Relationship Profiling over Social Networks: Reverse Smoothness from Similarity to Closeness

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Abstract

On social networks, while nodes bear rich attributes, we often lack the 'semantics' of why each link is formed– and thus we are missing the 'road signs' to navigate and organize the complex social universe. How to identify relationship semantics without labeled links? Founded on the prevalent *homophily* principle, we propose the novel problem of *Attribute-based Relationship Profiling* (ARP), to profile the closeness *w.r.t.* the underlying relationships (*e.g.*, schoolmate) between users based on their similarity in the corresponding attributes (*e.g.*, schools) and, as output, learn a set of *social affinity graphs*, where each link is weighted by its probabilities of carrying the relationships. As requirements, ARP should be *systematic* and *complete* to profile every link for every relationship– our challenges lie in effectively modeling homophily. We propose a novel *reverse smoothness principle* by observing that the similarity-closeness duality of homophily is consistent with the well-known *smoothness assumption* in graph-based semi-supervised learning– only the direction of inference is reversed. To realize smoothness over noisy social graphs, we further propose a novel holistic closeness modeling approach to capture 'high-order' smoothness by extending closeness from edges to paths. Extensive experiments on three real-world datasets demonstrate the efficacy of our proposed algorithm for ARP.

1 Introduction

While our social universe– like our social lives– is complex, they are critically missing 'road signs' to navigate. On general networks like Twitter and DBLP, the edges (*i.e.* links, connections) between nodes (*i.e.* users) are often *unlabeled*– without 'meanings'. Even on more personal networks like Facebook and LinkedIn– where we spend much time every day interacting with friends in our ego networks– our connections with and between friends are lacking the 'semantics', in terms of the underlying *relationships*, *e.g.*, schoolmate or colleague, resulting in cluttered social spaces and unorganized interactions. Such relationship semantics is crucial as 'road signs' to organize friends [7, 18, 5] and route information [2, 15, 27] in our social universe. Without labeled connections, can we automatically identify the underlying relationships? This paper aims at such *relationship profiling*, in an *unsupervised* manner, which is important for modeling social networks.

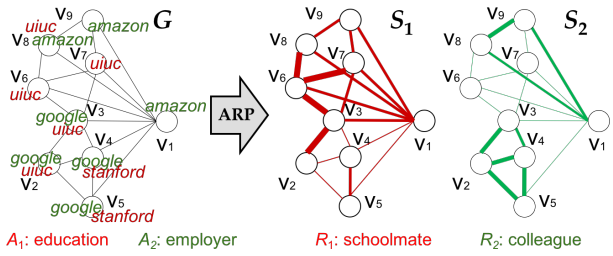
Without pre-defined relationships, what 'reasons' do we give as the semantics for each link? With the well-known phenomenon of *homophily* [12]– *i.e.*, *the tendency of individuals to stay close with similar others*, it is often the case that a connection between users is a result of such tendency, *i.e.*, it is formed due to their similarity in certain dimensions. Moreover, unlike existing works that consider homophily in a single dimension [13, 19, 25, 23], we stress that homophily is naturally *discriminative* in that different relationships correspond to different dimensions of similarity, *i.e.*, different attributes $\mathcal{A}$ lead to different relationships $\mathcal{R}$.

While no social network can capture all possible attributes and relationships, we observe that it is usually trivial to relate the most important relationships in a network to the particular attributes captured there. *E.g.*, in a professional network like LinkedIn, the most important relationships are schoolmate and colleague, which are the result of similar education and employer attributes; on a personal network like Facebook, friends are formed through relationships such as townsmen and hobby peers resulted from their similarity in hometown and hobby. Table 1 gives more intuitive examples of important relationships $\mathcal{R}$ and relating attributes $\mathcal{A}$ on different networks.

We thus propose the problem of *Attribute-based Relationship Profiling* (ARP), founded on the principle of homophily– to profile the underlying relationships $\mathcal{R}$ of each connection by their associated attributes $\mathcal{A}$. While the problem is *important*, as social networks

Network		Important relationships and relating attributes		
LinkedIn	$\mathcal{R}$	schoolmate	colleague	professional peer
	$\mathcal{A}$	education background	working experience	skill
Facebook	$\mathcal{R}$	townsman	hobby peer	acquaintance
	$\mathcal{A}$	hometown	sports, music, groups, *etc.*	check-ins, events, *etc.*
DBLP	$\mathcal{R}$	research group members	in-field collaborators	cross-field collaborators
	$\mathcal{A}$	publication	paper within the same fields	publication within different fields

Table 1: **Some intuitive examples of relationships $\mathcal{R}$ and attributes $\mathcal{A}$ on different social networks.**



(a) Graph G. (b) Social affinity graphs S_1 and S_2.

Figure 1: A toy example of a simple social network.

strives to help users organize their social universe and route information, it is also *novel*, and we are the first to identify it formally, to the best of our knowledge.

To illustrate, Figure 1(a) shows a network $\mathcal{G} = (\mathcal{V}, \mathcal{E}, \mathcal{A})$, where $\mathcal{V}$ is the set of nodes v_i and $\mathcal{E}$ that of connections e_{ij}. $\mathcal{G}$ has a set of M important attributes $\mathcal{A} = \{\mathcal{A}^m\}_{m=1}^M$ (*e.g.*, $\mathcal{A}^1$ = education, $\mathcal{A}^2$ = employer) with the value functions, *e.g.*, $\mathcal{A}^1(v_8)$ = uiuc, $\mathcal{A}^2(v_8)$ = amazon. Given $\mathcal{G}$ as *input*, ARP aims to profile $\mathcal{E}$ *w.r.t.* $\mathcal{A}$'s corresponding relationships $\mathcal{R} = \{\mathcal{R}^m\}_{m=1}^M$, by inferring its *relationship probabilities* $\{r_{ij}^m = p(e_{ij}|\mathcal{R}^m, \mathcal{A}^m)\}_{m=1}^M$, *i.e.*, how each link e_{ij} carries $\mathcal{R}$. As *output*, ARP constructs a set of *social affinity graphs* $\mathcal{S} = \{\mathcal{V}, \mathcal{E}, \mathcal{R}\} = \{\mathcal{S}^m\}_{m=1}^M$, *i.e.*, graphs sharing the same structure of $\mathcal{G}$, where each link e_{ij} in $\mathcal{S}^m$ is now weighted by $r_{ij}^m \in \mathcal{R}^m$ indicating how it carries $\mathcal{R}^m$. *E.g.*, as Figure 1(b) shows, for $\mathcal{A}^1$ = education, ARP outputs the affinity graph $\mathcal{S}^1$ for $\mathcal{R}^1$ = schoolmate, and similarly, for $\mathcal{A}^2$ = employer, it outputs $\mathcal{S}^2$ for $\mathcal{R}^2$ = colleague. To visualize, we plot the thickness of a link to indicate its weight in $\mathcal{R}$.

We stress that, as the homophily principle implies, ARP should be 'systematic' and 'complete'. On the one hand, individuals stay close because they are similar, and every link should have a probability to carry certain relationships. To this end, our profiling should be *systematic* to cover *every link*. *E.g.*, two links (e_{15} and e_{19}) may not carry a certain relationship (*e.g.*, schoolmate, because it is weak or weaker than other relationships), but we may still want to compare them in that dimension. On the other hand, as similar individuals may stay close, more 'similarity' leads to more 'closeness', and any relationships can co-occur in a link. To this end, our profiling should be *complete* to cover *every relationship* on a link. *E.g.*, two users (v_2 and v_3) may be both schoolmates and colleagues.

