Seedless Graph Matching via Tail of Degree Distribution for Correlated Erdős-Rényi Graphs

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Abstract—The graph matching problem refers to recovering the node-to-node correspondence between two correlated graphs. A previous work theoretically showed that recovering is feasible in sparse Erdős-Rényi graphs if and only if the probability of having an edge between a pair of nodes in one of the graphs and also between the corresponding nodes in the other graph is in the order of \(\Omega(\log(n)/n)\), where \(n\) is the number of nodes. In this paper, we propose a graph matching algorithm which obtains correct matching with high probability in Erdős-Rényi graphs for the region of \(\Theta(\log(n)/n)\) without using a seed set of pre-matched node pairs as an input. The algorithm assigns structurally innovative features to high-degree nodes based on the tail of empirical degree distribution of their neighbor nodes. Then, it matches the high-degree nodes according to these features, and finally obtains a matching for the remaining nodes. We evaluate the performance of proposed algorithm in the regions of \(\Theta(\log(n)/n)\) and \(\Theta(\log^2(n)/n)\). Experiments show that it outperforms previous works in both regions.

Index Terms—Graph Matching, Network Alignment, Erdős-Rényi Graphs.

1 INTRODUCTION

Graph matching (or network alignment) between two correlated graphs is the problem of finding bijection mapping between the nodes in one graph to the nodes in the other graph according to structural similarities between them. If the two graphs have exactly the same structure, the problem reduces to the graph isomorphism problem, but in general, the two graphs are only similar, which makes the problem more challenging.

Graph matching arises in various applications in different fields including computer vision [1], pattern recognition [2], autonomous driving [3], computational biology [4], [5], and social networks [6]. For instance, in computational biology, protein-protein interactions (PPI) can be modeled as graphs. PPI graphs of different species can be aligned by solving the graph matching problem which can be useful in investigating evolutionary conserved pathways or reconstructing phylogenetic trees [7].

Graph matching algorithms can be classified into two main categories: I) seed-based algorithms, and II) seedless algorithms. Seed-based graph matching algorithms work based on a set of pre-matched nodes from the two graphs, called seeds [8], [9], [10], while seedless algorithms do not require any seed set as input [2]. Moreover, in order to assist the matching procedure, some algorithms employ node or edge features as a side information (e.g., user names or locations in de-anonymization of social networks [11], [12]), while some other matching algorithms do not require such prior knowledge and only utilize the structural similarities between the two graphs as the most important feature in solving the problem [13]. In this paper, we focus on designing seedless graph matching algorithms which do not require either any input seed set, or any input features

for the nodes or edges as side information and work solely based on structural similarities between the two correlated graphs.

Most of the seed-based graph matching algorithms rely on the idea of percolation, in which the algorithm starts from a small set of pre-matched nodes (seeds), and gradually expands the set of matched nodes by applying some rules on the neighbor nodes of previously matched nodes. The pioneering method in this category, which succeeded in de-anonymizing a social network with millions of nodes, was introduced by Narayanan and Shmatikov [6]. They empirically observed that the proposed algorithm is very sensitive to the size of the seed set. If the size of seed set is too small, the algorithm could not percolate, but if the size exceeds a threshold, the algorithm could successfully percolate and de-anonymize a large portion of the entire network. Yartseva and Grossglauser [14] later proved that such phenomenon happens in random bigraph models. Later, Kazemi et al. [15] proposed a percolation-based method called “NoisySeed” algorithm. The main advantage of this algorithm, as the name implies, is that the initial seed set can include some incorrectly matched pairs as well. The required size for the seed set as well as the tolerable number of incorrect matches have been investigated in [15]. Recently, Zhang et al. [16] proposed a graph matching algorithm that can align two graphs in multi-levels including the node level as the finest granularity given a prior similarity matrix.

Compared with the above solutions, the seedless algorithms do not require pre-matched node pairs as an input. In the literature, several seedless methods have been proposed based on convex relaxations of graph matching problem. For instance, in [17], matching problem is relaxed as a quadratic programming problem, and then, the solution is projected into zeros and ones in order to recover the mapping between nodes of two graphs. Some other seedless algorithms rely
on computing graph edit distance between the two graphs, which is basically the minimum number of edge deletions or insertions required to convert one of the graphs to the other one [2, 18]. Methods based on convex relaxations or graph edit distance are often much more time consuming than other seedless graph matching algorithms [19].

