $|G|$.

Obviously, if the algorithm is parallel scalable, then for a given G, it *guarantees* that the more processors are used, the less time it takes to solve A on G. It allows us to process big graphs by adding processors when needed. If an algorithm is not parallel scalable, we may not get reasonable response time *no matter how many* processors are used.

We say that problem A is *parallel scalable* if there exists a parallel scalable algorithm for it. Unfortunately, parallel scalability is *not* warranted for all problems, *e.g.,* it is beyond reach for graph simulation [15]. The good news is as follows.

Theorem 6: EIP *is parallel scalable.* □

As a proof, we outline a parallel algorithm for EIP, denoted by Match_c. Given Σ, $G = (V, E, L)$, η and a positive integer n, it computes $\Sigma(x, G, \eta)$ by using n processors. Note that Match_c is *exact*: it computes precisely $\Sigma(x, G, \eta)$.

To present Match_c, we use the following notations. (a) We use d to denote *the maximum radius* of $R(x, y)$ at node x, for all GPARs R in Σ. (b) For a node $v_x \in V$, $G_d(v_x)$ is *the d-neighbor* of v_x in G (see Section 4.2). (c) We denote by L the set of all *candidates* v_x of x, *i.e.,* nodes in G that satisfy the search condition of x in $q(x, y)$.

Algorithm. Match_c capitalizes on the data locality of subgraph isomorphism (see Section 4.2). It works as follows.

(1) *Partitioning.* It divides G into n fragments $\mathcal{F} = (F_1, \ldots, F_n)$ in the same way as algorithm DMine (Section 4.2), such that F_i's have roughly even size, and $G_d(v_x)$ is contained in one F_i for each $v_x \in L$. This is done in parallel. In particular, $G_d(v_x)$ can be constructed in parallel by revising BFS (breadth-first search), within d hopes from v_x. Each fragment F_i is assigned to a processor S_i for $i \in [1, n]$.

(2) *Matching.* All processors S_i compute local matches in F_i *in parallel*. For each candidate $v_x \in L$ that resides in F_i, and for each GPAR $R(x, y)$: $Q(x, y) \Rightarrow q(x, y)$ in Σ, S_i checks whether v_x is in $P_R(x, G_d(v_x))$, $P_Q(x, G_d(v_x))$ and $P_q(x, G_d(v_x))$, and whether v_x has an outlink labeled q.

(3) *Assembling.* Compute $\mathsf{conf}(R, G)$ for each R in Σ by assembling the partial results of (2) above. This is also done *in parallel*: first partition L into n fragments; then each processor operates on a fragment and computes partial sup-

port. These partial results are then collected to compute $\mathsf{conf}(R, G)$. Finally, output those v_x when there exists a GPAR R such that $v_x \in P_R(x, G)$ and $\mathsf{conf}(R, G) \geq \eta$.

Analysis. To show that Match_c is parallel scalable, observe the following. (1) Step 1 is in $O(|L||G_d^m|/n)$ time, since BFS is in $O(|G_d^m|)$ time, where G_d^m is the largest d-neighbor for all $v_x \in L$. (2) Step 2 takes $O(t(|G_d^m|, |\Sigma|)|L|/n)$ time, where $t(|G_d^m|, |\Sigma|)$ is the worst-case sequential time for processing a candidate v_x. (3) Step 3 takes $O(|L||\Sigma|/n)$ time. (4) By $|L| \leq |V|$, steps 1 and 2 take much less time than $t(|G|, |\Sigma|)$, since $t(,)$ is an exponential function by Proposition 5, unless P = NP. (5) In practice, $t(|G_d^m|, |\Sigma|)|L| \ll t(|G|, |\Sigma|)$ since $t(,)$ is exponential and G_d^m is much smaller than G. Indeed, (a) in the real world, graph patterns in GPARs are typically small, and hence so is the radius d; as argued in Section 4.2, $G_d(v_x)$ is thus often small. Putting these together, we have that the parallel cost $T(|G|, |\Sigma|, n) < O(t(|G|, |\Sigma|)/n)$, and better still, the larger n is, the smaller $T(|G|, |\Sigma|, n)$ is.