While natural, these dual requirements of homophily (and thus relationship semantics) have not been met by most existing works. Although the problem of ARP is novel, by similarly leveraging the homophily insight, several social mining methods have exploited relationship semantics as their *intermediate results*, but in a rather limited form– due to the failure to model homophily appropriately: First, in *attribute profiling* works [2, 7, 21, 23], the homophily modeling is *not complete*, by restricting to *one* relationship per link. Second, in *community detection* works [11, 16, 24, 26], it is *not systematic*, by targeting at each *community* instead of links, which forces links in the same community to carry the same relationship, and leaves out those outside or between communities. As Sec. 4 will show, such improper models fall short for relationship profiling.

Thus, to address ARP, our key challenges center around effectively modeling homophily:

Challenge 1: Systematic and Complete Homophily. As ARP requires, and as the nature of homophily implies, we should realize homophily over every link (systematicness) and for every relationship (completeness), which most existing work failed to satisfy. What is a principled mechanism for implementing homophily, so that every link can be properly understood through multiple relationships?

Insight: Reverse Smoothness Principle. Over a graph, homophily bridges two kinds of 'proximities' between users, *i.e.*, *similarity*, measuring how similar two users share for attributes $\mathcal{A}$, and *closeness*, measuring how close two users link through a relationship $\mathcal{R}$. Interestingly, we observe that, as this similarity-closeness duality is natural, it has been explored in graph-based semi-supervised learning (GSSL) [28, 30, 31]. GSSL models the *smoothness assumption*, *i.e.*, *points close to each other are likely to share labels*, which helps to infer from closeness (of links) to similarity (of labels) over a given, as *input*, *data affinity graph*, in a systematic (over every

link) and complete (for every label) manner.

Surprisingly, while the smoothness assumption is remarkably consistent with homophily, their connection has only been exploited in a non-discriminative way that considers a unique relationship and mixes up all attributes [23]. As our key insight is to leverage the modeling of smoothness to realize systematic and complete homophily, we note that our direction of inference for ARP is focused on the opposite to GSSL: from attributes to relationships. Therefore, we propose the reverse smoothness principle (details are in Appendix A) and a probabilistic model in Sec. 2, to infer from given similarity (of attributes $\mathcal{A}$) to latent closeness (of relationship $\mathcal{R}$) and construct, as *output*, a *social affinity graph*. We stress that, from similarity to closeness, the focus of ARP is exactly the opposite to that of GSSL– and this reverse smoothness has not been explored to date.

Challenge 2: Robust Homophily. While the reverse smoothness principle allows us to relate attributes and relationships by implementing homophily, due to the incompleteness and ambiguity of attributes and links in real-world networks, similarity can not be computed and closeness can not be enforced directly between every pair of nodes. How to realize homophily robustly over such noisy social networks?

Insight: Holistic Closeness Modeling. Traditional smoothness is only considered on direct edges between pairs of nodes by GSSL on the data affinity graph. It works because every edge exists and every pair-wise closeness is enumerated. In real-world networks where attributes are incomplete and ambiguous, and nodes with similar attributes do not always share an edge, such a scheme is useless.

To deal with real-world networks, we propose a holistic closeness modeling approach (details and implementations are in Sec. 2, Appendix A and B), to leverage similarity between every pair of nodes– even though they may not have a direct link– by capturing the closeness between nodes based on *paths*, instead of *edges*. In other words, from edges to paths, we extend the traditional smoothness modeling to *higher-order* smoothness, so as to fully exploit the available attribute and link information on an incomplete ambiguous graph.

We intuitively explain the idea of this approach by continuing on the running example in Figure 1. It is intuitive to say that e_{68} is very likely to carry relationship schoolmate, because v_6 and v_8 have the same education attribute. However, tricky questions arise due to the incomplete and ambiguous attributes. *E.g.*, consider e_{19}, where neither of v_1 or v_9 has available education attribute, and e_{23}, where both v_2 and v_3 have multiple attributes. The holistic closeness modeling approach leverages paths that connect attributed nodes to profile edges they bypass. *E.g.*, paths $v_8 - v_9 - v_1 - v_7$ and $v_5 - v_2 - v_3 - v_4$ bypass e_{19} and e_{23}, respectively, so they add belief on e_{19} to carry relationship schoolmate and e_{23} to carry relationship colleague. In a nutshell, the approach exploits data redundancy in the neighborhood to complete and disambiguate relationships.

Summary. In this paper, based on our novel reverse smoothness principle and holistic closeness modeling approach, we develop a probability framework of Attribute-based Relationship Profiling (ARP), which leverages user attributes and link structures to reliably estimate the proper relationship semantics in social networks. Specifically, we preserve reverse smoothness on the graph based on an interpretable probability experiment, and we achieve holistic modeling by measuring closeness through standard random walks. An efficient path finding algorithm is designed to solve our justifiable MLE objective. Finally, experiments on three real-world datasets comprehensively demonstrate the effectiveness and efficiency of our ARP framework.

2 Model

Maximizing the production of a similarity term and a closeness term is a standard way of preserving smoothness on the graph [28, 31]. However, the objective function is rather heuristically designed for optimization purposes and the scales of learned quantities are arbitrary.

The objective of ARP is to estimate a complete set of relationship probabilities systematically on each link. Moreover, this has to be done based on incomplete and ambiguous user attributes and link structures. We develop a unified probabilistic framework to derive the objective function of reverse smoothness and precisely learn the proper relationship probabilities through holistic closeness modeling.

We note that existing probabilistic models in graph-based settings only consider the inference from closeness to similarity on the comprehensive data affinity graphs, instead of the inference in the opposite direction on the incomplete and ambiguous social graphs as we consider [4, 6, 20].

2.1 Probabilistic Reverse Smoothness

To learn the systematic and complete relationship probabilities based on user attributes, we apply our novel reverse smoothness principle (Principle 2 in Appendix A) by designing a set of simulated probability experiments.

We start from the description of the probability space. To model closeness between users v_i and v_j, we

define a *user closeness event* that v_i and v_j are close on the graph and use a random variable $p(v_i \sim v_j)$ to denote the probability of this event. Therefore, we have the *sample space* $\Omega = \mathcal{V}^2$. We assume that $(v_i \sim v_j)$ follows the multinomial distribution on Ω and have $\sum_{i=1}^{N}\sum_{j=1}^{N} p(v_i \sim v_j) = 1$. We aim to estimate $p(v_i \sim v_j)$ based on observed attribute similarity.

Since we only observe attributes $\mathcal{A}$ directly from the network rather than the similarity $f(a_i, a_j)$, we firstly use intuitive examples to explain how to compute $f(a_i, a_j)$.

Consider $\mathcal{R} =$ schoolmate and $\mathcal{A} =$ university. For a single categorical attribute with multiple distinct values like this, a simple way to compute $f(a_i, a_j)$ is to assign 1 to it if a_i and a_j include at least one same value and 0 otherwise. This is basically doing the OR operations among the AND results between users on each distinct value of the specific attribute.