Spectral methods are another type of seedless algorithms which match nodes based on eigenvalues and eigenvectors of a transformation of the graph’s adjacency matrix [20], [21], [22]. The main idea in these methods is to obtain Laplacian matrices from adjacency matrices of the two graphs and then compute the eigenvectors and eigenvalues of these Laplacian matrices. Next, \( k \) number of eigenvectors corresponding to top \( k \) eigenvalues are selected to construct a \( k \)-dimensional feature vector for every node. From these feature vectors, the nodes in two graphs can be matched based on a distance metric.

Besides to the above seedless algorithms, several machine-learning based algorithms have been proposed that match nodes based on a set of features which are extracted by processing additional information from nodes, e.g., user-names or locations in social networks [12], [23], [24]. As mentioned before, the proposed method in this paper works merely based on structural similarities between the two graphs, and does not require any additional features.

Recently, few seedless graph matching algorithms have been proposed for Erdős-Rényi graphs. Barak et al. [23] presented a matching algorithm that finds certain small subgraphs that appear in both graphs, based on which a set of seeds is formed accordingly. Next, a percolation algorithm extends the selected seeds to match all the nodes. This algorithm is designed for Erdős-Rényi graphs with average node degrees in the range \([n^{\epsilon(1)}, n^{1/153}]\) or \([n^{2/3}, n^{1-\epsilon}]\), where \( \epsilon \) is a small positive constant. This range covers very sparse or very dense Erdős-Rényi graphs. Compared with this algorithm, the proposed solution in this paper works on Erdős-Rényi graphs with average node degrees of order \( \log(n) \). Dai et al. [23] proposed another matching algorithm for Erdős-Rényi graphs called canonical labeling. In the first step of this algorithm, the nodes in the two graphs are sorted according to their degrees. Then, the top \( h \) highest degree nodes in two graphs are matched based on the sorted lists. In the second step, each remaining node \( j \) gets a binary vector of length \( h \). Entry \( i \) of this vector is equal to one if node \( i \) is connected to \( i \)-th node in the sorted list. Otherwise, this entry is set to zero. The nodes are then matched according to these binary feature vectors. Our experiments show that the canonical labeling does not have good performance in the graphs with average node degrees of order \( \log(n) \) or even \( \log^2(n) \). Ding et al. [19] proposed a matching algorithm for Erdős-Rényi graphs with average node degree in three regions including \( \Theta(\log^2(n)) \). In this algorithm, every node is assigned a feature vector containing empirical degree distribution of its neighbors. Then, the minimum distance on these features are used to match the nodes. This algorithm has a relatively higher accuracy in Erdős-Rényi graphs with average degree of \( \log^2(n) \), but our experiments show that it has poor performance for the graphs with average node degree of order \( \log(n) \).

In this paper, we propose a seedless graph matching algorithm for correlated Erdős-Rényi graphs. The proposed algorithm has two main steps: In the first step, for each node \( i \) in any of two correlated graphs which is among the top highest degree nodes in that graph, we construct a feature vector containing degrees of nodes like \( j \) having the following two properties: I) Node \( j \) should be in the neighborhood of node \( i \). II) Its degrees is in the tail of empirical degree distribution of nodes in neighborhood of node \( i \). Due to this property of the proposed algorithm, we call it “Tail Degree Signature (TDS)” graph matching algorithm. In the second step, we compute a distance metric between any pair of feature vectors and execute Hungarian algorithm [27] on the matrix of distances to generate a seed-set. Afterwards, we can feed this seed-set to NoisySeed algorithm [8] and obtain the final matching. We evaluate the performance of TDS algorithm for Erdős-Rényi graphs with average degree of order \( \log(n) \) and \( \log^2(n) \). Experiments show that TDS algorithm outperforms other related works for the case of average degree of order \( \log(n) \) and also \( \log^2(n) \).