Remark. Algorithm DMine (Section 4.2) takes $t(|A|/n, k)$ time and is parallel scalable if the problem size $|A|$ is measured as $|G|+|Q|+|\Sigma|$ [29]. Indeed, if one wants all candidate GPARs R with $\mathsf{supp}(R, G) \geq \sigma$, then $|\Sigma|$ is the size of the output, and $|\Sigma|$ is not large (due to small d and large σ).

5.2 Optimization Strategies

Algorithm Match_c just aims to show the parallel scalability of EIP. Its cost is dominated by step 2 for matching via subgraph isomorphism. To reduce the cost, we develop algorithm Match that improves Match_c by incorporating the following optimization techniques. To simplify the discussion, we start with a single GPAR $R(x, y) : Q(x, y) \Rightarrow q(x, y)$.

Early termination. For each candidate $v_x \in L$ that resides in fragment F_i, we check whether *there exists* a match G_x of P_R in which v_x matches x. As soon as one G_x is verified a match of P_R, we include v_x in $P_R(x, F_i)$, *without* enumerating *all* matches of P_R at v_x. This is done locally at F_i: by our partitioning strategy, $G_d(v_x)$ is contained in F_i.

Guided search. To identify G_x at v_x, Match starts with pair (x, v_x) as a partial match m, and iteratively grows m with new pairs (u, v) for $u \in P_R$ and $v \in G_d(v_x)$ until a complete match is identified, *i.e.,* m covers all the nodes in P_R. A complete m induces a subgraph G_x. It is in PTIME to verify whether m is an isomorphism from P_R to G_x.

To grow m, Match performs *guided search* based on *k-hop neighborhood sketch*. For each node v in G, a k-hop sketch $K(v)$ is a list $\{(1, D_1), \ldots, (k, D_k)\}$, where D_i denotes the distribution of the node labels and their frequency at i hop of v. Given a pair (u, v) newly added to m and a pattern edge (u, u') in Q, Match picks "the best neighbor" v' of v such that the pair (u', v') has a high possibility to make a match. This is decided by assigning a score $f(u', v')$ as $\sum_{i\in[1,k]}(D_i - D'_i)$, where $D'_i \in K(u')$, $D_i \in K(v')$, and $D_i - D'_i$ is the total frequency difference for each label in D_i. Indeed, (1) v' does not match u' if for some i, $D_i - D'_i < 0$; and (2) the larger the difference is, the more likely v' matches u'. If (u', v') does not lead to a complete m, Match backtracks and picks v'' with the next best score $r(u', v'')$.

Example 10: Consider GPAR R_1 of Fig. 1. For its designated node x, the 2-hop neighborhood sketch $L_2(x)$ in P_{R1} contains pair (1, D_1={(city,1), (cust,1), (French Restaurant, 4)}) and (2, D_2={(city,1),(cust,1),(French Restaurant, 4)}).

Given R_1 and G_1 of Fig. 2, Match identifies $P_{R_1}(x, G_1)$ as follows. (1) It finds $P_{q_1}(x, G)$=$\{\mathsf{cust}_1\text{-}\mathsf{cust}_4, \mathsf{cust}_6\}$, while cust_5 accounts for $\mathsf{supp}(\bar{q}_1, G_1)$. (2) It computes $P_{R_1}(x, G_1)$ by verifying candidates v_x from $P_q(x, G_1)$, and calculates $f(x, v_x)$ in G_1, *e.g.,* $L_2(\mathsf{cust}_2)$ = {(1, D_1 = {(city, 1), (cust, 2), (French Restaurant, 8)}), (2, D_2={(city, 1), (cust, 2), (French Restaurant, 8)})}. Hence $f(x, \mathsf{cust}_2) = 5 + 5 = 10$. Match then ranks candidates cust_2, cust_1, cust_3, cust_4, where cust_6 is filtered due to mismatched sketches. (2) At cust_2, Match starts from (x, cust_2), and extends to (x', cust_3) since $f(x', \mathsf{cust}_3)$ is the highest. It continues to add pairs (city, NewYork), (French Restaurant, LeBernardin) and three pairs for French Restaurant[3]. This completes the match, and cust_2 is verified a match. (3) Similarly, Match verifies cust_1 and cust_3, and finds $P_{R_1}(x, G_1) = \{\mathsf{cust}_1, \mathsf{cust}_2, \mathsf{cust}_3\}$.

