On the Performance of a Canonical Labeling for Matching Correlated Erdős-Rényi Graphs

Osman Emre Dai*, Daniel Cullina†, Negar Kiyavash*, and Matthias Grossglauser‡

* Department of Electrical and Computer Engineering, University of Illinois at Urbana-Champaign
  Email: {osmand2,kiyavash}@illinois.edu
† Department of Electrical Engineering, Princeton University
  Email: dculima@princeton.edu
‡ School of Computer and Communication Sciences, École Polytechnique Fédérale de Lausanne
  Email: matthias.grossglauser@epfl.ch

Abstract

Graph matching in two correlated random graphs refers to the task of identifying the correspondence between vertex sets of the graphs. Recent results have characterized the exact information-theoretic threshold for graph matching in correlated Erdős-Rényi graphs. However, very little is known about the existence of efficient algorithms to achieve graph matching without seeds.

In this work we identify a region in which a straightforward \(O(n^2 \log n)\)-time canonical labeling algorithm, initially introduced in the context of graph isomorphism, succeeds in matching correlated Erdős-Rényi graphs. The algorithm has two steps. In the first step, all vertices are labeled by their degrees and a trivial minimum distance matching (i.e., simply sorting vertices according to their degrees) matches a fixed number of highest degree vertices in the two graphs. Having identified this subset of vertices, the remaining vertices are matched using a matching algorithm for bipartite graphs.
I. INTRODUCTION

Graph matching (GM) (also called graph alignment or network reconciliation) refers to a class of computational techniques to identify node correspondences across related networks based on structural information. GM has applications in a variety of domains, including data fusion, privacy, computer vision, and in computational biology. For example, in computational biology, a coarse description of the metabolic machinery of a particular species is via a protein-protein interaction (PPI) network, which essentially captures which protein can react with which other protein in that species. Across species, the PPI networks tend to be strongly correlated, because evolution transfers metabolic processes from species to species. Therefore, by identifying correspondences among proteins in different species (so-called orthologs), one is able to transfer biological knowledge from one species to the other. However, crucially, the actual proteins tend to be chemically different across species, because random mutations alter these proteins over time without affecting their function. It is therefore not possible to find correspondences between proteins in different species simply by examining their amino-acid sequences. GM computes such correspondences by exploiting the correlation across networks in different species.

A similar challenge arises in social networks: suppose a set of users have accounts in several social networks. It is plausible that their links in these networks would be correlated, in the sense that given \( u \) and \( v \) are linked in the first network, it makes it conditionally more likely that they are connected in the second. This can help network reconciliation (e.g., if one wants to create a single network out of several component networks), and it can hurt privacy (e.g., by exploiting one public network to de-anonymize a private network whose node identities have been obfuscated).

While a lot of prior work on GM is heuristic in nature, a clean mathematical treatment of the problem first posits a stochastic model over two random graphs. One parametrization of this model assumes a generator graph \( G \), and then generates two correlated observable graph \( G_{a,b} \) by sampling the edge set of \( G \) twice, independently. An equivalent formulation, adopted in this paper, consider a joint distribution that generate both graphs without the assumption of an underlying true graph. Given this random graph model, we can recover the perfect alignment as the matching of the vertex sets under the assumption that pairs of vertices in one graph tend to be adjacent if and only if their true matches are adjacent in the other graph. This can be considered as a generalization of the problem of identifying graph isomorphisms, which corresponds to matching graphs where edges are not just likely but certain to be the same in both graphs.

In this paper, to the best of our knowledge, we present the first algorithm that possesses the following advantages: (i) it is seedless, i.e., it does not require side-information in the form of pre-matched pairs to operate; (ii) under a well-studied stochastic graph model, the regime where the algorithm matches perfectly can be characterized; and (iii) the algorithm incurs an \( O(n^2 \log n) \) computational cost in the size of the graph, enabling the alignment of large networks.

Our algorithm proceeds in two phases: during the first phase, for a fixed threshold parameter \( h \), the \( h \) highest-degree vertices in both graphs are matched in the natural way (highest degree to highest, second-highest to second-highest, and so forth). In the second phase, each remaining vertex is labeled with a binary vector of length \( h \) that encodes its adjacency to the set of \( h \) highest-degree vertices. The final matching is then generated via a minimum-distance matching over the labels in both graphs. Note that the second phase is equivalent to the matching of two bipartite graphs given the matching of one of their partite sets.

We evaluate the performance of the algorithm on the correlated random graph model of asymptotic size and determine conditions for the reliable performance of the algorithm. This result relies on an achievability result on the matching of bipartite graphs as an intermediary step, which is of independent interest.