2 Problem Definition

Graph matching is problem of identifying a bijection mapping between nodes in two structurally similar graphs. Let \( G_a(V_a,E_a) \) and \( G_b(V_b,E_b) \) be two graphs with node sets \( V_a \) and \( V_b \) of size \( n \), and edge sets \( E_a \) and \( E_b \). We denote the edge between nodes \( i \) and \( j \) by \((i,j)\). Let mapping function \( \pi : V_a \rightarrow V_b \) denote a one-to-one mapping between nodes of \( G_a \) and \( G_b \). The goal in the graph matching problem is to select a matching \( \hat{\pi} \) from \( n! \) different possible mapping functions in the symmetric group \( S_n \) such that:

\[
\hat{\pi} = \arg\min_{\pi \in S_n} \| A(G_b) - P_{\pi}^T A(G_a) P_{\pi} \|_F^2,
\]

where \( \| \cdot \|_F \) is Frobenius norm and \( A(G_a) \) and \( A(G_b) \) are the adjacency matrices for \( G_a \) and \( G_b \), respectively. Moreover, the matrix \( P_{\pi}^T A(G_a) P_{\pi} \) is a simultaneous row/column permuted version of \( A(G_a) \), and \( P_{\pi} \) is the permutation matrix corresponding to mapping \( \pi \) which is defined as:

\[
P_{\pi}[i,j] = \begin{cases} 1 & : i \in V_a, \ j \in V_b, \ j = \pi(i), \\ 0 & : \text{otherwise}. \end{cases}
\]

In other words, the objective function in Equation (1) measures the number of mis-matched edges between relabeled version of graph \( G_a \) based on mapping \( \pi \) and graph \( G_b \). In the worst case, solving the above optimization problem is NP-hard [28].

We assume that \( G_a \) and \( G_b \) are two correlated Erdős-Rényi graphs where the original graph \( G(V,E) \) is generated with parameter \( p \), i.e., there is an edge between any two nodes with probability \( p \). Then, two correlated graphs \( G_a \) and \( G_b \) are constructed where edge sets \( E_a \) and \( E_b \) are sampled from \( E \) with probability \( s \). In other words, every edge in edge set \( E \) is in \( E_a \) and \( E_b \) with probability \( s \), independently.
The vertex set $V_a$ is the same as $V$, but $V_b$ is a permuted version of $V$ according to mapping $\pi^*$. The matching algorithm tries to recover $\pi^*$ given only $G_a$ and $G_b$. For correlated Erdős-Rényi graphs, it can be shown [3] that maximum a-posteriori (MAP) estimation is equivalent to minimizing the objective function in Equation (1). Furthermore, MAP estimator finds the ground truth matching, i.e., $\pi = \pi^*$ with high probability if and only if $p s^2 = \Omega(\log(n)/n)$ [29].

### 3 Tail Degree Signature (TDS) Algorithm

Our proposed graph matching algorithm consists of four steps: I) Two small node subsets are selected from $G_a$ and $G_b$. II) For every node in the two selected subsets, a feature vector is extracted. III) Based on these feature vectors, the nodes in the two subsets are matched. IV) The matched nodes are provided as seeds to a percolation algorithm which matches all the nodes by extending the initially matched nodes, i.e., the provided seeds.

#### 3.1 Node Selection

**Method:** In the first step, $\tilde{n}$ number of nodes are selected from each of the two graphs in order to be matched in the next step. Let $V_a \subset V$ and $V_b \subset V$ denote the two selected subsets. Note that $|V_a| = |V_b| = \tilde{n}$ and $\tilde{n} << n$, i.e., the size of these subsets are small relative to the graph size. Ideally, we would like to have $\pi^*(i) \in V_b$ for any $i \in V_a$. In other words, the corresponding node of every node in the selected set $V_a$ is in $V_b$ and vice versa. Since we do not have access to the correct mapping $\pi^*$, it is challenging to select the sets $V_a$ and $V_b$ with such property. Herein, we select subsets $V_a$ and $V_b$ as $\tilde{n}$ highest-degree nodes from $V_a$ and $V_b$, respectively.

**Rationale:** We claim that for every node $i \in V_a$, its corresponding node is in $V_b$ with significant probability. We prove this claim in the following.