We may also include numerical attributes like age, which may help produce better attribute similarities among schoolmates. We can normalize the difference between the values of a_i and a_j into $[0, 1]$ by dividing the largest difference among all pairs, and similarity equals one minus the normalized difference. Then we combine similarities on multiple attributes by simply doing a generalized AND operation.

With a score $f(a_i, a_j)$ computed for each pair of users v_i and v_j describing their similarity on $\mathcal{A}$, we estimate their closeness in $\mathcal{R}$ in the following simulated probability experiments. Each time, we pick up a pair of users v_i and v_j from Ω according to $f(a_i, a_j)$ and observe that they are close on the graph. We require that the probability of randomly picking up $(v_i \sim v_j)$ is proportional to $f(a_i, a_j)$. Therefore, after a sufficiently large number of experiments, the likelihood of observing the user closeness events boils down to

$$L = \prod_{i=1}^{N}\prod_{j=1}^{N} p(v_i \sim v_j)^{f(a_i,a_j)}. \tag{2.1}$$

By maximizing L, we ensure that each pair of users are necessarily close on the social affinity graph $\mathcal{S}$ according to their attribute similarity in $\mathcal{A}$, while not too close under the constraints of multinomial distribution. Thus the objective of preserving reverse smoothness over the graph is fulfilled.

2.2 Holistic Closeness Modeling To precisely estimate relationship probabilities, we develop a holistic model of user closeness based on random walks on $\mathcal{S}$ (more details and motivating examples are in Appendix A). While closeness can be asymmetric, we consider it in a symmetric way under the setting of undirected graphs. The framework generalizes trivially to directed graphs.

In standard random walks, edge weights $\mathcal{R}$ determine the one-step transition probabilities of the random walker on the graph, *i.e.*, $p(v_j|v_i) = \frac{r_{ij}}{d_i}$, where $d_i = \sum_{j\in\mathcal{N}(v_i)} r_{ij}$ and $\mathcal{N}(v)$ is the set of nodes that share an edge with v [4, 14]. $p(v_j|v_i)$ measures the edge-wise closeness on $\mathcal{S}$.

We propose to further measure path-wise (holistic) closeness. Consider a random walk on $\mathcal{S}$. Starting from a specific node v_i, besides jumping directly to v_j, the random walker can pass through several nodes between v_i and v_j with the corresponding transition probabilities before finally reaching v_j. The probability of the random walker to reach v_j from v_i through all possible paths accurately measures the holistic closeness between v_i and v_j on $\mathcal{S}$.

In order to capture and formalize holistic closeness, we bring out the notion of *reachability* in random walk [9, 29]:

$$R(v_i \sim v_j) = \sum_{l\in l(v_i\sim v_j)} r(l), \tag{2.2}$$

where $l(v_i \sim v_j)$ is the set of all paths connecting v_i and v_j, and $r(l)$ is the reachability through the specific path l in a random walk. Although we focus on the reachability in only one direction, closeness is modeled symmetrically because we consider similarities in both directions equally.

Suppose all possible paths connecting v_i and v_j are known. We systematically enumerate reachability w.r.t. paths of different lengths and then add them up into a uniform representation. Specifically, we use $l_{kh}(v_i \sim v_j)$ to denote the hth path of length k between v_i and v_j. Suppose $l_{kh}(v_i \sim v_j) = v_{h_1} - v_{h_2} - \ldots - v_{h_{k+1}}$. At each step from v_{h_i} to $v_{h_{i+1}}$, the transition probability is $\frac{r_{h_i h_{i+1}}}{d_{h_i}}$. We also consider the decay factor α to denote the impact of longer walks. Therefore, the reachability under the measure of $l_{kh}(v_i \sim v_j)$ is

$$p_{kh}(v_i \sim v_j) = \alpha^k \prod_{s=1}^{k} \frac{r_{h_s h_{s+1}}}{d_{h_s}}. \tag{2.3}$$

In this form of multiplication, since the weight of the whole path is proportional to the weight of each edge and sub-path along that path, the closeness among nodes is naturally coupled and transmitted along the path.

Suppose there are totally H paths of length k connecting v_i and v_j, then we have

$$p_k(v_i \sim v_j) = \sum_{h=1}^{H} p_{kh}, \tag{2.4}$$

Considering all paths of different lengths connecting

v_i and v_j, we have

$$p(v_i \sim v_j) = \sum_{k=1}^{K} p_k, \tag{2.5}$$

where K is the maximum length of paths we consider. To fully implement reachability as in Eq.2.2, K should be set to $+\infty$. However, it is usually sufficient to set K to small numbers like 3 or 4, due to the small world phenomenon, which makes longer paths less important [22]. According to [29], the ignored reachability on paths longer than K is bounded by α^{K+1}, and in practice, we can dynamically increase K to compute incremental reachability. In Sec. 4, we show the impact of different α and K.

Combing Eq.2.3, Eq.2.4 and Eq.2.5, we get the reachability between v_i and v_j measured by the whole graph as

$$p(v_i \sim v_j) = \sum_{k=1}^{K} \sum_{h=1}^{H} \alpha^k \prod_{s=1}^{k} \frac{r_{h_s h_{s+1}}}{d_{h_s}}. \tag{2.6}$$

However, finding all possible paths connecting v_i and v_j is non-trivial. Therefore, an efficient path enumerating algorithm is devised especially for our scenario in Appendix B.

2.3 Interpretation We give an interpretation of how our probabilistic framework works in a random-walk perspective.

Combining Eq.2.1 and Eq.2.6, we get the likelihood function connecting path-wise user closeness with attribute similarity,

$$L = \prod_{i,j} \left(\sum_{k=1}^{K} \sum_{h=1}^{H} \alpha^k \prod_{s=1}^{k} \frac{r_{h_s h_{s+1}}}{d_{h_s}}\right)^{f(a_i, a_j)}. \tag{2.7}$$

Consider a random walk on the graph. By constraining edge weights through path-wise closeness measured by reachability on the graph, we are actually requiring the random walker to 'prefer' paths connecting nodes with similar attributes, instead of always choosing an edge to go with uniform probabilities. This idea is similar to the supervised random walk in [1]. But instead of generating ad hoc features for edges, we directly manipulate edge weights through paths, and thus the actual correspondence between edges and paths is preserved. As a result, for each edge or sub-path, the more paths connecting nodes with similar attributes pass through it, the more probable it will be visited by the random walker in the stationary distribution, and thus is more probable to be formed due to the attribute similarity under consideration. Since there are many paths connecting each pair of attributed nodes and each path consists of multiple edges and sub-paths, many relationships among un-attributed nodes can be effectively profiled given only a few pairs of attributed nodes. Thus the problems of missing and overlapping attributes are both well addressed.

To show that our model essentially preserves reverse smoothness, we extract the generalized objective function of SSL as

$$J_{SSL} = \sum_{i,j} C_{ij} S_{ij}, \tag{2.8}$$

where closeness (C) and similarity (S) are implemented in various ways due to different intuitions and measurements [30, 28, 8]. Maximizing Eq.2.8 with proper regularization essentially preserves smoothness by reducing the difference between C and S. To contrast, we write the log-likelihood of ARP from Eq.2.7 as

$$J_{ARP} = \sum_{i,j} f(a_i, a_j) \log\left(\sum_{k=1}^{K} \sum_{h=1}^{H} \alpha^k \prod_{s=1}^{k} \frac{r_{h_s h_{s+1}}}{d_{h_s}}\right). \tag{2.9}$$

In this equation, $f(a_i, a_j)$ implements S while $\log(p(v_i \sim v_j))$ implements C. The correspondence between Eq. 2.8 and 2.9 indicates the effectiveness of ARP in preserving the reverse smoothness on the social affinity graph.