The remainder of the paper is organized as follows: In Section II, we survey the relevant prior work on the problem of graph matching in large networks. In Section III, we introduce our notation, formalize the problem, and present our model of correlated graphs and correlated bigraphs. In Section IV, we state our main result, present the conditions on the successful performance of the two steps of the algorithm, and finally provide the proof for our main result. In Section V, we suggest some directions for future work.
II. RELATED WORK

The graph matching problem has been studied in a diverse set of fields and with different applications in mind. First, a line of work focuses on GM as a mode of attack on private information. An adversary tries to de-anonymize a network that is publicly released, but where node identities have been deliberately obfuscated. Obviously, there are also legitimate applications for GM: for example, similar approaches have been proposed to reconcile databases, by aligning their database schema \[1, 2\]. One such scenario considers the possibility of manipulating the network prior to its release, such that an identifiable sub-network is created \[3\] through a form of “graph steganography”. In another scenario, the attacker uses queries to attempt to locate the node of a given user \[4\]. Yet other scenarios assume the availability of some kind of side information, such as community assignments \[5, 6\] or subsets of identified vertices (seeds) \[7, 8, 9\]. One important method making use of such side information is the so-called percolation method, which starts from the seeds vertices to iteratively grow the matching until the whole graph is identified \[10, 11\].

In computational biology, PPI network alignment algorithms typically rely on both structural and biological information (in particular, the amino acid sequences of the proteins). Many heuristics have been developed, which typically try to minimize a cost function that is a convex combination of structural similarity and of sequence similarity. A few prominent examples include IsoRank \[12\], the GRAAL family \[13, 14\], MAGNA and its successor MAGNA++ \[15\], and SPINAL \[16\]. All of these methods are purely heuristic in nature, and have been evaluated without the availability of a ground truth. Their relative merits are a matter of ongoing debate in the computational biology community.

We show in this paper that efficient graph matching is possible without any side information. Henderson et al. propose one such method that performs matching based on expressions of structural features of vectors \[17\]. The proposed features are of two kinds: neighborhood features, constructed only using information on immediate neighbors of the vertex, and recursive features, which include information from a wider region of around the vertex with every iteration. Also, \[18\] present a heuristic that builds a matching in phases; matched nodes in one phase serve as distance fingerprints for additional nodes in the next phase.

Non-iterative approaches for graph matching have also been suggested. We especially note the study by Mitzenmacher et al. \[19\] that proposes performing graph matching based on algorithms to determine graph isomorphisms. Defining the problem of graph matching as a generalization of the isomorphism problem, it becomes possible to attempt to match graphs using some very efficient algorithms developed for the setting of isomorphic graphs. We consider one such algorithm.

Studies on the information-theoretical bound of the graph matching problem first given by Pedarsani et al. \[20\] and further developed by Cullina et al. \[21\], have established conditions beyond which no algorithm can succeed. These fundamental bounds provide the main benchmark against which our algorithm will be compared below.

III. MODEL

A. Notation

For a graph \(G\) we denote its vertex set and edge set as \(V(G)\) and \(E(G)\), respectively. Alternatively we write \(G = (V; E)\) where \(V = V(G)\) and \(E = E(G)\). For a bipartite graph \(H\) we denote \(H = (A, B; E)\) where \(A\) and \(B\) are the partite sets and \(E = E(H)\). For any vertex \(v \in V(G)\) let \(N_G(v)\) be the set of its neighbors in \(G\), \(d_G(v)\) its degree and \(\Delta_G(v)\) its complementary degree. The maximum degree in graph \(G\) is denoted by \(\Delta(G)\). When referring to graphs distinguished by their subscript (e.g. \(G_a, G_b\)), we use a shorthand notation to denote neighborhoods, degrees etc. as follows \(N_a(v) = N_{G_a}(v), d_a(v) = d_{G_a}(v), d_{\pi}(v) = d_{G_{\pi}}(v)\). For a set \(X\), let \(X^k\) be set of vectors of length \(k\) with entries from \(X\). We will use \([k]\) as the index set for these vectors. We denote vectors in lower case bold font, e.g. \(v = (v_1, v_2, \ldots, v_k) \in V^k\).

For any \(n \in \mathbb{N}\), \([n]\) denotes the set of all integers from 1 to \(n\). We denote by Bin\((n; p)\) the binomial distribution with \(n\) trials and event probability \(p\).

B. Problem Definition

Let \(G_a = (V_a; E_a)\) and \(G_b = (V_b; E_b)\) be graphs and let \(M : V_a \rightarrow V_b\) be a bijection between their vertex sets. We say that these graphs are correlated if the edge set of one provides information about the edge set of the other.
We are interested in the case of simple positive correlation: conditioning on the event \( \{u, v\} \in E_a \) makes the event \( \{M(u), M(v)\} \in \mathcal{E}_b \) more likely. The details of our random graph model are given in Section III-D. Our problem consists of matching each vertex in \( G_a \) to its corresponding vertex in \( G_b \) based on the correlation of the edge sets, or equivalently recovering \( M \).

### C. Matching algorithm

Our proposed matching algorithm is closely related to the algorithm originally presented for the graph isomorphism problem in [22] and subsequently used for graph matching in the adversarial setting [19]. The algorithm assigns a canonical label to each vertex in both graphs. The labels are then used to perform matching by minimizing the label distance between vertex pairs across the graphs. This is done in two steps, in the first step vertices are labeled with their degrees and the small subset of the vertices with high-degrees are identified.

