VERSACHI: Finding Statistically Significant Subgraph Matches using Chebyshev's Inequality

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ABSTRACT

Approximate subgraph matching, which is an important primitive for many applications like question answering, community detection, and motif discovery, often involves large labeled graphs such as knowledge graphs, social networks, and protein sequences. Effective methods for extracting matching subgraphs, in terms of label and structural similarities to a query, should depict accuracy, computational efficiency, and robustness to noise. In this paper, we propose VERSACHI for finding the top-k most similar subgraphs based on 2-hop label and structural overlap similarity with the query. The similarity is characterized using Chebyshev's inequality to compute the chi-square statistical significance for measuring the degree of matching of the subgraphs. Experiments on real-life graph datasets showcase significant improvements in terms of accuracy compared to state-of-the-art methods, as well as robustness to noise.

CCS CONCEPTS

• Information systems → Information systems applications; Data mining;

KEYWORDS

Subgraph Similarity, Approximate Matching, Statistical Significance, Chi-Square, Labeled Graph, Chebyshev's Inequality

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1 INTRODUCTION

With the growth of Open Linked Data in the form of knowledge graphs, social networks, bioinformatic structures, and road networks, efficient graph mining poses a challenging problem [2, 45]. Such large data sources are represented as labeled graphs, where entities are modeled as vertices, while their relationships are captured by edges, with labels defining the attributes of entities and relations.

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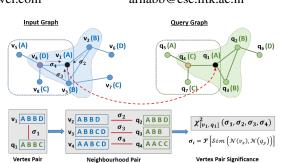


Figure 1: Two-hop neighborhood similarity based computation of χ^2 statistical significance for vertex match in VERSACHI.

Subgraph querying is used across several domains including frequent pattern search in data mining [30], community detection in IR [24], question answering in NLP [36], object recognition in computer vision [6], and route planning [10]. The problem of subgraph match querying entails the extraction of subgraphs from an underlying graph having similar structure and labels to a given query [29, 33].

Traditional approaches for exact structural and label matching based on isomorphism are computationally infeasible. Thus, approaches based on pruning [26, 39, 50], indexing [42, 44], filtering [8, 20], and dynamic programming [22] have been proposed. However, they fail to scale for modern web-scale graph applications, wherein approximate subgraph matching was explored [29, 31] to extract similar subgraphs, with exact matches or with slight variations in structural elements and label mismatches. For example, in bioinformatics, approximate subgraph matching enables the detection of candidate regions in genome, that might have undergone abnormal mutations, for studying the associated medical effects [43, 51]. Although approximate subgraph extraction have been well studied [3, 18, 29, 31, 44, 47], efficiently finding matching subgraphs with improved runtime and accuracy remains an important problem. **Problem Statement.** Consider $\mathcal{G} = (\mathcal{V}_{\mathcal{G}}, \mathcal{E}_{\mathcal{G}}, \mathcal{L}_{\mathcal{G}})$ to be an input graph, where $\mathcal{V}_{\mathcal{G}}$ and $\mathcal{E}_{\mathcal{G}}$ denote the vertex and edge sets respectively, while $\mathcal{L}_{\mathcal{G}} : \mathcal{V}_{\mathcal{G}} \to \Gamma$ maps the vertices in \mathcal{G} to a finite label (or attribute) set Γ . A similar query graph is considered: $Q = (\mathcal{V}_Q, \mathcal{E}_Q, \mathcal{L}_Q)$. Without loss of generality, we assume that the graph G is deterministic, undirected, vertex labeled, and does not contain hyper-edges. The problem of approximate subgraph matching aims to find the top-k subgraphs of G that are best matching (maximum similarity) to Q in terms of vertex label and edge overlap. In our context, VERSACHI finds the top-k statistically significant subgraphs of \mathcal{G} as the best approximate matches of Q.