Given $P_{R_1}(x, G_1)$, Match only needs to verify cust_5 for Q_1 in R_1; it finds $Q_1(x, G_1) = P_{R_1}(x, G_1) \cup \{\mathsf{cust}_5\}$. It also finds $\mathsf{supp}(q, G_1) = 5$ (cust_1–cust_4, cust_6), $\mathsf{supp}(\bar{q}, G_1) = 1$ (cust_5), and computes $\mathsf{conf}(R_1) = \frac{3*1}{1*5} = 0.6$. □

Algorithm Match. Given a set Σ of GPARs, Match revises step (2) of Match_c by checking whether v_x matches x via guided search and early termination; it reduces redundant computation for multiple GPARs by extracting common subpatterns of GPARs in Σ [32]. It remains parallel scalable following the same complexity analysis for Match_c.

6. EXPERIMENTAL STUDY

Using real-life and synthetic graphs, we conducted three sets of experiments to evaluate (1) the scalability of algorithm DMine, (2) the effectiveness of DMine for discovering interesting GPARs, and (3) the scalability of algorithm Match for identifying potential customers in large graphs.

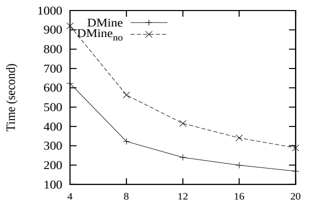
Experimental setting. We used two real-life graphs: (a) *Pokec* [3], a social network with 1.63 million nodes of 269 different types, and 30.6 million edges of 11 types, such as *follow*, *like*; and (b) *Google+* [20], a social graph with 4 million entities of 5 types and 53.5 million links of 5 types.

We also designed a generator for synthetic graphs $G = (V, E, L)$, controlled by the numbers of nodes $|V|$ (up to 50 million) and edges $|E|$ (up to 100 million), with L drawn from an alphabet $\mathcal{L}$ of 100 labels.

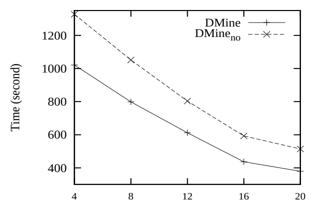
Pattern generator. To evaluate Match, we generated GPARs R controlled by the numbers $|V_p|$ and $|E_p|$ of nodes and edges in P_R, respectively. (1) We found 48 meaningful GPARs on each of *Pokec* and *Google+*, with labels drawn from their data (domain, social groups). (2) For synthetic graphs, we also generated 24 GPARs with labels drawn from $\mathcal{L}$. We denote the size of a GPAR R as $|R|$= $(|V_p|, |E_p|)$.

Algorithms. We implemented the following, all in Java. (1) Algorithm DMine, compared with (a) $\mathsf{DMine}_{\mathsf{no}}$, its counterpart without optimization (incremental, reductions and bisimilarity checking), and (b) GRAMI [13], an open source frequent subgraph mining tool [1]. Since GRAMI uses *a single machine* [1], we only compared the interestingness of patterns found by GRAMI with GPARs discovered by DMine. (2) Algorithm Match, compared with (a) Match_c (Section 5.1), (b) disVF2, a parallel implementation of VF2 for EIP, and (c) Match_s, Match by using the method of [38] instead of VF2.