In the second step, the remaining vertices are labeled with signature vectors based on their adjacencies with the high-degree vertices identified in step one.

This second step ignores all edges between unidentified vertices, effectively treating the graph as a bipartite graph. Therefore, the second step may be considered separately as an algorithm to match two bipartite graphs with one unidentified partite set. In the remainder of this paper, we refer to the first step as the high-degree matching algorithm and the second step as the bipartite matching algorithm.

**Definition 1.** For a \( n \)-vertex graph \( G \), let \( \delta_G = (\delta_{G,1}, \delta_{G,2}, \cdots, \delta_{G,N}) \) be the degree sequence of \( G \). Thus \( \delta_{G,1} \) is the maximum degree and \( \delta_{G,n} \) is the minimum degree.

The high-degree sorting function \( f_h \) takes as input a graph \( G \) on the vertex set \( V \) and lists the \( h \) highest-degree vertices, sorted by degree. More precisely, \( f_h(G) \) is some vector \( w = (w_1, w_2, \cdots, w_h) \in V^h \) of distinct vertices such that \( \delta_G(w_i) = \delta_{G,i} \).

The degree sequence of \( G \) is always uniquely defined. \( f_h(G) \) is uniquely defined only if the first \( h \) entries of \( \delta_G \) are strictly decreasing. If multiple high-degree vertices have the same degree, \( f_h(G) \) lists them in some arbitrary order.

The high-degree matching of graphs \( G_a \) and \( G_b \) corresponds to the index-by-index matching of vertices of \( f_h(G_a) \) and \( f_h(G_b) \). We refer to the set of \( h \) vertices that appear in \( f_h(G_a) \) as \( H_a \), the set of \( h \) vertices that appear in \( f_h(G_b) \) as \( H_b \), and when they are the same we say \( H_a = H_b = H \). The bipartite matching algorithm labels each vertex in \( V_a \setminus H_a \) by a binary vector encoding its adjacency with vertices in \( H_a \). These labels, which we refer to as signatures, are defined as follows:

**Definition 2.** Given graph \( G \) and vertex-valued vector \( w = (w_1, w_2, \cdots, w_h) = f_h(G) \), the signature function \( \text{sig}_G \) takes as input vertex \( u \in V(G) \) and returns the signature label of the vertex such that,

\[
\text{sig}_G(u) = \{0, 1\}^h \quad \text{and} \quad \text{sig}_G(u)_i = \mathbb{1}\{u, w_i\} \in E(G) \}
\]

where \( \mathbb{1}\{\cdot\} \) denotes the indicator function of an event. We use the shorthand notation \( \text{sig}_a(u) = \text{sig}_{G_a}(u) \), \( \text{sig}_b(u) = \text{sig}_{G_b}(u) \) when referring to graphs \( G_a \) and \( G_b \).

The bipartite matching algorithm matches vertices in \( V \setminus H \) such as to minimize the Hamming distance between pairs of signatures of matched vertices. In our analysis we consider a naive approach matching each vertex in one graph to the vertex with the closest signature in the other graph. Notice that any graph matching approach limited to signatures ignores all information pertaining to edges among the unmatched set of vertices.

The steps of the matching algorithm are summarized in Algorithm 1. We refer to the estimated matching as \( \hat{M} \). We say the algorithm is successful when \( \hat{M} = M \).

**Algorithm 1** Canonical Labeling Matching

**Input:** \( G_a = (V_a, E_a), G_b = (V_b, E_b), h \)

**Output:** Estimated matching \( \hat{M} : V_b \to V_a \)

1: **Step 1:** High-degree matching
2: \( w_a = f_h(G_a) \)
3: \( w_b = f_h(G_b) \)
4: for \( i \in [h] \) do
5: \( \hat{M}(w_{b,i}) = w_{a,i} \)
6: end for

7: **Step 2:** Bipartite matching
8: \( H_a = \{w_{a,i} : i \in [h]\} \)
9: \( H_b = \{w_{b,i} : i \in [h]\} \)
10: for vertex \( v \in V_b \setminus H_b \) do
11: \( \hat{M}(v) = \arg \min_{u \in V_a \setminus H_a} |\text{sig}_a(u) - \text{sig}_b(v)| \)
12: end for
D. Correlated Erdős-Rényi Graphs

We perform our analysis on correlated Erdős-Rényi (ER) graphs \[21\]. Under the basic ER model of random graphs, \( G \sim ER(n; p) \) is a random graph on \( n \) vertices where any two vertices share an edge with probability \( p \) independent from the rest of the graph. Under the correlated graph model, \((G_a, G_b) \sim ER(n; (p_{11}, p_{10}, p_{01}, p_{00}))\) are a pair of graphs on the same set of \( n \) vertices where the occurrences of an edge \( e = \{u, v\} \) between any pair of vertices \( u, v \) is independent and identically distributed with the following probabilities:

\[
(1) \quad \mathbb{I}\{e \in E(G_a)\}, \mathbb{I}\{e \in E(G_b)\} = \begin{cases} (1, 1) & \text{w.p. } p_{11} \\ (1, 0) & \text{w.p. } p_{10} \\ (0, 1) & \text{w.p. } p_{01} \\ (0, 0) & \text{w.p. } p_{00} \end{cases}
\]

The marginal probabilities are then defined as:

\[
p_{1*} = p_{11} + p_{10} \quad p_{*1} = p_{11} + p_{01} \quad p_{0*} = p_{01} + p_{00} \quad p_{0*} = p_{10} + p_{00}
\]

We denote the vector of probabilities as \( p = (p_{11}, p_{10}, p_{01}, p_{00}) \). Note that all probabilities are functions of \( n \). We limit our interest to sparse graphs and only consider \( p \) such that \( \lim_{n \to \infty} p_{00} = 1 \).