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State-of-the-art. (Sub-)graph matching has been extensively studied, and the existing body of work can be broadly categorized into two groups – *exact* methods and *approximate* heuristics. Since graph isomorphism is quasi-polynomial [4] and subgraph isomorphism is NP-complete [12], earlier works on exact graph matching such as Swift-Index [42], VF2 [13, 26], PathBlast [28], SAGA [47], Iso-Rank [44] and GraphGrep [20] to name a few, explored pruning and indexing techniques. To tackle incomplete and noisy data, approximate matching techniques tolerate small amounts of structural and label mismatches. These methods usually rely on identifying candidate vertices, whose neighborhoods are then progressively expanded in a greedy manner - providing compute efficiency, although with possibly sub-optimal results. Initial approaches like TALE [48], C-Tree [59], GString [25] and SAPPER [58] were based on indexing techniques and graph distance measures to compute the degree of similarity. The use of pattern matching, semantic-based search, and graph decomposition for finding matching subgraphs were explored in gIndex [54], FG-Index [9], iGraph [23], Grafil [55], GPTree [57], cIndex [7], iGQ [52], and SIM-T [31]. Surveys on the rich literature of graph matching can be found in [11, 19, 34, 53]. Recent techniques like NeMa [29] and GFinder [33] adopt a combination of efficient indexing and graph traversal based cost measure to efficiently identify candidate matching regions, while VELSET [18] and NAGA [18] use statistical measure to mine subgraphs that demonstrate significant deviations from the background distribution when matched to a query. Approximate graph matching in the context of probabilistic graphs have also been studied [1, 21, 27, 32, 35, 45, 56]. Preliminaries. Statistical significance models the relationships between the observations and the factors that affect the system. The pvalue [37] measures the probability of attributing an observed event to chance or randomness. Since extreme events are rare, they exhibit a smaller p-value or a higher statistical significance. Since, computation of p-value is exponential, the *Pearson's chi-square statistic* (χ^2) has been shown to provide an estimate [38] of the "goodness-of-fit" of the set of observations. It is computed as the normalized squared difference between the expected and observed occurrence counts of the different outcomes. Mathematically, $\chi^2 = \sum_{\forall i} \left[(O_i - E_i)^2 / E_i \right]$, where O_i and E_i are the observed and expected number of occurrences, respectively, for all outcomes i. The Chebyshev's inequality [46] models the probability of deviation for a random variable in terms of the number of standard deviations from the distribution mean. Thus, for a random variable X with finite mean μ and non-zero variance δ^2 , we have $\Pr(|X - \mu| \ge t \cdot \delta) \le 1/t^2$ for any t > 0 ($t \in \mathbb{R}$). Intuitively, the degree of label and structural overlap (i.e., similarity) between a query and its matching subgraph would demonstrate significant deviations (due to high similarity) from the expected characteristics (considering a random subgraph). The Chebyshev's inequality can be used to characterize the difference in terms of the number of standard deviations away from the mean to compute the statistical significance of candidate matching subgraphs. Such techniques have been studied for sequence mining [15, 16, 41], substring matching [14], subgraph similarity [1, 18], and clique finding [17]. Contributions. In this paper, we propose the Vertex Neighborhood Aggregation for Statistically Significant Subgraphs via Chebyshev

Inequality (VERSACHI) algorithm for efficient top-k subgraph matching based on statistical significance. We identify candidate neighborhood regions matching an input query by using *two-hop* label and structural overlap based similarity. The deviation of the observed similarity, from the underlying distribution is then characterized by Chebyshev's inequality and represented as symbols. Based on statistical significance, matching candidate regions are identified and explored in a greedy manner, to obtain the best matching subgraph to the query. Observe that VERSACHI adopts the methodology of [17] for finding subgraph matches, while differing from [18] in symbol computation and neighborhood similarity. Initial empirical results on real and synthetic datasets showcase our proposed framework to outperform existing techniques in accuracy and robustness to noise.