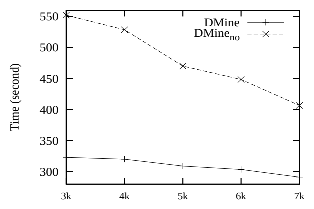
Fragmentation and distribution. We revised the algorithm of [36] to evenly partition graph G into n fragments (see Section 4.2). We find that the gap between maximum and



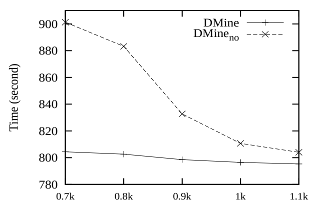
(a) DMine: Varying n (Pokec)



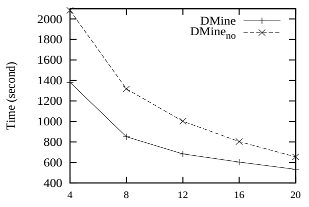
(b) DMine: Varying n (Google+)



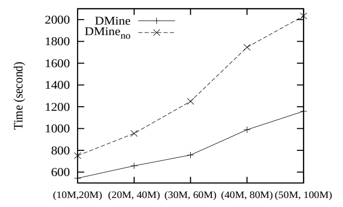
(c) DMine: Varying σ (Pokec)



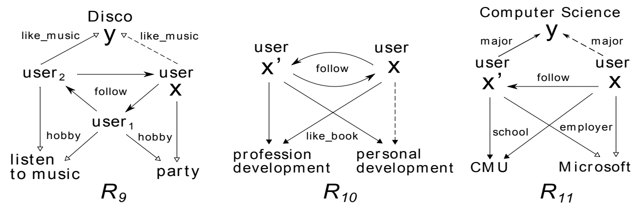
(d) DMine: Varying σ (Google+)



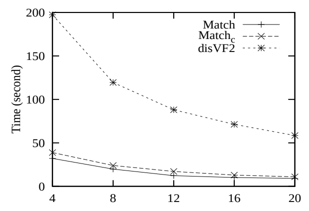
(e) DMine: Varying n (Synthetic)



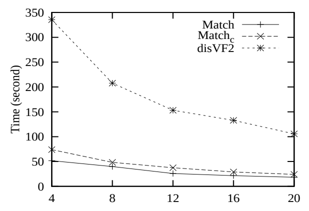
(f) DMine: Varying $|G|$ (Synthetic)



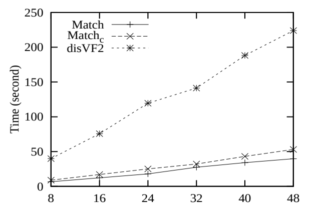
(g) real-life GPARs: case study



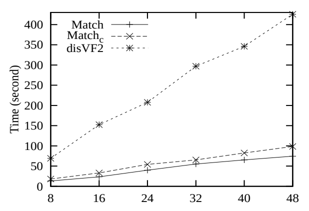
(h) Match: Varying n (Pokec)



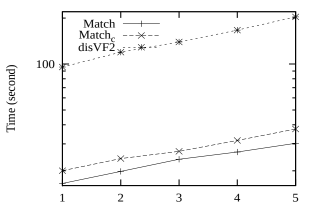
(i) Match: Varying n (Google+)



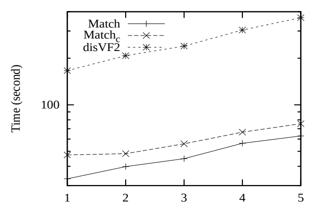
(j) Match: Varying $\|\Sigma\|$ (Pokec)



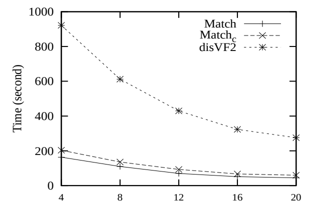
(k) Match: Varying $\|\Sigma\|$ (Google+)