The model that we have just described generates a pair of graphs on the same vertex set \( V \). To convert these graphs to a pair of correlated graphs on distinct vertex sets, the vertices of \( G_b \) can be relabeled using the bijection \( M : V \to V_b \). This relabeling hides the association between the vertex sets and makes the alignment recovery problem nontrivial. For the analysis of Algorithm 1, it is more convenient to work with pairs of graphs on the same vertex sets rather than work with \( M \) explicitly so we will do this for the remainder of the paper.

In the case of bipartite graphs we use an analogous model. We denote the distribution as \( ER(h, k; p) \) for pairs of correlated graphs with left vertex set of size \( h \) and right vertex set of size \( k \). For random bipartite graphs \((B_a, B_b) \sim ER(h, k; p)\), a left vertex \( u \), and a right vertex \( v \), the pair of random variables \((\mathbb{I}\{(u, v) \in E(B_a)\}, \mathbb{I}\{(u, v) \in E(B_b)\})\) have the same distribution as (1).

IV. ANALYSES AND RESULTS

Our main result is a condition under which Algorithm 1 successful recovers the graph matching.

**Theorem 3.** Let \( G_a = (V; E_a) \) and \( G_b = (V; E_b) \) such that \((G_a, G_b) \sim ER(n, p)\) where \( p \) is a function of \( n \) such that \( p_{11} \leq o(1) \),

\[
p_{11} \geq \omega \left( \frac{\log^{7/5} n}{n^{1/5}} \right) \quad \text{and} \quad p_{01} + p_{10} \leq o \left( \frac{p_{11}^5}{\log^6 n} \right).
\]

Then Algorithm 1 with parameter \( h \) such that \( \frac{\log n + o(1)}{p_{11}} \leq h \leq O \left( \frac{\log n}{p_{11}} \right) \) exactly recovers the matching between the vertex sets of \( G_a \) and \( G_b \) with probability \( 1 - o(1) \).

[Fig. 1] compares our achievability region with that of the more challenging adversarial scenario \[19\]. It also gives the information theoretic achievability region \[21\]. We only consider the symmetric case, where \( p_{10} = \Theta(p_{01}) \). The \( x \)-axis shows \( \frac{\log p_{11}}{\log n} \) and the \( y \)-axis shows \( \frac{\log p_{11}}{\log n} \). Note that in the region \( x < -2 \), the number of edge differences between the pairs of graphs is zero under the adversarial model and is zero with high probability under the random

\[
-2 - \frac{17}{9} \quad \frac{\log p_{11}}{\log n} \quad -1 \quad -\frac{1}{2} \quad 0 \quad \frac{\log p_{11}}{\log n} \quad -\frac{1}{7} \quad -\frac{1}{5} \quad 0
\]

Fig. 1: Comparison of regions of achievability for symmetric noise \((p_{10} = \Theta(p_{01}))\): (A) region achievable by Algorithm 1 under the adversarial model \[19\], \[23\], (AUB) region achievable by Algorithm 1 under the random graph model, (AUBUC) theoretical achievability region for the random graph model \[21\].
In Appendix II-A we derive an expression for the probability generating function $F$. Let $a$ be a function of $\alpha \triangleq d_a(u) - d_a(v)$ for $u,v \in V(G)$, define $\rho \triangleq d_a(u) + d_v(v)$ and $d_\sigma(d) \triangleq \frac{d_a(d)}{p_{1*}}$. Let $\eta \in (0,\infty)$ be a function of $n$. If $d_a(u) - d_a(v) \geq (1 - \varepsilon)^{-1} \left( k + 4 \max(\eta, \sqrt{\rho - \eta}) \right)$, then $P[d_a(u) - d_a(v) - k \leq e^{-\eta}]$.