**Proposition 1.** Let $D^a_i$ and $D^b_{\pi^*(i)}$ denote the degrees of node $i$ in graph $G_a$ and its correspondence in graph $G_b$, respectively. The probability of degree of node $i$ in graph $G_a$ being greater than a threshold “$th$” given that the corresponding node’s degree in graph $G_b$ also being greater than the threshold $th$ is given as follows:

$$
\Pr(D^a_i \geq th | D^b_{\pi^*(i)} \geq th) = \frac{\sum_{k=th}^{n-1} F^2(th, k, s) B(n - 1, p; k)}{\sum_{k=th}^{n-1} F(th, k, s) B(n - 1, p; k)},
$$

where:

$$
B(n, p; k) = \binom{n}{k} p^k (1-p)^{n-k}, F(th, k, s) = \sum_{j=th}^{k} B(k, s; j).
$$

**Proof.** We can write the left hand side of Equation (3) as follows:

$$
\Pr(D^a_i \geq th | D^b_{\pi^*(i)} \geq th) = \frac{\Pr(D^a_i \geq th, D^b_{\pi^*(i)} \geq th)}{\Pr(D^b_{\pi^*(i)} \geq th)}.
$$

Let $D_i$ be the degree of corresponding node of $i$ in the original graph $G$. For the probability $\Pr(D^b_{\pi^*(i)} \geq th)$, we have:

$$
\begin{align*}
\Pr(D^b_{\pi^*(i)} \geq th) &= \sum_{k=th}^{n-1} \Pr(D^b_{\pi^*(i)} \geq th | D_i = k) \Pr(D_i = k) \\
&= \sum_{k=th}^{n-1} \Pr(D^b_{\pi^*(i)} \geq th | D_i = k) \Pr(D_i = k) \\
&= \sum_{k=th}^{n-1} \Pr(D^b_{\pi^*(i)} \geq th | D_i = k) B(n - 1, p; k) \\
&= \sum_{k=th}^{n-1} F(th, k, s) B(n - 1, p; k),
\end{align*}
$$

(a) The probability $\Pr(D^b_{\pi^*(i)} \geq th | D_i = k)$ is equal to zero for $k < th$. 
(b) According to definition of $B(n - 1, p; k)$ and the fact that the degree of node in the original graph $G$ has Binomial distribution with parameters $n - 1$ and $p$. 
(c) Given $D_i = k$, the distribution of $D^b_{\pi^*(i)}$ is Binomial with parameters $k$ and $s$. Thus, the probability $\Pr(D^b_{\pi^*(i)} = j | D_i = k)$ is equal to $B(k, s; j)$ and we can imply that: $\Pr(D^b_{\pi^*(i)} \geq th | D_i = k) = \sum_{j=th}^{k} B(k, s; j) = F(th, k, s)$ according to definition of function $F$.

Now, we derive the probability $\Pr(D^a_i \geq th, D^b_{\pi^*(i)} \geq th)$:

$$
\Pr(D^a_i \geq th, D^b_{\pi^*(i)} \geq th) = \sum_{k=0}^{n-1} \Pr(D^a_i \geq th, D^b_{\pi^*(i)} \geq th | D_i = k) \Pr(D_i = k) \\
= \sum_{k=th}^{n-1} \Pr(D^a_i \geq th, D^b_{\pi^*(i)} \geq th | D_i = k) \Pr(D_i = k) \\
= \sum_{k=th}^{n-1} \Pr(D^a_i \geq th | D_i = k) \Pr(D^b_{\pi^*(i)} \geq th | D_i = k) \\
= \sum_{k=th}^{n-1} \Pr(D^a_i \geq th | D_i = k) \sum_{j=th}^{k} B(k, s; j) \\
= \sum_{k=th}^{n-1} \sum_{j=th}^{k} B(k, s; j) B(n - 1, p; k),
$$

(a) $D^a_i$ and $D^b_{\pi^*(i)}$ are independent by fixing the value of $D_i$. 
(b) Due to the definition of function $F$.

Combining Equation (5) and Equation (6), we can derive Equation (3) and the proof is complete.