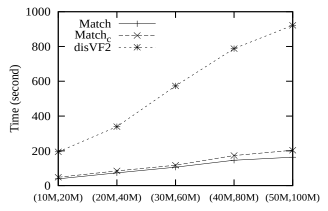
(l) Match: Varying d (Pokec)



(m) Match: Varying d (Google+)



(n) Match: Varying n (Synthetic)



(o) Match: Varying $|G|$ (Synthetic)

Figure 5: Performance evaluation

minimum time spent on different fragments by DMine is at most 14.4% (resp. 8.8%) of the time for processing fragments of *Pokec* (resp. *Google+*), and at most 6.0% (resp. 5.2%) of the time for identifying matches by Match. These indicate that the impact of skew from partitioning is fairly small.

We deployed the algorithms and n fragments on $n \in [4, 20]$ Amazon EC2 M3 instances, each has 2.6GHz 2vcpu with 7.5G memory, and 32GB SSD storage. Each experiment was run 5 times and the average is reported here.

Experimental results. We next report our findings. We fixed parameter $\lambda = 0.5$ for diversification in Exp-1.

Exp-1: Scalability of DMine. We first evaluated the scalability of DMine vs. DMine$_{no}$. We used $k = 10$, and found that different k had little impact. We found that GPARs mined in real-life graphs with infrequent edge labels usually denote unrelated facts. Hence we used 20 most frequent edge patterns, *i.e.,* graph patterns consisting of a single edge (with both node and edge labels), to grow GPARs in *Pokec*. We used all 5 types of edges in *Google+*.

Varying n. Fixing radius $d = 2$ and support $\sigma = 5000$ (500 for *Google+*), we varied the number n of processors from 4 to 20. The algorithms generated up to 300 patterns to be verified. As shown in Fig. 5(a) (resp. Fig. 5(b)), (1) DMine scales well with the increase of processors: the improvement is 3.7 (resp. 2.69) times when n increases from 4 to 20; and (2) it is on average 1.67 (1.37) times faster than DMine$_{no}$; this verifies that our optimization strategies effectively reduce confidence checking time, which is a major bottleneck in DMine$_{no}$. With 20 processors, DMine takes 168.3 (resp. 379) seconds on *Pokec* (resp. *Google+*).

Varying σ. Fixing $d = 2$ and $n = 4$, we varied σ from $3K$ to $7K$ (resp. 700 to 1100) on *Pokec* (resp. *Google+*). Figures 5(c) and 5(d) tell us the following. (1) All algorithms takes longer with smaller σ, because more patterns satisfy the support constraint and are checked. (2) DMine outperforms DMine$_{no}$ in all cases. Moreover, it is less sensitive to the increment of σ. This is because DMine checks much less patterns than DMine$_{no}$ due to its filtering strategy.

Using large synthetic graphs of size up to $(50M, 100M)$, we evaluated the impact of n, the size of G and radius d.

Varying n (Synthetic). Fixing $|G| = (10M, 20M)$, $d = 2$ and $\sigma = 100$, we varied n from 4 to 20. The results (Fig. 5(e)) are consistent with Figures 5(a) and 5(b). DMine takes 533.2 seconds over synthetic G with 20 processors.

Varying $|G|$ (Synthetic). Fixing $n = 16$, $d = 2$ and $\sigma = 100$, we varied $|G|$ from $(10M, 20M)$ to $(50M, 100M)$. As shown in Fig. 5(f), (1) both algorithms take longer on larger graphs; and (2) DMine outperforms DMine$_{\text{no}}$ by 1.76 times, verifying the effectiveness of our optimization methods.

Varying d. Fixing $n = 16$, $|G| = (50M, 100M)$ and $\sigma = 100$, we varied d from 1 to 3. We find that DMine and DMine$_{\text{no}}$ take longer over larger d (not shown), as expected. However, DMine is less sensitive to d, since its optimization strategies reduces GPAR candidates and checking time.