Proof: Let us denote the degree separations in the two graphs by $\alpha \triangleq d_a(u) - d_a(v)$ and $\beta \triangleq d_u(u) - d_b(v)$. Observe that the presence of the edge $\{u,v\}$ in $G_a$ does not affect $\alpha$. Thus we define $d_a(u) \triangleq |N_a(u) \setminus \{u\}|$, $d_a(v) \triangleq n - 2 - d_a(u)$, and $d_b(v) \triangleq n - 2 - d_a(u)$. The error event in the degree sequence, i.e. $d_a(u) - d_a(v) \leq k$, corresponds to $\beta \leq k$. By the Chernoff bound:

$$P[\beta \leq k|d_a(u), d_a(v)] \leq z^{-k}E[z^{\beta}|d_a(u), d_a(v)] \forall 0 < z \leq 1.$$  

In Appendix II-A we derive an expression for the probability generating function $F_{\beta}(z) \triangleq E[z^{\beta}|d_a(u), d_a(v)]$:

$$F_{\beta}(z) = z^\alpha \left( 1 + \frac{p_{10}}{p_{1*}} (z^{-1} - 1) \right)^{d_a(u)} \left( 1 + \frac{p_{10}}{p_{1*}} (z - 1) \right)^{d_a(v)} \left( 1 + \frac{p_{01}}{p_{0*}} (z - 1) \right)^{d_b(u)} \left( 1 + \frac{p_{01}}{p_{0*}} (z^{-1} - 1) \right)^{d_b(v)}.$$  

By applying $1 + x \leq e^x$ we get

$$F_{\beta}(z) \leq \exp \left\{ \alpha \log z + \left( \frac{p_{10}}{p_{1*}} d_a + \frac{p_{01}}{p_{0*}} d_b \right) (z - 1) + \left( \frac{p_{10}}{p_{1*}} d_a + \frac{p_{01}}{p_{0*}} d_b \right) (z^{-1} - 1) \right\}.$$  

Furthermore applying $\log x \leq x - 1$ we have

$$z^{-k}F_{\beta}(z) \leq \exp \left\{ \left( \alpha - k - \frac{p_{10}}{p_{1*}} d_a + \frac{p_{01}}{p_{0*}} d_b \right) (z - 1) + \left( \frac{p_{10}}{p_{1*}} d_a + \frac{p_{01}}{p_{0*}} d_b \right) (z^{-1} - 1) \right\}.$$  

Denote the coefficients by $r' \triangleq \alpha - k - \frac{p_{10}}{p_{1*}} d_a + \frac{p_{01}}{p_{0*}} d_b$ and $r \triangleq \frac{p_{10}}{p_{1*}} d_a + \frac{p_{01}}{p_{0*}} d_b$. Denote their difference as

$$\Delta r \triangleq r' - r = \alpha - k - \frac{p_{10}}{p_{1*}} d_a + \frac{p_{01}}{p_{0*}} d_a - \left( n - 2 \right) - \frac{p_{10}}{p_{1*}} d_a + \frac{p_{01}}{p_{0*}} d_b \left( n - 2 \right) - d_a.$$

$$= \alpha - k \left( \frac{p_{10}}{p_{1*}} + \frac{p_{01}}{p_{0*}} \right) (d_a - d_a) = \alpha \left( 1 - \frac{p_{01}}{p_{0*}} - \frac{p_{10}}{p_{1*}} \right) - k$$

The right hand side of the inequality in (2) is minimized at $z^* \triangleq \sqrt{r/r'}$. Taking the logarithm of both sides in (2) and evaluating at $z = z^*$ we get

$$\log F_{\beta}(z^*) \leq - \left( \sqrt{r} - \sqrt{r'} \right)^2 = -\Delta r \left( \sqrt{1 + r/\Delta r} - \sqrt{r/\Delta r} \right).$$

The inequality $\sqrt{1 + x^2} - x \geq \frac{1}{1 + 2x}$ holds for any $x \geq 0$. Specifically the choice of $x = \sqrt{r/\Delta r}$ results in

$$- \left[ \log F_{\beta}(z^*) \right] \leq \frac{\Delta r}{1 + 2 \sqrt{r/\Delta r}}.$$
Theorem 9. Define such that 
\[ \frac{\Delta r}{(1 + 2\sqrt{\Delta r})^2} \geq \frac{1}{4} \max \left\{ \Delta r', \Delta r \sqrt{\eta} \right\} \geq \frac{\Delta r}{4} \geq \eta \]
which implies \((z^*)^{-k} F_{\beta}(z^*) \leq e^{-\eta}\). Finally observe that \(\rho \geq r\) and therefore the condition in the statement of the lemma implies \(\Delta r \geq 4 \max \{ \eta, \sqrt{\eta} \}\). ■

Lemma 4 only concerns pairs of vertices. Next we present a condition on the graph sequence of \(G_a\) that guarantees with high probability the desired degree separation among high-degree vertices in \(G_b\). Recall that, by Definition 1, \(\delta_a\) and \(\delta_b\) denote the degree sequences in \(G_a\) and \(G_b\) respectively.

Corollary 5. Let \((G_a, G_b) \sim ER(n; p)\) where \(G_a = (V; E_a)\) and \(G_b = (V; E_b)\). Define \(\rho \triangleq \Delta(G_a) \frac{p_{0a}}{p_{1a}} + n \frac{p_{0a}}{p_{1a}}\) and \(\varepsilon \triangleq \frac{p_{0a}}{p_{0a}} + \frac{p_{0a}}{p_{1a}}\). Let \(h \in [n]\) and \(\eta\) be functions of \(n\). Let \(s\) be an integer such that \(s \geq h + \frac{1}{2} \log \left( \frac{p_{1a}}{p_{0a}} \right) + 1\). If
\[ \forall i \in [s], \quad \delta_{a,i} - \delta_{a,i+1} \geq (1 - \varepsilon)^{-1} \left( k + 4 \max \{ \eta, \sqrt{\rho \cdot \eta} \} \right) \]
then, with probability at least \(1 - (2h + 1) e^{-\eta} / (1 - e^{-\eta})\), \(f_h(G_a) = f_h(G_b)\) and \(\delta_{b,i} - \delta_{b,i+1} > k\) for any \(i \in [h]\).