Note that, unlike Eq. 2.8 that is designed purely based on intuitions and optimization purposes, our Eq. 2.9 is derived from a principled probabilistic framework, where probability interpretation of relationship semantics is naturally preserved, and the coupling of closeness and similarity is decided by the well defined simulated probability experiments.

3 Algorithm

Realizing our holistic smoothness model is to compute a parameter configuration $\mathcal{R}$, so that the likelihood of observing the user closeness event is maximized according to attribute similarity. For this purpose, we need to firstly find relevant paths that can be constructed by existing edges on the graph, and then optimize weights $\mathcal{R}$ on them.

3.1 Finding Paths on Graph According to Eq. 2.7, we need to find paths $l(v_i \sim v_j)$ for the pairs of nodes v_i and v_j with $f(a_i, a_j) > 0$. Unlike traditional path enumeration on graphs, our problem is quite unique, where we only care about *short* paths between *a small portion* of nodes.

Since shorter paths contribute more in our model, we devise an efficient path finding algorithm based on breadth-first search (BFS), so that we can tune path length K to avoid considering longer paths. In practice, $f(a_i, a_j)$ is usually very sparse, since there are numerous distinct values on $\mathcal{A}$ and many users do not have any meaningful value. Therefore, we only need to start from a very small number of nodes compared to $|\mathcal{V}|$. Finally, since we need to record the exact paths and avoid

repeated iterations when considering the same nodes in different levels of search, we borrow the efficient path descriptor $d(\cdot)$ from [17] to encode, record and retrieve paths between nodes with time complexity $O(1)$. It is also efficient to check if a certain node or edge is on a path and if two paths are the same by simply doing binary AND and XOR based on d, respectively.

Since path indexing and legitimacy checking are efficiently $O(1)$ with the path descriptor lists, the overall computational complexity of finding paths is $O(K|\mathcal{V}|^2)$. However, the actual computational time is much shorter than $K|\mathcal{V}|^2$. In each step of BFS, the numbers of considered nodes and neighbors are much less than $|\mathcal{V}|$. The efficiency of finding paths can be further improved by path caching and reusing, to fully utilize the path indexes. Specifically, we try to cache as many legitimate paths as possible after they are indexed. Therefore, the paths of length K can be directly reused when considering paths longer than K. As the number of paths goes exponentially with the length of the paths, it is usually impossible to keep all path indexes in cache and even memory. Motivated by the scale-free property of social networks [3], which leads to the frequent reuse of paths between a small number of high-degree hub nodes, we adopt the Least Recently Used (LRU) algorithm for path caching.

3.2 Optimizing Weights on Paths Now that the paths connecting each pair of nodes with similar attributes are found, we continue to optimize the log-likelihood function in Eq.2.9 and generate the relationship probabilities $\mathcal{R}$. We derive the gradient for r_{uv} as

$$\frac{\partial J}{\partial r_{uv}} = \sum_{i,j} f(a_i, a_j) \frac{N_{uv}(v_i \sim v_j)}{p(v_i \sim v_j)}. \tag{3.10}$$

In the equation,

$$N_{uv}(v_i \sim v_j) = \sum_{k=1}^{K} \sum_{h=1}^{H} I\{l_{kh}, e_{uv}\} \frac{p_{kh}(v_i \sim v_j)}{r_{uv}}, \tag{3.11}$$

where $I\{l_{kh}, e_{uv}\}$ is an indicator function computed from path l_{kh}. Specifically, $I\{l_{kh}, e_{uv}\}$ equals 1 if l_{kh} contains edge e_{uv}, and 0 otherwise. Therefore, $N_{uv}(v_i \sim v_j)$ is the sum of the products of all normalized edge weights except for r_{uv} along all paths that connect nodes v_i and v_j and also contain edge e_{uv}.

With Eq.3.10, we apply standard gradient ascent to solve for $\mathcal{R}$. As can be seen in Eq.3.11, for a specific edge e_{uv}, the more paths l_{kh}'s pass through it ($I\{l_{kh}, e_{uv}\}$ equals 1), the larger the derivative of the corresponding weight r_{uv} is, which substantiates our intuition of using paths connecting similarly attributed nodes to profile individual edges. In Eq.2.3, the denominator d_{h_s} exposes an l-1 norm on all weights in $\mathcal{R}$, encouraging sparse solutions. The penalty arises naturally within the probabilistic model and therefore no heuristic penalty terms to encourage sparsity is necessary.

Consider a specific pair of nodes v_i and v_j. Given Eq.2.3, $p_{kh}(v_i \sim v_j)$ is concave in $\mathcal{R}$. Moreover, since different paths connecting v_i and v_j found by SPPI never share the same edge, $p_k(v_i \sim v_j)$ and $p(v_i \sim v_j)$ in Eq.2.4 and Eq.2.5 are both concave in $\mathcal{R}$. Since log concave is still concave, the log-likelihood function in Eq.2.6 is a weighted sum of concave functions, which is not globally concave but has an upper bound. However, since $f(a_i, a_j)$'s are usually very sparse in social networks, we find the solution of our algorithm stable and almost always the global optimal in the experiments.

The runtime of ARP is dominated by finding paths. The runtime of optimization with gradient ascent is linear in $|\mathcal{V}|$. As we study in our experiments, convergence is reached usually within 20 iterations with step size empirically set to 0.05. As discussed before, the time of finding paths is much less than $K|\mathcal{V}|^2$, so the overall computation complexity of ARP is $O(K|\mathcal{V}|^2)$, comparable to many advanced attribute profiling and community detection algorithms [2, 7, 11].

For more details and analyses of the algorithm, please refer to Appendix B.

4 Experiments

In this section, we evaluate ARP with quantitive experiments and case studies on three real-world datasets.

4.1 Experimental Settings

Datasets. The first is the LinkedIn Ego Networks dataset (LEN) from [7]. It includes 268 ego networks, which contain about 19K users and 110K connections. Among them, about 30% users have attributes of 193 different universities and 375 different employers, which we use to generate training data. 8K connections are labeled by the ego users as carrying the relationships of schoolmates, colleagues or both, based on which we directly perform quantitive performance evaluations.

The second is the Facebook Ego Networks dataset (FEN) from [11]. It contains 10 ego networks of about 4K users and 88K connections. We choose all hometown, school and employer attributes out from the total 634 attributes, because they well indicate the relationships of townsman, schoolmate and colleague. Since there are no labeled relationships, we randomly split the users into training and testing sets. We input all users with their connections and attributes in the training set to all compared algorithms, and evaluate the learned relationships on connections between users

in the training set and users in the testing set. For quantitive evaluations, we label the relationship of townsman (schoolmate, colleague) on the connections between friends sharing the same attribute value of hometown (school, employer). Thus, there might be multiple relationships on the same connection.

The DBLP data we use were extracted on Jan 1st, 2017, which includes 3.7M publications from 1.8M authors. We generate nodes as authors and use three publication venues, KDD, VLDB and ICML, as node attributes. A uniform connection is generated between authors who have co-authored at least once in any of the considered venues. Since the authors and attributes are not anonymous, we present insightful case study results on some novel applications to show the effectiveness of our framework.