In graphs $G_a$ and $G_b$, every node $i$ is connected to any other node with probability $ps$, independent from other edges. Thus, every node’s degree has a Binomial distribution with parameters $n - 1$ and $ps$. Hence, we have for any node $i$ in graph $G_a$ or its correspondence in graph $G_b$:

$$
\Pr(D^a_i = k) = \Pr(D^b_{\pi^*(i)} = k) = B(n - 1, ps; k).
$$

(7)
Let \( N^{a,t}_{i} \) be the set of nodes in graph \( G_a \) whose distance from node \( i \) is exactly equal to \( t \), where \( t \in [1, \lambda] \), and \( \lambda \) is the maximum distance that is considered in the feature extraction procedure. For every node \( i \in \tilde{V}_a \) and every \( t \in [1, \lambda] \), set \( D(N^{a,t}_{i}) \) is formed as the degrees of the nodes in \( N^{a,t}_{i} \), i.e.,

\[
D(N^{a,t}_{i}) = \{ D^a_{i'} | i' \in N^{a,t}_{i} \}. \tag{11}
\]

Next, for a given integer parameter \( \theta \), we pick \( \theta \) of the smallest and \( \theta \) of the largest elements in \( D(N^{a,t}_{i}) \) and put them in feature vector \( \Phi^a_t \) of size \( 2 \theta \). Finally, feature vector \( \Phi^a_t \) is formed by concatenating vectors \( \Phi^a_t \) as follows:

\[
\Phi^a_t = \Phi^a_{t,1} | \Phi^a_{t,2} | \cdots | \Phi^a_{t,\lambda}. \tag{12}
\]

Thus, \( \Phi^a_t \) is a vector of size \( 2 \theta \lambda \). By a similar procedure, for every node \( j \in \tilde{V}_b \), feature vector \( \Phi^b_t \) is also formed. As an example of feature extraction procedure, suppose in Fig. 2(a), the set of nodes \( \tilde{V}_a \) is also shown in graph \( G_a \) and they are selected in \( \tilde{V}_a \). Similarly, nodes 12 and 9 are high-degree nodes in graph \( G_b \) and they are selected in \( \tilde{V}_b \). Fig. 2(c) shows the construction procedure of \( \Phi^a_t \) where \( N^{a,t}_{18} \) and \( D(N^{a,t}_{18}) \) are generated according to Fig. 2(b). Similarly, \( \Phi^b_t \), \( \Phi^a_t \) and \( \Phi^b_t \) are generated.

**Rationale:** In constructing the vector \( \Phi^a_t \), we select the degree of nodes in \( N^{a,t}_{i} \) which are in the tail region of empirical degree distribution of nodes in \( N^{a,t}_{i} \). Herein, we give an intuition why such selection is more preferable than considering nodes’ degrees outside of this region for \( t = 1 \). As we mentioned before, the degree distribution of node \( i \) in graph \( G_a \) or \( G_b \) is approximately normal distribution \( N(\mu, \sigma^2) \) with parameters \( \mu = (n - 1)ps \) and \( \sigma = \sqrt{(n - 1)(1 - ps)ps} \). Let \( U^a_t \) be the normalized degree of node \( i \) in graph \( G_a \), i.e., \( U^a_t = (D^a_{i} - \mu)/\sigma \). \( U^a_t \) is defined similarly in graph \( G_b \).

**Proposition 2.** If node \( j \in \tilde{V}_b \) is the corresponding node of a node \( i \in \tilde{V}_a \), i.e., \( j = \pi^*(i) \), then \( U^a_t \) and \( U^b_t \) are two correlated random variables with the correlation coefficient: \( \rho = s(1 - p)/(1 - ps) \). Otherwise, they are approximately uncorrelated for large \( n \).

**Proof.** To prove the statement of proposition, it is just needed to compute the following term for the two correlated random variables \( U^a_t \) and \( U^b_t \):

\[
\mathbb{E}\left[ D^a_{i}D^b_{\pi^*(i)} \right] = \mathbb{E} \left[ \sum_{k \neq i} \mathbb{I}_{i, k} \in E_a \right] \sum_{k' \neq \pi^*(i)} \mathbb{I}_{[\pi^*(i), k'] \in E_b} \right]
\]

\[
= \left( (n - 1)^2 - (n - 1) \right) (ps)^2 + \mathbb{E} \left[ \mathbb{I}_{i, k} \in E_a \right] \mathbb{I}_{[\pi^*(i), \pi^*(k)] \in E_b} \right]
\]

\[
= (n - 1)^2 - (n - 1) (ps)^2 + (n - 1) ps^2, \tag{13}
\]

where \( \mathbb{I}_{[\cdot]} \) is the indicator function.

(a) Due to the fact that the events \( \mathbb{I}_{[i, k] \in E_a} \) and \( \mathbb{I}_{[\pi^*(i), \pi^*(k)] \in E_b} \) are independent for \( k' \neq \pi^*(k) \).