2 VERSACHI ALGORITHM

This section describes the VERSACHI algorithm for extracting the top-k best approximate matching subgraphs from a target graph $\mathcal{G} = (\mathcal{V}_{\mathcal{G}}, \mathcal{E}_{\mathcal{G}}, \mathcal{L}_{\mathcal{G}})$, with respect to a query graph $\mathcal{Q} = (\mathcal{V}_{\mathcal{Q}}, \mathcal{E}_{\mathcal{Q}}, \mathcal{L}_{\mathcal{Q}})$. The working of VERSACHI comprises the following steps. The first 5 steps are *offline* and are done only once for a target graph, while the last 4 are *online* and take place when a query arrives.

1. Index Creation. Given a target graph \mathcal{G} , VERSACHI initially constructs two indexing lists summarizing the labels of the vertices and their neighbors. The first is an *inverted list*, $IL_{\mathcal{G}}$, that maps vertex labels to the corresponding list of vertices having the label. The second index, the *label neighbor list*, $LNL_{\mathcal{G}}$, stores the label information of the neighbors for each vertex in \mathcal{G} . A *label count vector* index, $LCV_{\mathcal{G}}(u)$, for each vertex u in \mathcal{G} is also constructed. It stores the count of occurrence of each label (for $|\Gamma|$ labels) in the neighborhood of u. This enables efficient computation of similarity between vertices as described next (step 4 onwards).

2. Similarity Measure. For a vertex pair (u, v) we use a modified *Tversky index*¹ [49] to define the *vertex similarity score* (η) :

$$\eta_{u,v} = |\mathcal{N}(u) \cap \mathcal{N}(v)| / (|\mathcal{N}(u) \cap \mathcal{N}(v)| + |\mathcal{N}(v) \setminus \mathcal{N}(u)|^{\gamma})$$
(1)

where $\mathcal{N}(u)$ is the set of labels in the neighborhood of u including the label of u itself. Observe, by setting $\gamma = 1$, we obtain the original Tversky index with $\alpha = 0$ and $\beta = 1$. Intuitively, the similarity of $u \in \mathcal{G}$ is maximized w.r.t. $v \in \mathcal{Q}$ when all neighbor labels of v are present in the neighbors of u (i.e., $\mathcal{N}(v) \subseteq \mathcal{N}(u)$). Since the presence of additional neighbors of $u \in \mathcal{G}$ should not affect the similarity, we set $\alpha = 0$ in the Tversky index. In essence, Eq. (1) captures the *neighborhood recall* of $v \in \mathcal{Q}$ provided by $u \in \mathcal{G}$ (thus, $\beta = 1$). The exponential *penalty factor*, γ , penalizes increasing mismatches in the neighborhood label overlap between vertex pairs. It captures fine differences in the neighborhoods by accentuating even smaller mismatches. Empirically, $\gamma = 3$ gave the best results.

3. Initialization. Using $LCV_{\mathcal{G}}(u)$ structures and similarity measure, VERSACHI computes the vertex similarity scores for every vertex pair in \mathcal{G} . This captures the underlying distribution. The expected similarity distribution across random neighborhoods of \mathcal{G} is captured via 3 characteristics computed using $\eta_{u,w} : \forall \langle u \in \mathcal{G}, w \in \mathcal{G} \rangle$.

(a) $\psi(\mathcal{G}) = \sum_{u,w \in \mathcal{G}} \eta_{u,w} / |\mathcal{V}_{\mathcal{G}}|$: *average* vertex similarity score for all vertex pairs in \mathcal{G} ,

(b)
$$\delta(\mathcal{G}) = \left(\sum_{u,w\in\mathcal{G}} (\eta_{u,w} - \psi(\mathcal{G}))^2 / (|\mathcal{V}_{\mathcal{G}}| - 1)\right)^{1/2}$$
 : standard

 $[\]overline{|S(X,Y)|} = \frac{|X \cap Y|}{|X \cap Y| + \alpha |X \setminus Y| + \beta |Y \setminus X|} \text{ for sets } X \text{ and } Y \text{ with parameters } \alpha, \beta \ge 0.$

deviation of the vertex similarity scores of \mathcal{G} , and

(c) $\triangle(\mathcal{G}) = \max_{u,w \in \mathcal{G}} \{ (|\eta_{u,w} - \psi(\mathcal{G})| / \delta(\mathcal{G}) \} : maximum \text{ deviation} of vertex similarity score from the average among all the vertex pairs in terms of standard deviations in <math>\mathcal{G}$.