The attributes captured in both LEN and FEN are incomplete and noisy. In such scenarios, we show that profiling the systematic and complete relationship semantics is generally useful in improving the performance of relationship prediction. Although both LEN and FEN are ego-networks, our framework is general to work on any non-ego-networks like DBLP. Moreover, on DBLP where the attributes are complete and precise, we show that our framework is still advantageous because it provides more insightful results.

Compared algorithms. The problem of ARP is novel, which is hardly addressed by previous literature. To comprehensively evaluate ARP, we adapt state-of-the-art algorithms from two groups.

Adapting attribute profiling algorithms. These algorithms aim at inferring user attributes based on both known attributes and network structure. Since the relationships they learn are implicit, we need to predict them based on the inferred attributes on the connected users. *E.g.*, we predict a relationship as schoolmate if the two connected users are inferred with the same university attributes.

- Relation neighbor classifier (RNC) [10]: it profiles user attributes *w.r.t.* labeled neighbors without learning.
- Discriminative relational classifier (DRC) [21]: it constructs a modularity-based feature as latent social dimensions to help learn user attributes.
- EdgeExplain [2]: it improves on traditional label propagation [30, 31] by leveraging a softmax function to solve for a global optimal assignment of both user attributes and relationships.
- BLA [23]: it jointly infers link and attribute probabilities by addressing smoothness from two directions on social graphs.

Adapting community detection algorithms. We adapt community detection algorithms that use node attributes to characterize communities, which have a side effect of profiling links at a coarse granularity. We refer to the attribute assignment of each community and predict all relationships based on the most prominent attribute. *E.g.*, we predict all relationships in a community as schoolmate if a university attribute is the most prominent there.

- PCL-DC [26]: it unifies a conditional model for link and a discriminative model for content analysis.
- Circles [11]: it designs a generative model of edges *w.r.t.* profile similarity to detect overlapping communities.
- CESNA [24]: it designs a generative model of edges and attributes to detect overlapping communities.
- CoProfiling [7]: it profiles attributes and community memberships through iterative coordinate descent.

Instead of producing a set of relationship probabilities for each link like ARP, all baselines can only produce categorical labels.

Metrics. For performance evaluations, we compute precision, recall and F1 score over all predictions of each relationship as commonly done in related works [7]. The presented results are the averages over 10 times of the same procedures. We also conduct significance tests with p-value 0.01.

To further understand the results, we evaluate the relationships profiled by different algorithms *w.r.t.* the systematicness and completeness criteria as we discussed in Sec. 1. We compute the number of all links in the network (E), the number of profiled links (P) and the number of links profiled with multiple relationships (M). To measure the systematicness, we compute $S = P/E$, and to measure completeness, we compute $C = M/P$.

We also measure the actual runtimes of different algorithms on a typical PC with dual 2.3 GHz Intel i7 processors and 8GB memory.

4.2 Performance Comparison on LEN On the LEN dataset, ARP is quantitively evaluated against all baselines. Given a uniform social network, the task is to identify relationships that are discriminatively related to user attributes. Here we aim to identify schoolmates, who are likely to share the same university attributes, and colleagues, who are likely to share the same employer attributes. Evaluation is done on the user labeled relationships.

We run ARP on the university and employer attributes and predict the probabilities of schoolmate and colleague relationships on each link. To perform quantitive evaluations, we convert the probabilities into binary predictions for each relationship by thresholding at value θ^m. For attribute learning algorithms, we predict schoolmates if the two connected users are inferred with the same university attribute; for community detection algorithms, we predict schoolmates if a certain university is the most prominent attribute for the detected community that contains both connected users.

We select the best parameters for all algorithms via standard 5-fold cross validation. The parameters we set for ARP are $K = 3$, $\alpha = 0.8$, $\theta^1 = 0.4$ and $\theta^2 = 0.7$.

Algorithm	Schoolmates			Colleagues		
	P	R	F1	P	R	F1
RNC	0.613	0.548	0.579	0.358	0.467	0.405
DRC	0.885	0.472	0.616	0.603	0.442	0.510
EdgeExplain	0.782	0.618	*0.690*	0.530	0.642	*0.581*
BLA	0.648	*0.683*	0.665	0.416	*0.697*	0.521
PCL-DC	0.932	0.498	0.649	0.654	0.516	0.577
Circles	0.937	0.431	0.590	0.512	0.428	0.466
CESNA	0.813	0.492	0.613	0.502	0.538	0.519
CoProfiling	**0.969**	0.487	0.648	*0.691*	0.453	0.547
ARP	*0.941*	**0.793**	**0.861**	**0.705**	**0.782**	**0.742**

Table 2: **Performance comparison on LEN.**

Table 2 shows performance comparison on LEN. The scores all passed the significance tests with p-value 0.01. ARP constantly ranks first among the 8 algorithms on F1 score, while other methods have varying performance, which indicates the robustness and universal advantages of our approach on precisely profiling individual links. By looking into the scores, we find that ARP can effectively improve recall, while maintaining comparable precision to the baselines. It shows the effectiveness of our model to systematically and completely profile relationships along paths connecting users with similar attributes.

We present systematicness and completeness evaluations in Table 3, where the ratios are averaged through 10 random training-testing splits. As clearly shown, the attribute profiling algorithms usually profile only one relationship for every connection, while the community detection algorithms predict no relationship at all on some connections. ARP is the only one that implements systematic and complete homophily by profiling every connection *w.r.t.* every relationship.

Algorithm	RNC/DRC	EdgeExplain	BLA	PCL-DL
Systematicness	100%	100%	100%	88.7%
Completeness	0%	15.7%	78.2%	64.0%

Algorithm	Circles	CESNA	CoProfiling	ARP
Systematicness	83.6%	86.2%	91.4%	100%
Completeness	81.2%	72.9%	0%	100%

Table 3: **Systematicness and completeness of profiled relationships on LEN.**

We present the average runtime of different algorithms on LEN in Figure 2. For ARP, we compare the runtime with and without path caching and reusing, as discussed in Appendix B (the additional runtime without path caching is marked as yellow). The runtime of ARP is comparable to the baselines.

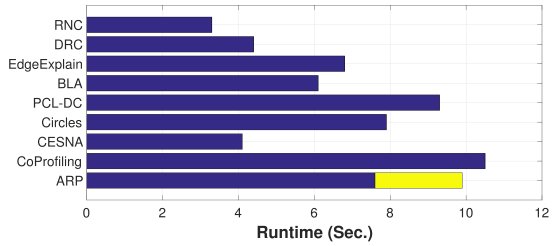
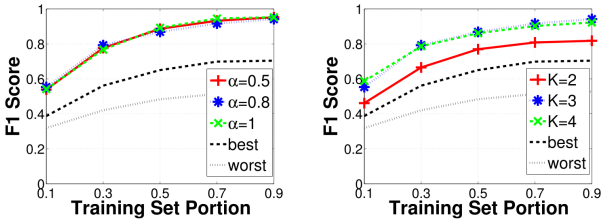


Figure 2: **Runtime comparison on LEN.**

4.3 Performance and Parameter Study on FEN

We run experiments on FEN with varying portions of training and testing sets to comprehensively evaluate the performance of ARP. We also closely study the impact of the two intrinsic parameters of ARP, *i.e.*, α, the decay factor, and K, the maximum length of paths.