Proof: See Appendix III.

The results in Corollary 5 depend on the maximum degree of \(G_a\), so we need the following upper bound.

Lemma 6. Let \(G \sim ER(n; p)\) with \(p \geq \omega \left( \frac{\log n}{n} \right)\). For any constant \(\epsilon > 0\), we have \(P[\Delta(G) \geq pn(1 + \epsilon)] \leq o(1)\).

Proof: For any vertex \(u \in V(G)\), \(d_G(u) \sim \text{Bin}(n-1; p)\). By the Chernoff bound, for any \(D \in \mathbb{N}\) and \(z \in [1, \infty]\)
\[ P[d_G(u) \geq D] \leq z^{-D} \mathbb{E}\left[z^{-d_G(u)}\right] \leq z^{-D} \left[1 + p(z - 1)\right]^{n-1}. \]
Applying \(1 + x \leq e^x\) to both terms this becomes \(\log P[d_G(u) \geq D] \leq D(z^{-1} - 1) + p(n - 1)(z - 1)\). The right hand side is minimized for \(z^* = \sqrt{\frac{D}{p(n-1)}}\) which gives us \(\log P[d_G(u) \geq D] \leq - \left(\sqrt{D} - \sqrt{p(n-1)}\right)^2\).

Let \(D = (1 + \epsilon)p(n-1)\). By the union bound, the probability that the maximum degree is at least \(D\) is at most
\[ nP[d_G(u) \geq D] \leq n \exp \left(-p(n-1) \left(\sqrt{1 + \epsilon} - 1\right)^2\right) \leq n \exp (-\omega(\log n)) \leq o(1). \]

Corollary 5 relies on \(G_a\) having a degree sequence whose largest terms are sufficiently separated. We now present a condition that guarantees a given degree separation for almost all random graphs.

Theorem 7. (23) Theorem 3.15 Let \(h \in \mathbb{N}\) and \(c \in \mathbb{R}^+\) functions of \(n\) such that \(h = o(n)\) and \(c = o(1)\). Then, with probability \(1 - o(1)\), in \(G \sim ER(n; p)\)
\[ \delta_i - \delta_{i+1} \geq c \frac{np(1-p)}{\log n} \left( \frac{np(1-p)}{\log n} \right)^{1/2} \quad \text{for each} \quad i \in [h]. \]

We are now in a position to present a result on the performance of the high-degree matching step of our algorithm.

Definition 8. Let \(E^{11}_a\) be the event that the lists of the \(h\) highest-degree vertices in \(G_a\) and \(G_b\) are the same, i.e. \(f_h(G_a) = f_h(G_b)\). This is the “high-degree match” event. Let \(E^{11}_a\) be the event that \(\delta_{a,i} > \delta_{a,i+1} + 2\) for all \(i \in [h]\). Define \(E^{11}_b\) analogously for \(\delta_b\). These are the “degree separation” events.

Theorem 9. Let \((G_a, G_b) \sim ER(n; p)\) where \(p\) is a function of \(n\) such that \(p_{00} = 1 - o(1)\). Moreover let \(h \in [n]\) such that \(\omega(\log n) \leq h \leq o(n)\). If
\[ \max \left\{ \left(\log h\right)^2, n(p_{01} + p_{10}) \log h \right\} \leq o \left( \frac{np_{11}}{h^4 \log n} \cdot \frac{p_{11}}{p_{1*}} \right), \]

(4)
then \( P \left[ E^H \land E^S_a \land E^S_b \right] \geq 1 - o(1) \).

**Proof:** To apply Corollary 5, \( \eta \) and \( s \) must satisfy \( s \geq h + \frac{1}{\eta} \log \left( \frac{h}{n} \right) \). We pick \( \eta \) such that \( s = \left[ h + \frac{1}{\eta} \log \left( \frac{h}{n} \right) \right] \) and \( \log h + \omega(1) \leq \eta \leq O(\log h) \). The condition \( h \geq \omega(\log n) \) guarantees that \( s \leq h(1 + o(1)) \).