4. Symbol Categorization. The degree of matching between a target graph vertex and a query vertex is captured in VERSACHI by the amount of deviation of the vertex pair similarity score (in terms of the number of standard deviations) from the underlying expected distribution (computed above). The standard deviations are discretized using the *step size* parameter, κ . It also determines the total number of possible symbols, $\tau = \lceil (\Delta(\mathcal{G}) - 1)/\kappa \rceil$. The set of category symbols, therefore, is $\Sigma = \{\sigma_1, \sigma_2, \cdots, \sigma_\tau\}$. Smaller values of κ is preferred for differentiating between finer-grained structural mismatches.

For a pair of vertices u, w, its similarity is characterized using the symbol $\sigma_i, 1 \le i \le \tau$. The first symbol, σ_1 , spans the range of standard deviations up to $1 + \kappa$, i.e., $\sigma_1 : 0 \le |\eta_{u,w} - \psi(\mathcal{G})|/\delta(\mathcal{G}) < 1 + \kappa$. Subsequent symbols cover step size standard deviations each, $\sigma_i : 1 + (i - 1) \cdot \kappa \le |\eta_{u,w} - \psi(\mathcal{G})|/\delta(\mathcal{G}) < 1 + i \cdot \kappa$ for $2 \le i \le \tau$. **5. Expected Probabilities of Symbols.** The expected probability of occurrence associated with the category symbols is next computed using the *Chebyshev's inequality*. Observe, the deviation of vertex pair similarity from the mean can be in negative or positive direction.

Since we are interested in vertices that have higher similarity than the mean (to capture higher matching), we only discretize the similarity (into symbols) when it is greater than the mean. For all similarities that are lesser than the mean, we fold them into symbol σ_1 . Thus, assuming symmetric one-sided Chebyshev's inequality, the occurrence probability of symbol σ_i is $\Pr(\sigma_i) = \frac{1}{2} \left[\frac{1}{(1+(i-1)\cdot\kappa)^2} - \frac{1}{(1+i\cdot\kappa)^2} \right]$ for $2 \le i \le \tau$, and $\Pr(\sigma_1) = 1 - \sum_{j=2}^{\tau} \Pr(\sigma_j)$.

We also empirically evaluated the variant where the deviation in both the positive and negative side of the mean are considered (i.e., without folding). However, it produced no changes in our results. Since a very low similarity (large negative deviation) can potentially have large chi-square values and, thus, produce false matching results, VERSACHI uses the one-sided version.

Note that all the above steps are *offline* operations and performed only once for a target graph \mathcal{G} .

6. Candidate Pair Mapping. Upon arrival of a query graph Q, the *online* processing starts with the construction of indexes IL_Q , LNL_Q , and LCV_Q , analogously to G. For each *label* in Q, VER-SACHI creates *candidate pairs* between the vertices of G and Q having the same label. These candidate pairs form the initial seed vertex for extracting matching subgraphs (to the query) via greedy neighborhood search. Formally, the candidate pairs generated are $CP = \{ \langle v \in G, q \in Q \rangle \mid \mathcal{L}_G(v) = \mathcal{L}_Q(q) \}.$

7. Vertex Symbol Sequence. For a candidate pair $\langle v \in \mathcal{G}, q \in Q \rangle$, VERSACHI computes the vertex pair similarity score, $\eta(v, q)$, and characterizes the similarity score by assigning a category symbol based on the deviation from the expected similarity distribution (as discussed previously). The category symbol $\sigma_{\langle v,q \rangle}$ captures the one-hop neighborhood similarity for vertices *v* and *q* (see Eq. (1)).