To compute the F1 scores, the similar process for LEN has been done to all compared algorithms to yield a binary prediction for each of the townsman, schoolmate and colleague relationships on each connection.



(a) Varying α while $K = 3$ (b) Varying K while $\alpha = 0.8$

Figure 3: **Performance study on FEN.**

Figure 3 shows results on FEN for townsman with $\theta^1 = 0.2$. The results for schoolmates and colleagues are similar. In Figure 3(a), the decay factor α does not significantly influence the performances. This is probably because we only consider short paths. In Figure 3(b), when K is set to 2, only two-step paths are considered, which leads to poor results. When K is set to larger values like 3, the holistic modeling approach becomes effective and the results are much better. Note that $K = 3$ and $K = 4$ always yield similar results, which indicates that the importance of paths is dominated by short ones. By setting K to values like 3, we can run ARP efficiently by avoiding irrelevant edges.

Due to space limit, more experiments and case study results are placed in Appendix C. Readers are also welcome to explore our Github project[1] for more interesting novel applications and visualizations enabled by ARP. All codes are available under the same directory.

[1]https://github.com/yangji9181/ARP2017

5 Conclusion

While ARP is a novel problem that can be viewed as an essential part of problems such as attribute learning and community detection, we emphasize that this problem itself is important, complex and of great research value. As a unique solution, we propose to learn relationship semantics in a principled probabilistic way, which characterizes the formation of each user relationship in social networks based on user attributes. Since ARP enables automatic labeling of relationships in an unsupervised way, the roles that different relationships play in various networks can be rigorously studied, such as promoting certain messages and shaping specific groups.

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Relationship Profiling over Social Networks: Reverse Smoothness from Similarity to Closeness [Supplementary Materials]

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Appendix A: Detailed Motivations and Concepts

In real-world networks, while links should bear different relationships, they are not explicitly labeled. We argue that being connected in a network does not mean being equally close in reality, and being close does not mean being equally close in every perspective. Since important relationships in social networks are usually discriminatively related with some particular attributes captured by the networks, we propose to leverage user attributes to decipher the hidden relationship semantics of uniform links.

Challenges. The challenges of ARP lie in the effective modeling of homophily– to be systematic and complete as well as robust.. The former is difficult due to the lack of a principled way to infer relationships from attributes, and the later is hard because of incomplete and ambiguous information in real social networks.

Principle: Reverse Smoothness. We notice that there is a systematic connection between attributes and relationships as we desire, which has been explored by the principled framework of graph-based semi-supervised learning (GSSL) [11, 12]. Specifically, GSSL models two proximities on the graph: *closeness* and *similarity*. Consider GSSL in the social network setting. For each user attribute $\mathcal{A}$, an *affinity graph* $\mathcal{R}$ is used to encode user closeness in terms of the corresponding relationship. Then the value of every user on $\mathcal{A}$ can be learned based on $\mathcal{R}$.

As an example, consider v_1, v_5 and v_6 in Figure 1(a) of the main paper. GSSL assumes that closeness in $\mathcal{R}$ is already given. Therefore, if w_{16} is larger than w_{15}, the unknown education attribute of v_1 will be more likely to be predicted as a_6 (UIUC) than a_5 (Stanford), due to the following principle of GSSL.

Principle 1. *(Smoothness Principle) If two nodes v_i and v_j are close on the affinity graph R, their attributes a_i and a_j should be similar [11, 12].*

The focus of GSSL is thus on attribute inference, which goes from closeness to similarity on the graph.

Interestingly, the focus of ARP is the opposite of GSSL, *i.e.*, from similarity to closeness. In ARP, *e.g.*, we only know there is an edge e_{13} between v_1 and v_3. We are interested in the closeness on e_{13} in terms of schoolmate and colleague.

Inspired by GSSL, we intuitively reverse the smoothness principle into the following, which allows us to learn $\mathcal{R}$ by systematically enforcing closeness based on similarity, leading to a novel and unique solution to the ARP problem.

Principle 2. *(Reverse Smoothness Principle) If two users v_i and v_j share similar attributes on $\mathcal{A}$, they should be close on the social affinity graph in terms of $\mathcal{R}$.*

Based on this principle, it is intuitive to implement homophily by probabilistically estimating the closeness on every link in terms of each relationship $\mathcal{R}$ based on the similarity of its related attributes $\mathcal{A}$. The resulting social affinity graphs naturally encode the systematic and complete relationship semantics in the network.

Approach: Holistic Closeness Modeling. Our situation in the real-world graph setting is more complex than that of GSSL. While GSSL can enumerate all pair-wise closeness on each edge and enforce similarity accordingly, the opposite is hard to do in social networks with missing and ambiguous information.

Firstly, attributes are incomplete. Consider v_1 and v_9 in Figure 1 of the main paper. Since the education attribute a_1 and a_9 are missing, we have no idea how similar they are, and thus how close e_{19} should imply in terms of schoolmate. Moreover, even if attributes are complete, closeness cannot be simply enforced on every edge, because similarity can be ambiguous. This is due to the direction of inference, *i.e.*, friends of relationship $\mathcal{R}$ must share the same related attribute $\mathcal{A}$,

while similar in $\mathcal{A}$ does not necessarily mean close in $\mathcal{R}$. *E.g.*, consider v_2 and v_3 in Figure 1 of the main paper. If v_2 and v_3 are schoolmates, they must share the same education attribute such as UIUC. However, sharing the same education attribute does not necessarily imply the relationship of schoolmates. In fact, they may be colleagues, because they also share the same employer attribute of Google, or both. If we simply enforce closeness on e_{23}, the results will be ambiguous.

To further leverage our reverse smoothness principle and robustly learn the social affinity graph $\mathcal{S}$, we propose to put smoothness constraints and closeness measures onto the whole graph, rather than limiting them to direct edges. Specifically, we define a *path* to be a sequence of non-repeating edges connecting two nodes and use *reachability* to measure closeness as a sum of all weighted paths between two nodes. Then we constrain closeness measured by reachability according to attribute similarity. The intuition is that, the more similar attributes v_i and v_j share, the closer they should be on the graph, and therefore the more paths of shorter lengths and larger weights should connect them.

Continue our example in Figure 1 of the main paper. Inferring r_{19} in terms of schoolmate is challenging due to missing *education* attributes of v_1 and v_9. However, similarity between v_7 and v_8 can be used to estimate the closeness on path $v_7 - v_1 - v_9 - v_8$, which indirectly estimates the closeness on e_{19}. As a result, e_{19} is likely to carry relationship schoolmate, basically because v_1 and v_9 share many friends from UIUC such as v_7 and v_8.

Moreover, continue the discussion from Figure 1 of the main paper about v_2 and v_3, where e_{23} is ambiguous. If we combine closeness measured by multiple paths containing e_{23}, we will end up with a higher probability of e_{23} to be formed due to Google rather than UIUC, mainly because of the short path $v_4 - v_3 - v_2 - v_5$ containing e_{23} between v_4 and v_5 with Google.

By constraining closeness measured with reachability on paths, we effectively utilize the constraints between each pair of nodes v_i and v_j with meaningful attributes onto all edges along the paths connecting v_i and v_j, much beyond their direct edges, if any. Among those edges, many are likely to connect nodes without meaningful values of particular attributes, but in this way, they can still get properly constrained and thus well estimated. Moreover, since each edge can be a component of multiple constrained paths, multiple signals from nearby nodes are combined to disambiguate the semantics of that single edge, yielding much more robust results.