Exp-2: Effectiveness of DMine. We manually examined GPARs discovered by DMine from *Pokec* and *Google+*. Three GPARs are shown in Fig. 5(g), with support above 100:

(1) R_9 (*Pokec*): *if x follows* user$_1$*,* user$_1$ *follows* user$_2$*,* user$_2$ *follows x,* user$_1$ *and* user$_2$ *share the hobby to* listen to music*, x and* user$_1$ *share the hobby of* party*, and if* user$_2$ *likes* Disco *music, then x likes* Disco. This suggests regularity between types of music people like and their friends' hobbies.

(2) R_{10} (*Pokec*): *if x and x' follow each other and both like books of* profession development*, and if x' likes books about* personal development*, then so does x.* This suggests that potential customers x favor books liked by their friends.

(3) R_{11} (*Google+*): *if x follows x', both x and x' went to* CMU*, both x and x' are employees of* Microsoft*, and if x' was majored in* CS*, then x was also likely majored in* CS. This indicates a social pattern between Microsoft employees and CMU computer science students.

We also found that most patterns mined by GRAMI are cycles of users. These patterns, although quite frequent, reveals little insight about entity associations.

GPARs *with different metrics.* We also evaluated different confidence metrics for GPARs (Section 3). Given a GPAR R, we define its (1) PCA confidence [17] $\mathsf{PCAconf}(R, G)$ as $\frac{\mathsf{supp}(R,G)}{\mathsf{supp}(Q\bar{q},G)}$, and (2) image-based $\mathsf{Iconf}(R, G)$ by replacing $\mathsf{supp}(\cdot, G)$ in $\mathsf{conf}(R, G)$ with the image-based support [7].

We evaluated prediction precision of these metrics for social networks following [17]. We partitioned *Pokec* into two fragments F_1 (as training data) and F_2 (for cross validation), and selected 5 predicates as in Exp-1 from F_1. We set $\lambda = 0$ to focus on the relevance of GPARs, and mined top 10, 30 and 60 GPARs from F_1 with highest conf, PCAconf and Iconf, respectively. We evaluate the precision for each GPAR R as $\mathsf{prec}(R)=\frac{\mathsf{supp}(R,F_2)}{\mathsf{supp}(Q,F_2)}$, indicating correctly predicted customers in F_2, constrained by GPARs mined from F_1.

	top 10	top 30	top 60
PCAconf	0.276	0.280	0.277
Iconf	0.267	0.273	0.265
conf	0.423	0.388	0.381

As shown in the table above, (1) DMine is able to identify GPARs that "predict" predicates with average precision up to 42.3%, and (2) GPARs ranked by our conf metric provides better prediction precision than PCAconf and Iconf.

Exp-3: Scalability of Match. Finally, we evaluated (1) the scalability of Match with the number n of processors, and the impacts of (2) the number $\|\Sigma\|$ of GPARs in Σ, (3) the maximum radius d of GPARs in Σ, and (4) the size $|G|$ of graphs. We started with real-life graphs and fixed $\eta = 1.5$.

Varying n. Fixing $\|\Sigma\| = 24$, $|R| = (5, 8)$ and $d = 2$, we varied n from 4 to 20. Figures 5(h) and 5(i) report the results on *Pokec* and *Google+*, respectively, which tell us the following.

(1) Match, Match$_c$ and Match$_s$ allow a high degree of parallelism. For instance, Match is 3.52 (resp. 3.54) times faster when n increases from 4 to 20 on *Pokec* (resp. *Google+*). This is consistent with Theorem 6. The algorithms are efficient. In particular, Match takes 9.1 seconds on social graph *Pokec* with 20 processors, and it scales better than Match$_c$ and disVF2. We find that Match$_s$ and Match have very similar performance, and thus we report Match only.

(2) Our optimization strategies are effective. (a) Compared to disVF2, Match$_c$ and Match are 4.79 and 6.24 times faster on average, since for each GPAR $R : Q \Rightarrow q$, disVF2 invokes two isomorphic checks at each candidate v_x (one for P_R and one for $Q_{\bar{q}}$) vs. one by Match$_c$ and Match; this justifies *the need for new algorithms for* EIP instead of applying conventional pattern matching algorithms. (b) Match is 1.2 and 1.35 times times faster than Match$_c$ on *Pokec* and *Google+*, respectively, demonstrating the effectiveness of early termination and guided search, without enumerating all matches.