We next compute "second-order" candidate pairs between the vertex sets adjacent to v and q. A *greedy* best mapping based on the vertex pair similarity score is used to compute the second-order candidate pairs. Similar to $\langle v, q \rangle$, each second-order candidate pair is assigned a category symbol based on the deviation of its similarity

score from the expected. The initial category symbol $\sigma_{\langle v,q \rangle}$ is aggregated with the second-order category symbols to form the *vertex* symbol sequence, $O_{\langle v,q \rangle}$, for the candidate pair $\langle v,q \rangle$.

As an example, consider Fig. 1 depicting an initial candidate pair between vertices v_1 and q_1 (both having label A) with category symbol σ_1 assigned to it (using Eq. (1)). The adjacent vertices of v_1 ({ v_2, v_3, v_4 }) and the neighbors of q_1 ({ q_2, q_3, q_4 }) are then greedily best-matched based on vertex pair similarity to obtain the "second-order" candidate pairs. For instance, v_2 and q_2 provides the best match with the same label and the same neighborhood labels and, thus, forms the next candidate pair (with, say, category symbol σ_2). Subsequently, v_3 and q_3 are matched having the same label and partial neighborhood overlap (consider to be assigned symbol σ_3). Finally, the candidate pair $\langle v_4, q_4 \rangle$ is obtained with category symbol σ_4 . The corresponding vertex symbol sequence, $O_{\langle v_1, q_1 \rangle} = \{\sigma_1, \sigma_2, \sigma_3, \sigma_4\}$, associated to $\langle v_1, q_1 \rangle$, captures the twohop similarity between the candidate pair vertices v_1 and q_1 (Fig. 1). **8. Statistical Significance.** The computed symbol sequence $O_{\langle v, q \rangle}$ signifies the degree of matching between the two-hop neighborhoods of v and q. Assuming d to be the *degree* of q, since mapping is performed for the neighbors of q, the length of $O_{\langle v,q \rangle}$ is d. Thus, the expected occurrence counts of category symbol σ_i is $E[\sigma_i] =$ $d \cdot \Pr(\sigma_i)$. The *observed occurrence counts* of the category symbols are directly obtained from $O_{\langle v,q \rangle}$. Using the observed and expected counts, VERSACHI computes the *chi-square statistics*, $\chi^2_{(v,a)}$, for all the candidate pairs obtained in CP (see step 6).

9. Approximate Matching. The candidate pairs along with their computed chi-square values, $\langle v, q, \chi^2_{\langle v,q \rangle} \rangle$, are inserted into a *primary max-heap* structure. The candidate pair with the largest χ^2 value is extracted (assume $\langle v, q \rangle$) for initializing the top-1 matching subgraph, $Match^{(1)}$, and is considered as the starting seed vertex for greedy expansion to find matching subgraph region for the query Q.

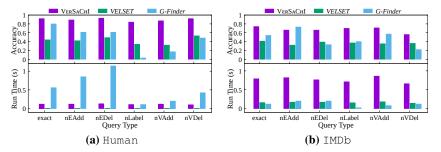
Next, candidate pairs between the adjacent vertices of the extracted seed pair (v and q) are constructed (as in step 6) and pushed into a *secondary max-heap* structure. As before, the vertex symbol sequence of the candidate pairs in the secondary heap are constructed, their statistical significances computed, and the pair with the highest χ^2 value is extracted and added to $Match^{(1)}$. This process is iterated till the secondary heap is empty, or the size of $Match^{(1)}$ equals the number of vertices in Q. The subgraph obtained in $Match^{(1)}$ is reported as the *top-1 best approximate matching subgraph* for Q.