Appendix B: Details of our Algorithms

Efficiency. In practice, $\mathcal{A}$ is usually very sparse, because for every specific attribute, there are numerous distinct values and many users do not have any meaningful values. Therefore, most $f(a_i, a_j)$ computed on $\mathcal{A}$ will be 0 or very small as can be ignored, which means we only need to consider a very small number of pairs of nodes compared to $|\mathcal{V}|^2$.

We develop the Sensor Propagating with Path Indexing (SPPI) algorithm for optimizing our model. SPPI is based on the idea of label propagation on graphs [5]. But instead of labels, we generate a sensor at a starting node s and propagate it to every possible direction at each step, and index the edges it goes through. We call it a sensor because each time it touches a new node t, it detects whether a legal path from s to t has been detected. If yes, we can retrieve the exact edges on that path by looking up the indexes. Another important task of the sensor is to act as a marker, so at each step of propagation, we only consider a small subset of $\mathcal{V}$ with the sensors on.

We formally present the procedures of SPPI in Algorithm 1. To implement our path indexer D, we borrow the idea of *path descriptor* from [7]. A path descriptor $d(\cdot)$ is a pair of bit vectors for each path l as $d(l) = \{V, E\}$. V is a bit vector of $|\mathcal{V}|$ items with $V_i = 1$ if node $v_i \in l$ and $V_i = 0$ otherwise. E is a bit vector of $|\mathcal{E}|$ items with $E_i = 1$ if edge $e_i \in l$ and $E_i = 0$ otherwise. For v_i and v_j, we use $D(i, j)$ as a list of path descriptors to index all paths connecting them. With the path descriptor d and index matrix D, it is easy to encode, record and retrieve multiple paths connecting any two nodes with time complexity $O(|\mathcal{E}|)$. It is also efficient to check if a certain node or edge is on a path and if two paths are the same by simply doing binary AND and XOR on d.

SPPI is different to exhaustive search in several ways. Firstly, it is based on breath-first search (BFS), so that as shorter paths contribute more in our model, we can tune K to avoid the consideration of longer paths and save computation time. Secondly, it is more efficient than brute force BFS by utilizing the sensor vector and path descriptor lists and checking the legitimacy of propagation directions at each step, avoiding repeated iterations when considering the same nodes in different levels of search. Thirdly, it is specially suited to the optimization of our model, because after each execution, it finds paths from a starting node to all nodes with similar attributes on the graph, while avoiding enumerating paths connecting other nodes.

Correctness. We evaluate the correctness of SPPI by checking the completeness and non-repetitiveness of the algorithm. In *Step 8*, by requiring $v_j \notin l$, we require that the next node to be propagated to is not already in the path being considered, so no loopy paths can be

generated; by requiring $l + e_{ij} \notin D(I, j)$, we guarantee that each path is generated only once. Moreover, in *Step 10* and *Step 14*, we ensure that all and only nodes with the newly propagated sensors on are considered at each step, so the same nodes are not considered multiple times in different search levels. Finally, in *Step 6*, since we always try to propagate the sensors through every possible edge, we make sure that every simple path is considered.

Since path indexing and legitimacy checking are efficiently $O(1)$ with the path descriptor lists, the overall computational complexity of finding paths is $O(K|\mathcal{V}|^2)$. However, the actual computational time is much shorter than $K|\mathcal{V}|^2$. In each step of BFS, the numbers of considered nodes and neighbors are much less than $|\mathcal{V}|$. The efficiency of finding paths can be further improved by path caching and reusing, to fully utilize the path indexes. Specifically, we try to cache as many legitimate paths as possible after they are indexed. Therefore, the paths of length K can be directly reused when considering paths longer than K. As the number of paths goes exponentially with the length of the paths, it is usually impossible to keep all path indexes in cache and even memory. Motivated by the scale-free property of social networks [2], which leads to the frequent reuse of paths between a small number of high-degree hub nodes, we adopt the Least Recently Used (LRU) algorithm for path caching.

Algorithm 1 SPPI algorithm

procedure SPPI ▷ Input

$\mathcal{G}(\mathcal{V}, \mathcal{E})$: the graph.

K: the maximum length of paths we consider.

I: the source node from which we want to find all paths to other nodes in the graph.

▷ Output

$D(I, j), j = 1 \dots |\mathcal{V}|$: each $D(I, j)$ is a list of path descriptors describing paths between v_I and v_j.

▷ Variables we use

Φ: a bit vector of length $|\mathcal{V}|$, where $\Phi(i)$ marks if there is a sensor on node v_i.

▷ Initialize

$\Phi(I) \leftarrow 1, \forall j \neq I, \Phi(j) \leftarrow 0$

$\forall j, D(I, j) \leftarrow null$

▷ Iteration

for $k = 1 : K$ **do**

  for all i in $1 : |\mathcal{V}|$ with $\Phi(i) == 1$ **do**

    for all j in $1 : |\mathcal{V}|$ with $e_{ij} == 1$ **do**

      for each path l in $D(I, i)$ **do**

        if $v_j \notin l$ && $l + e_{ij} \notin D(I, j)$ **then**

          $D(I, j) = D(I, j) + (l + e_{ij})$

          $\Phi(j) \leftarrow 1$

        end if

      end for

    end for

    $\Phi(i) \leftarrow 0$

  end for

end for

return $D(I, j), j = 1 \dots |\mathcal{V}|$

end procedure

Appendix C: More Related Works

Although we are the first to formally define the problem of ARP, since relationship semantics is critical for various tasks on social networks, algorithms in recent literature have already been intensively solving the related problems to ours. However, while they commonly believe in homophily and connect attributes and relationships with it, they do not correctly interpret the nature of homophily as complete and systematic. According to their main objectives, they can be categorized into two groups. The first group applies homophily to learn attributes through relationships, assuming that relationships on each link are mutually exclusive [1, 3, 8]. While they implicitly learn relationships, they do not compute the complete semantics on each link. The second group utilizes homophily to detect communities, assuming that each community of nodes are connected through the same relationships [4, 6, 9, 10]. They compute the semantics of communities, rather than the systematic semantics on links.

The first group of algorithms can produce systematic but not complete relationship semantics. Since attribute learning aims to infer the missing attributes of every node, systematic relationship semantics can usually be retrieved afterwards by looking at the inferred attributes of nodes on each side of a link. The recent work EdgeExplain [1] is the closest to ours, which optimizes relationships jointly with attributes. However, it assumes that each link should only carry one relationship. The discriminative relational learning [8] exploits community features as latent social dimensions to aid attribute classification. Therefore, each link is only understood through one attribute chosen by the classification method applied on the two linked nodes. The Co-Profiling [3] algorithm attempts to learn both user attributes and circles via searching for the reasons of link formation. Each clink is then understood through one reason within one of the non-overlapping circles it detects. Considering two users that are both colleagues and schoolmates, those algorithms force the result to be either of them, which is partial and does not always reflect the truth. In contrast, ARP will yield two close probabilities w.r.t. the two relationships.