(b) The probability of existing an edge between nodes \( i \)
and $k$ in the original graph $G$ is equal to $p$. Moreover, the probability of having that edge in both graphs $G_a$ and $G_b$ is $s^2$. Hence, the expectation of event in the second sum would be $ps^2$.

Thus, the correlation coefficient between $D^a_i$ and $D^b_{\pi^*(i)}$ would be:

$$\rho = \frac{E[D^a_i D^b_{\pi^*(i)}] - \mu^2}{\sigma^2} = s(1-p)/(1-ps). \quad (14)$$

Similarly, for the case of $j \neq \pi^*(i)$, it can be shown that $\rho = s(1-p)/((n-1)(1-ps))$. Thus, the two random variables are approximately uncorrelated for large $n$ if $j \neq \pi^*(i)$.

Based on the above observation, we can model the two random variables $U^a_i$ and $U^b_{\pi^*(i)}$ as follows: $U^a_{\pi^*(i)} = \rho U^a_i + \sqrt{1-p^2}Z$ where $Z$ is an independent standard normal variable. To show the advantage of selecting nodes’ degrees in the tail of degree distribution, we define the following two metrics between any two nodes $i \in V_a$ and $j \in V_b$:

$$\Delta^ij_{\text{tail}} = \frac{1}{2} \int_{-\infty}^{-\frac{1}{2}} |\hat{U}^a_i(x) - \hat{U}^b_j(x)|dx + \frac{1}{2} \int_{\frac{1}{2}}^{\infty} |\hat{U}^a_i(x) - \hat{U}^b_j(x)|dx \quad (15)$$

and

$$\Delta^ij_{\text{center}} = \frac{1}{2} \int_{-\frac{1}{2}}^\frac{1}{2} |\hat{U}^a_i(x) - \hat{U}^b_j(x)|dx,$$

where $\hat{U}^a_i(x)$ and $\hat{U}^b_j(x)$ are the empirical distribution obtained from observing samples of $U^a_i$ and $U^b_j$, respectively. In fact, $\Delta^ij_{\text{tail}}$ and $\Delta^ij_{\text{center}}$ represent the total variation.
Algorithm 1 Percolation algorithm.

Input: $G_a, G_b, S, r$

Output: $\Pi$

1: $\mu \leftarrow 0$
2: for all pairs $(i, j) \in S$ do
3: $\forall (i', j') : i' \in N_i^{a, 1}, j' \in N_j^{b, 1}$ : increment $\mu(i', j')$
4: if $\mu(i', j') \geq r$ then
5: if $(i', x) \notin \Pi, \forall x \in V_a$ and $(y, j') \notin \Pi, \forall y \in V_a$ then
6: Add $(i', j')$ to set $\Pi$
7: $T \leftarrow S$
8: while $\Pi - T \neq \emptyset$ do
9: Randomly select pair $(i, j) \in \Pi - T$ and add it to set $T$
10: $\forall (i', j') : i' \in N_i^{a, 1}, j' \in N_j^{b, 1}$ : increment $\mu(i', j')$
11: if $\mu(i', j') \geq r$ then
12: if $(i', x) \notin \Pi, \forall x \in V_a$ and $(y, j') \notin \Pi, \forall y \in V_a$ then
13: Add $(i', j')$ to set $\Pi$

$\text{cost} = \frac{1}{n} \sum_{(i, j) \in S} X_{ij}$ (16)

In other words, by running Hungarian algorithm, we form a seed set that has minimum mean of similarity distance over all possible choices.

As an example, Fig. 2(d) shows $l_2$-norm distances between every pair of constructed feature vectors $\Phi_i^a$ and $\Phi_j^b$ from Fig. 2(c). This forms a $2 \times 2$ matrix since $n = 2$. The Hungarian algorithm runs on this matrix in order to find $\tilde{n}$ pairs with the mentioned property. Here, it matches nodes 5 and 18 in graph $G_a$ to nodes 12 and 9 in graph $G_b$, respectively.