Vertices extracted from the primary and secondary heaps are marked as "done" to prevent duplicate entries in the heap structures, and ensuring that the same region is not repeatedly explored. To retrieve more *top-k* approximate matches for a query, the secondary heap is reset and the process is re-run, starting from picking the currently best candidate pair (with highest statistical significance) from the primary heap. This is repeated until k matches are obtained. **Complexity Analysis**

Assume graph \mathcal{G} to contain *n* vertices, *m* edges and $|\Gamma|$ unique labels. Index construction (offline phase) requires O(n) space for $IL_{\mathcal{G}}$, O(m) for $LNL_{\mathcal{G}}$, $O(n \cdot |\Gamma|)$ for $LCV_{\mathcal{G}}$, and $O(\tau)$ for symbol probabilities. The overall space complexity of VERSACHI, therefore, is $O(n+m+\tau+n\cdot|\Gamma|)$. The time taken for index construction are O(n) for $IL_{\mathcal{G}}$, and O(m) for both $LNL_{\mathcal{G}}$ and $LCV_{\mathcal{G}}$. Computing the target

Dataset	# Vertices	# Edges	# Unique Labels	Dataset /	Accuracy					Running Time (sec)				
Human	4,674	86,282	44	Algorithm	Human	HPRD	Protein	Flickr	IMDb	Human	HPRD	Protein	Flickr	IMDb
HPRD	9,460	37,081	307	VELSET [18]	0.42	0.65	0.37	0.75	0.53	0.01	0.01	0.16	0.13	1.31
Protein	43,471	81,044	3	· · · · · · · · · · · · · · · · · · ·										
Flickr	80,513	5.9M	195	G-Finder [33]	0.45	0.12	0.47	out of memory		0.55	0.01	0.12	out of n	
IMDb	428,440	1.7M	22	VERSACHI	0.90	0.81	0.67	0.84	0.87	0.12	0.06	0.77	1.98	6.90
(a)									(b)					

Table 1: (a) Summary of the datasets characteristics. (b) Overall accuracy and runtime performance of the algorithms on the different datasets.



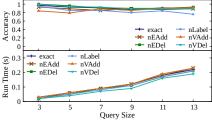


Figure 2: Performance for different query types on Human and IMDb datasets.

Figure 3: Performance with query size on Human dataset.

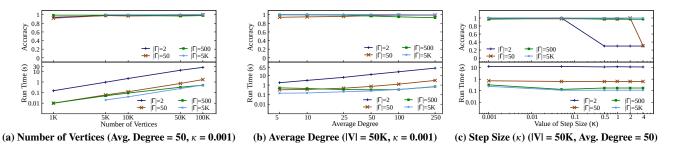


Figure 4: Performance of VERSACHI on Barabási-Albert graphs with varying (a) number of vertices (n), (b) average degree, and (c) step size (κ).

graph underlying distribution requires traversal of $LCV_{\mathcal{G}}$ for each vertex pair in \mathcal{G} . Thus, total *offline* time is $O(n+m+n^2 \cdot |\Gamma|) \approx O(n^2)$.

Once a query arrives, for each query vertex, candidate pairs (with same label) are constructed using the inverted indices. Assuming uniform label distribution in \mathcal{G} , the number of candidate pairs is $O(n_Q \cdot n/|\Gamma|)$. For each candidate pair, vertex symbol sequence generation (both initial and "second-order") takes $O(\rho \cdot |\Gamma|)$ time where ρ is the maximum degree in \mathcal{G} . Since χ^2 computation takes $O(\tau)$ time, the overall runtime of VERSACHI is $O(n_Q \cdot n/|\Gamma|)$.