The second group of algorithms can produce complete but not systematic relationship semantics. As they evolve, many community detection algorithms nowadays attempt to characterize communities through attributes. Examples include generative models like CESNA [9] and Circles [4] and other frameworks like PCL-DC [10] and CODICIL [6]. They all explicitly model the node attributes that cause communities to form and compute a weight matrix characterizing communities w.r.t. attributes. Relationship semantics can then be generated by assuming that links within the same communities carry the same relationships. Therefore, multiple relationships can be associated on each link, if the two linked nodes belong to multiple overlapping communities. However, since they only compute the community semantics, the relationship semantics computed from their results are coarse. To be more specific, there is no way to understand every link, such as those between different communities and outside of any communities. Moreover, they fail to distinguish individual links within the same community. Unlike them, ARP aims to profile relationships in a finer granularity. Rather than relying on the detection of communities, it utilizes the local paths to precisely understand every link as long as a path goes through it.

Appendix D: Case Studies on DBLP

One advantage of ARP over the compared algorithms is that it can estimate the probability of each connection to carry each relationship. On LEN and FEN, we convert the probabilities into binary outputs in order to present quantitive comparisons with the baselines. However, the application of ARP is much broader than binary predictions. We use DBLP to present some insightful results derived from the relationship probabilities, which only ARP can generate.

Consider some interesting novel applications on DBLP. One of them is to find out people's closest co-authors within different research fields. *E.g.*, two authors might study similar problems in data mining, but very different problems in database. Thus, how can we identify people's closest co-authors given a specific field? Another interesting application is to identify the closest pairs of authors within each field of study, *i.e.*, who study the closest problems and collaborate most in a specific field? Considering specific relationships, such problems are novel and naturally different from general graph ranking.

We show that problems like these are direct applications of ARP. By modeling publication venues as user attributes and co-authorship as user connections, ARP accurately computes the closeness among authors *w.r.t.* different fields.

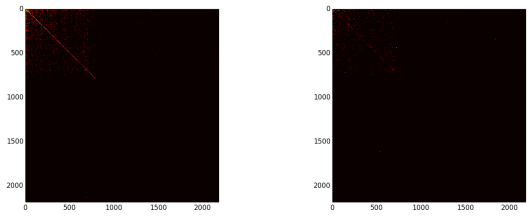
Consider three representative venues that correspond to three different but related fields. Table 1 shows the relationship specific closeness learned by ARP and normalized into multinomial distributions over each pair of authors. While relationships can be multiple and vary across connections, ARP completely retrieves them in all aspects. As we identify the authors, we observe that the relationships between some specific pairs of authors are quite interesting, *e.g.*, Jiawei Han and Xiaolei Li. We see that they are very close in VLDB, a bit close in KDD, but far away in ICML. To interpret the results, we look into the data and find that among the three conferences considered, the two authors have direct collaborations only in VLDB, which explains for the corresponding strong closeness. Nevertheless, they both directly work with authors like Dong Xin and Hong Cheng, who have collaborations in KDD. While the truth is that some of the papers that Jiawei Han and Xiaolei Li co-authored in VLDB are quite related to data mining (KDD), such semantics is hidden but effectively retrieved through paths connecting Dong Xin and Hong Cheng and then annotated to the relationship between Jiawei Han and Xiaolei Li by ARP.

Authors	KDD	VLDB	ICML
Jiawei Han, Philip S. Yu	**0.65**	*0.35*	0
Jiawei Han, Xiaolei Li	*0.04*	**0.96**	0
Jiawei Han, Tianbao Yang	*0.17*	0	**0.83**
Christos Faloutsos, Hanghang Tong	**0.86**	*0.13*	0.01
Divesh Srivastava, H. V. Jagadish	*0.03*	**0.97**	0
Corinna Cortes, Mehryar Mohri	*0.14*	0	**0.86**

Table 1: **Multi-aspect author relationships.**

Authors	(A) Holistic	(B) Single
Jiawei Han, Chi Wang	1.00/1st	1.00/1st
Christos Faloutsos, Hanghang Tong	0.95/2nd	1.00/1st
Hynne Hsu, Mong-Li Lee	0.93/3rd	0.72/10th
Jiawei Han, Philip S. Yu	0.90/4th	0.63/18th
Christos Faloutsos, Lei Li	0.85/5th	0.72/10th

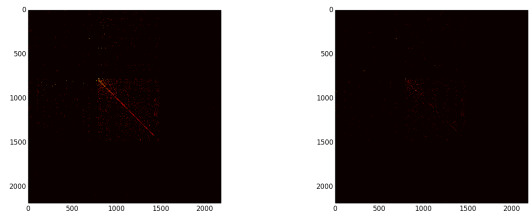
Table 2: **Rank list of closest authors on KDD.**



(a) By holistic path model (b) By single edge model

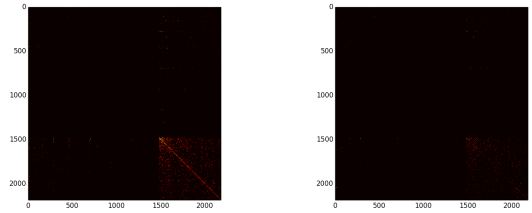
Figure 1: **Collaborations in KDD are highlighted.**

In Table 2, pairs of authors are ranked with their relative closeness in the research field of data mining *w.r.t.* the KDD conference. Column (A) shows the results of holistic modeling, where we set $K = 3$ and $\alpha = 0.8$ to consider indirect collaborations. The results are intuitive because the top ranked pairs of authors



(a) By holistic path model (b) By single edge model

Figure 2: **Collaborations in ICML are highlighted.**



(a) By holistic path model (b) By single edge model

Figure 3: **Collaborations in VLDB are highlighted.**

are indeed those who collaborate most in the field. To show that the results in Column (A) are non-trivial as cannot be simply computed by counting the number of collaborated papers, we also provide in Column (B) the results without holistic modeling, which are less intuitive. *E.g.*, although Han and Yu work quite closely on data mining, the closeness between them decreases from 0.90 to 0.63 and their rank drops from $4th$ to $18th$, merely because their many indirect collaborations are ignored. The situations are similar for many other pairs such as Faloutsos and Li.

Next, we demonstrate the power of our holistic closeness model by visualizing the computed collaboration matrices in different fields in comparison with those computed by the single edge model. In Figure 1-3, the x and y axis are the same set of researchers. As we can see, the collaboration matrices are naturally sparse. While the three relationships cluster on different locations (thus among different set of authors), some collaborations indeed bare multiple relationships (the same red dots appear in multiple figures). Also, it is interesting to see that in the KDD plot, the red dots scatter quite strictly in the top-left corner, which means that only data mining people collaborate in data mining a lot. However, in both the ICML plot and the VLDB plot, while most red dots scatter in the corresponding locations (the center-center and bottom-right), some obviously appear in the ICML-KDD and VLDB-KDD locations. It clearly indicates that many data mining people also collaborate in machine learning and database. It is true because data mining people need to know both machine learning and database, but not vise versa. Moreover, in both Figure 2 and 3, there is almost no red dot in the VLDB-ICML squares, which means database people seldom collaborate in machine learning conferences and vise versa.

In the collaboration matrices computed by single edge models, the same insightful observations are much harder to make. The red dots are much sparser, especially in the cross-field locations. *E.g.*, in the Figure 2(b), we can hardly observe the collaborations in machine learning between data mining researchers and machine learning researchers, as we can observe clearly in the Figure 2(a).

Due to space limit, for clearer views of the plots and more interesting results, please visit our Github project[1].

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[1] https://github.com/yangji9181/ARP2017