Applying Lemma 6, we have

\[
\rho = \Delta(G_a) \frac{p_{10}}{p_{11}} + n \frac{p_{01}}{p_{0*}} \leq (1 + \epsilon)np_{10} + n \frac{p_{01}}{p_{0*}} \leq (1 + \epsilon + o(1))n(p_{10} + p_{01}).
\]

Define \( c \triangleq s^{4 \log n/n_{pi}} \left( 1 - \frac{p_{10}}{p_{11}} - \frac{p_{01}}{p_{0*}} \right)^{-1} \left( 2 + 4 \max \{ \eta, (\rho \cdot \eta)^{1/2} \} \right) \). By \( p_{00} = 1 - o(1) \) we have \( 1 - \frac{p_{01}}{p_{11}} - \frac{p_{10}}{p_{0*}} \approx \Theta \left( \frac{p_{0*}}{p_{11}} \right) \). Together with the upper bounds on \( \eta, h, \) and \( s \), we get

\[
c \leq O(1) \left( \frac{h^{4} \log n}{np_{11}} \right) \left( \frac{p_{11}}{p_{11}} \right)^{1/2} \max \left\{ \log h, (n(p_{01} + p_{10}) \log h)^{1/2} \right\}.
\]

From (4), we have \( c \leq o(1) \).

By Theorem 7, with probability \( 1 - o(1) \), we have a minimum separation of \( 2 + 4 \max \{ \eta, (\rho \cdot \eta)^{1/2} \} \) among the top \( s \) degrees in \( G_a \sim ER(n, p_{11}) \). Then Corollary 5 implies that the probability that \( f_{h}(G_a) \neq f_{h}(G_b) \) is at most \( s e^{-\eta} \leq (1 + o(1))he^{-\log h - \omega(1)} \leq o(1) \).

### B. Bipartite graph matching

We will need the following method of specifying an induced bipartite subgraph. Let \( G \) be a graph on the vertex set \( V \) and let \( U \subseteq V \). Let \( w \in (V \setminus U)^{h} \) be vector of \( h \) distinct vertices. Define \( G[U, w] \) to be the bipartite graph with left vertex set \( U \), right vertex set \( \{h\} \), and edge set

\[
E(G[U, w]) = \{(u, j) \in U \times \{h\} : (u, w_j) \in E(G)\}.
\]

Recall that in Algorithm 1 we have \( w_a = f_{h}(G_a) \) and \( w_b = f_{h}(G_b) \). By Definition 2, the signature of any \( u \in U \) is the edge indicator function for \( G_a[u], w_a \):

\[
\text{sig}_a(u) \in \{0, 1\}^h \quad \text{and} \quad \text{sig}_a(u)_{i} = \mathbb{1}\{(u, i) \in E(G_a[u], w_a)\}.
\]

We define an analogous signature scheme for bipartite graphs to be used for the bipartite matching step.

**Definition 10.** Given the bipartite graph \( B = (V, [h]; E) \), the bipartite signature function \( \text{sig}_B \) takes as input vertex \( u \in V \) and returns the signature label of the vertex such that

\[
\text{sig}_B(u) \in \{0, 1\}^h \quad \text{and} \quad \text{sig}_B(u)_{i} = \mathbb{1}\{(u, i) \in E\}
\]

When referring to signatures on bipartite graphs that are distinguished only by their subscripts (e.g. \( B_a \) and \( B_b \)) we only denote the signatures in shorthand notation, e.g. \( \text{sig}_a(u) = \text{sig}_{B_a}(u) \), \( \text{sig}_a(u) = \text{sig}_{B_b}(u) \).

We restate the second half of Algorithm 1 as the bipartite graph matching algorithm in Algorithm 2.

Suppose that we have bipartite graphs \( B_a = (V_a, [h]; E_a) \) and \( B_b = (V_b, [h]; E_b) \) such that \( |V_a| = |V_b| \). Assume there is an exact correspondence between the vertex sets, expressed by the matching \( M : V_b \to V_a \). Algorithm 2 is guaranteed to map vertex \( u \in V_b \) to \( M(u) \in V_a \) if

\[
|\text{sig}_a(M(v)) - \text{sig}_b(u)| > |\text{sig}_a(M(u)) - \text{sig}_b(u)| \quad \text{for any} \ v \in V_b \setminus \{u\}. \quad (5)
\]

Hence verifying the equality above for any ordered pair of vertices \( (u, v) \in V_b^2 \) guarantees that the algorithm perfectly matches all vertices.

In the remainder of the section, in order to avoid cumbersome notation, we assume that, without loss of generality, \( V_a = V_b = V \) and the true matching is the trivial matching \( M(v) = v \) for any \( v \in V \).
To analyze Algorithm 2 for random bipartite graphs, we need the following lemma which bounds the probability that a pair of vertices are mismatched. This corresponds to the failure of [5] for either one of the vertices.

**Lemma 11.** Let bipartite graphs $B_a = (\{u, v\}, \{h\}; E_a)$ and $B_b = (\{u, v\}, \{h\}; E_b)$ be distributed according to $(B_a, B_b) \sim ER(2, h; p)$. 

Define $E^M(B_a, B_b)$ to be the “mismatch event” i.e. the event where either of the following inequalities hold:

$$|\text{sig}_a(v) - \text{sig}_b'(u)| \leq |\text{sig}_a'(u) - \text{sig}_b(u)| \quad \text{or} \quad |\text{sig}_a'(u) - \text{sig}_b'(v)| \leq |\text{sig}_a(u) - \text{sig}_b'(v)|.$$  

Then $P[E^M(B_a, B_b)] \leq 2 \exp(-h \rho^2)$ where $\rho = \sqrt{p_00p_1* + p_11p_0* - \sqrt{p_10p_0* + p_01p_1*}}$.