3 EXPERIMENTS

In this section, we discuss the empirical setup and evaluation of the VERSACHI algorithm, and its comparison to existing approaches. **Datasets.** We evaluate the performance of the algorithms on real datasets from 3 different domains: (i) *Biological Networks:* protein-protein interaction graphs of Human, HPRD [5] and Protein [40]; (ii) *Social Interaction:* social interaction network between users of the image and video hosting site Flickr, with the label of each user (vertex) denoting the group that she belongs to [40]; and (iii) *Knowledge Graph:* IMDb [40] containing named-entities like movies, actors, etc., along with their relationships. The characteristics of the

datasets are shown in Table 1(a). Synthetically generated *Barabási-Albert* graphs are also used to study the scalability of VERSACHI. **Query.** Query graphs (connected) are constructed (from the dataset) by initially selecting a random vertex, and exploring its neighborhood till n_Q vertices are visited. These are referred to as *exact queries*. To study the performance of the algorithms in presence of noise, exact query graphs were perturbed by introducing structural and label noise randomly by (i) modifying vertex labels (*nLabel*), or (ii) inserting or deleting vertices (*nVAdd* and *nVDel* resp.), or (iii) adding or deleting edges (*nEAdd* and *nEDel* resp.). The number of perturbations are limited to 2. Further, for each scenario, we generate queries with sizes varying from 3 to 13 (at intervals of 2), with 20 query graphs extracted for each size. Thus, for each dataset, we consider ($6 \times 6 \times 20$) = 720 queries, and report average results.

Evaluation. The efficiency of the algorithms are measured in terms of edge retrieval accuracy (using the labels of end vertices), that is, the fraction of edges of the query graph Q that are present in the matching subgraph retrieved. Additionally, we report the average runtime required (per query) by the different approaches to extract the approximate matching subgraphs. Since the introduced perturbations do not exist in the original graph, the exact query (for

obtaining the noisy query) is considered as the ground truth. For *Barabási-Albert* graphs we use exact queries only.

Baselines. We compare the performance of VERSACHI algorithm against the following: (i) *VELSET* [18], a statistical significance based approach for exploring candidate regions with partial label match; and (ii) *G-Finder* [33], a graph traversal based indexing for dynamic filtering and refinement of candidate match neighborhoods. **Index.** The maximum index size taken by VERSACHI in our experiments is 1.4 GB for the Flickr graph, while the highest offline computation time is 32783.44 seconds, for IMDb dataset.

Setup. All experiments were implemented in C++ and were conducted on an Intel(R) Xeon(R) 2.60GHz CPU E5-2697v3 with 500GB of RAM. G-Finder was obtained from github.com/lihuiliullh/GFinder and evaluated on a Visual Studio 2015 C++ platform.

Empirical Results

From Table 1(b), we observe that VERSACHI has a significantly better accuracy than the competing algorithms for finding the best matching subgraphs with more than 20% accuracy improvements (averaged across varying query types and sizes). The run-time of VERSACHI is slightly more than the other approaches due to the twohop neighborhood similarity computation. In absolute terms, though, it is quite practical. Overall, with a slight increase in compute time, VERSACHI offers a substantial accuracy gain. (*G-Finder* crashes due to out-of-memory issues for Flickr and IMDb datasets.)

Fig. 2 depicts the performance for different query types. (Results on the other datasets are similar and are, thus, omitted due to space constraints). VERSACHI achieves better accuracy across all the different query types, with slight increase in runtime. Fig. 3 shows that with increase in query size, the runtime increases linearly (across query types), while the accuracy remains largely unaffected.

Fig. 4 studies the scalability of VERSACHI using synthetic *Barabási-Albert* graphs. The runtime is seen to increase linearly, with increase in number of vertices and average degree, conforming to the analysis of Sec. 2. The accuracy of VERSACHI is unaffected in these scenarios. With increase in the *step size* κ , accuracy decreases, as the number of symbols decreases, limiting the power of VERSACHI to differentiate between finer differences in neighborhood mismatches between the graphs, while the runtime remains mostly constant.

4 CONCLUSIONS

This paper proposed a scalable and highly accurate algorithm, VER-SACHI, for approximate labeled graph querying. It shows significantly better accuracy than the competing methods across datasets and noise. Our framework is generic enough to accommodate other similarity measures and application-dependent tail distributions.

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