Varying $\|\Sigma\|$. Fixing $n = 8$ and $d = 2$, we varied $\|\Sigma\|$ from 8 to 48. As shown in Figures 5(j) and 5(k), (1) all algorithms take longer time with larger $\|\Sigma\|$, as expected; (2) Match is less sensitive to $\|\Sigma\|$ than Match$_c$ and disVF2; (3) the improvement of Match over the others is greater on larger Σ. These are because optimization by early termination and guided search works better for more GPARs in Σ.

Varying d. Fixing $n = 8$ and $\|\Sigma\| = 20$, we varied d from 1 to 5. As shown in Figures 5(l) and 5(m) (in *logarithmic scale*), all algorithms take longer time with larger d, since more nodes in the d-neighbors of candidates need to be visited. Nonetheless, Match and Match$_c$ are less sensitive to d than disVF2 due to their optimization techniques (data locality leveraged by Match$_c$, and early termination by Match).

Synthetic graphs. Using larger synthetic graphs, we evaluated the impact of n. Fixing $|G| = (50M, 100M)$, $d = 2$, $\eta = 1.5$ and $\|\Sigma\| = 24$, we varied n from 4 to 20. As shown in Fig. 5(n), the result is consistent with its counterparts on real-life graphs (Figures. 5(h) and 5(i)). The improvement for Match is 3.65 times when n increases from 4 to 20.

Fixing $n = 4$, $\|\Sigma\| = 24$, $\eta = 1.5$ and $d = 2$, we varied $|G|$ from $(10M, 20M)$ to $(50M, 100M)$. As shown in Fig. 5(o), (1) all the algorithms take longer on larger $|G|$, as expected; (2) Match performs the best, and is less sensitive to $|G|$ than the others; and (3) despite Proposition 5, Match is reasonably efficient: when $|G| = (50M, 100M)$, Match takes 163 seconds with 4 processors, while disVF2 takes 922 seconds.

Summary. We find the following. (1) It is not very expensive to mine diversified top-k GPARs in large social networks. For instance, DMine takes 533.2 seconds on graphs with $|G|$ = (10M,20M) by using 20 processors, when $k = 10$, $\sigma = 100$ and $d = 2$. (2) The number of candidate GPARs is not very large (up to 300), and hence DMine is "parallel scalable" (Section 5.1): it is 3.2 times faster on average when n increases from 4 to 20, on real-world social networks. (3) Moreover, discovered GPARs based on our conf metric predict more precise potential customers in social networks than its PCA and image-based counterparts. (4) Match is parallel scalable: it is 3.53 times faster on average when n increases from 4 to 20 over real-life social networks. (5) It is practical to apply GPARs to large graphs: on graphs with $|G| = (50M, 100M)$ and a set Σ of 24 GPARs, Match takes less than 45 seconds with 20 processors. (6) Our optimization strategies are effective: DMine outperforms DMine$_{no}$ by 1.52 times, and Match is 1.27 and 6.24 times faster than Match$_c$ and disVF2, respectively, on real-life graphs, on average.

7. CONCLUSION

We have proposed association rules with graph patterns (GPARs), from syntax, semantics to support and confidence metrics. We have studied DMP and EIP, for mining GPARs and for identifying potential customers with GPARs, respectively, from complexity to parallel (scalable) algorithms. Our experimental study has verified that while DMP and EIP are hard, it is feasible to discover and make practical use of GPARs. We contend that GPARs provide a promising tool for social media marketing, among other applications.

We are currently exploring real-life social graphs to experiment with. Another topic for future work is to extend GPARs by supporting graph patterns as consequent, and by allowing other matching semantics such as graph simulation.

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