Let $\tilde{n}_{\text{correct}}$ and $\tilde{n}_{\text{incorrect}}$ denote the number of correct and incorrect seeds in seed set $S$, respectively. Hence, $\tilde{n} = \tilde{n}_{\text{correct}} + \tilde{n}_{\text{incorrect}}$. We define the accuracy of matching high degree nodes as $\tilde{n}_{\text{correct}}/\tilde{n}$. Therefore, the maximum value of this accuracy is given in Equation (9). For $n = 100$, the maximum accuracy is shown in Fig. 4.

Complexity Analysis: Time complexity of seed selection step is in the order of $O(n^3)$ since finding similarity matrix $X$ is in the order of $O(n^2)$ and executing Hungarian algorithm is in the order of $O(n^3)$.

3.4 Percolation

Seed set $S$ consists of $\tilde{n}$ node pairs. This initial seed set is fed to the percolation algorithm introduced in [8] in order to match all the $n$ nodes. As shown in Algorithm [1] the percolation algorithm works based on assigning a score $\mu$ to all node pairs $(i, j)$, where $i \in G_a$ and $j \in G_b$. Scores $\mu$ are initially set to zero. The algorithm consists of two main parts. In the first part (lines 2-6), all node pairs in seed set $S$ are iteratively visited (line 2). In every iteration, score $\mu(i', j')$ is incremented for all $i' \in N_i^{a, 1}$, i.e., neighbors of $i$ in $G_a$, and all $j' \in N_j^{b, 1}$ (lines 3). Next, pair $(i', j')$ is added as a new match if $\mu(i', j')$ passes a certain threshold $r$, and if neither $i'$ nor $j'$ have been matched before (lines 4-6). Basically, the percolation algorithm matches node $i'$ in
Fig. 4. Comparing the accuracy of TDS (the proposed solution) with DP and Laplacian seedless graph matching algorithms in (a) $p = \log(n)/n$ and (b) $p = \log^2(n)/n$ regions. Here, $n = 1000$.

$G_a$ with node $j'$ in $G_b$ if $r$ neighbors of $i'$ in $G_a$ have been matched with $r$ neighbors of $j'$ in $G_b$.

The final matching $\Pi$ is formed in the second part of the algorithm (lines 7-13). Here, a set $T$ is initialized to $\mathcal{S}$ (line 7), and then, all node pairs in $\Pi - T$ are iteratively visited in random order. All visited node pairs are added to $T$ in order to avoid selecting a previously-visited node pair (lines 8-9). The rest of the algorithm (lines 10-13) is similar to the first part (lines 3-6).

**Complexity Analysis:** Time complexity of the percolation step is $O(n^3p^2)$. The first part (lines 2-6) and the second part (lines 8-13) of the percolation algorithm run in $O(nD_{\text{avg}})$ and $O(nD_{\text{avg}}^2)$, respectively. The average degree of a node is $D_{\text{avg}} = p(n - 1)$. Therefore, we can imply that the total time complexity of the percolation step is $O(n^3p^2)$.

4 Experimental Evaluation

In this section, we compare our proposed algorithm, called tail degree signature (TDS), with recent seedless graph matching algorithms on Erdős-Rényi graphs with $p = \log(n)/n$ and $p = \log^2(n)/n$. In particular we experiment with degree profile (DP) algorithm [19] and a spectral method called Laplacian algorithm [20], [21], [22].

Fig. 4(a) shows accuracy of the proposed algorithm for different values of $s$. Every point shows the average accuracy for 50 randomly-generated Erdős-Rényi graphs with $p = \log(n)/n$ and $n = 1000$. The proposed TDS algorithm achieves much higher accuracy compared to degree profile (DP) and Laplacian algorithms.

Fig. 4(b) presents the same comparison as Fig. 4(a) but for Erdős-Rényi graphs with $p = \log^2(n)/n$. In this region, TDS does not employ percolation. In other words, $n$ is set equal to $n$ in order to match all nodes without using the percolation algorithm. TDS has better performance compared to DP in $p = \log^2(n)/n$ region.

5 Conclusion

In this paper, we proposed a seedless graph matching algorithm for correlated Erdős-Rényi graphs. We introduced node features based on tail of degree distribution in order to match high-degree nodes and generate a seed set. From the obtained seed, we matched the remaining nodes in two graphs by a percolation method. We showed that this approach has advantages with respect to matching high-degree nodes based on center of degree distributions. Our experiments showed that our algorithm outperforms other related works for the average degree of order $\Theta(\log(n))$ and $\Theta(\log^2(n))$.

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