**Proof:** Define the random variable $\gamma = |\text{sig}_a(v) - \text{sig}_b'(u)| - |\text{sig}_a'(u) - \text{sig}_b(u)|$. We bound the probability of $\gamma \leq 0$ using the Chernoff bound: $P[\gamma \leq 0] \leq \mathbb{E}[\gamma^2]$ for all $0 < z \leq 1$. The generating function $F_z(\gamma) \triangleq \mathbb{E}[\gamma^2]$ is given as $F_z(\gamma) = \left[1 + q_0(z - 1) + q_1(z^{-1} - 1)\right]^h$ where $q_0 = p_00p_1* + p_11p_0*$ and $q_1 = p_10p_0* + p_01p_1*$. (See Appendix II-B for derivation.) Applying $1 + x \leq e^x$ and evaluating the function at $z^* = \sqrt{\frac{q_1}{q_0}}$, we get $\log F_z(z^*) \leq -h \left(\sqrt{q_0} - \sqrt{q_1}\right)^2$. Hence for $\rho = \sqrt{q_0} - \sqrt{q_1}$ we have $P[\gamma \leq 0] \leq \exp(-h \rho^2)$.

Notice that for the analogous $\gamma' = |\text{sig}_a'(u) - \text{sig}_b'(v)| - |\text{sig}_a(u) - \text{sig}_b(v)|$ the same bound holds. The event $E^M(B_a, B_b)$ is equivalent to $\{\gamma \leq 0 \lor \gamma' \leq 0\}$. Thus by the union bound $P[E^M(B_a, B_b)] \leq 2 \exp(-h \rho^2)$. \hfill \qed

The performance of the Algorithm 2 depends on the sparsity of the graph and the size of the partite sets.

**Remark 12.** Let $(B_a, B_b) \sim ER(k, h; p)$. Then for each $u, v \in [k]$, the subgraphs induced by $\{u, v\}$ and $\{h\}$ have joint distribution $ER(2, h; p)$. By Lemma 11 the probability that Algorithm 2 mismatches $u$ with $v$ or $v$ with $u$ is at most $2 \exp(-h \rho^2)$. Then, by the union bound over all $\binom{k}{2}$ pairs of vertices, Algorithm 2 correctly recovers the matching between $B_a$ and $B_b$ with probability at least $1 - k(k - 1) \exp(-h \rho^2)$ and the algorithm is correct with probability $1 - o(1)$ when $h \geq \frac{2 \log k + \omega(1)}{\rho'}$.

In our analysis of Algorithm 1 the situation is similar yet not quite as simple as the one described in Remark 12. After we find the lists of high degree vertices in $G_a$ and $G_b$, we obtain a pair of induced bipartite subgraphs: $G_a[V_a \setminus H_a, w_a]$ and $G_b[V_b \setminus H_b, w_b]$. When the high-degree vertex lists are the same, i.e. $w_a = w_b$, Algorithm 2 can be applied, but bipartite graphs do not have the joint distribution $ER(n - h, h, p)$, required for Remark 12. This is due to the fact that we used edge information to partition the original vertex set, so the edges are not independent of this partition. However, this dependence is weak. In Section IV-C we will apply Lemma 11 after careful conditioning.

C. General matching algorithm

Recall that $w_a = f_h(G_a)$ and $w_b = f_h(G_b)$. For $U = \{u_1, u_2\} \subseteq V$, the induced bipartite subgraphs $(G_a[U, w_a], G_b[U, w_b])$ determine whether Algorithm 1 mismatches $u_1$ with $u_2$ or $u_2$ with $u_1$. However, these graphs do not have a correlated ER joint distribution, so we define a related pair of induced bipartite subgraphs.

**Definition 13.** Let $G_a$ and $G_b$ be graphs on vertex set $V$. For set $U = \{u_1, u_2\} \subseteq V$, and $h \in \mathbb{N}$, define

$$w_a^U = f_h(G_a[V \setminus \{u_1, u_2\}]) \quad \text{and} \quad B_a^U = G_a[U, w_a^U],$$

i.e. $(u, i) \in E(B_a^U) \iff \{u, u_i^U\} \in E(G_a)$ for any $u \in U$ and $i \in [h]$. Define $w_b^U$ and $B_b^U$ analogously. Let $\mathcal{E}_a(U)$ be the event $w_a^U = w_b^U$.

We emphasize that in both $B_a^U$ and $B_b^U$ the left vertex set is $\{u_1, u_2\}$ and the right vertex set is $[h]$, so the vertex sets are not random variables.

We start by stating a result on conditional independence of the high-degree neighborhoods of a pair of vertices.

**Lemma 14.** Let $(G_a, G_b) \sim ER(n; p)$ be correlated graphs on the vertex set $V$ and let $U = \{u_1, u_2\} \subseteq V$. Then

$$B_a^U \sim ER(2, h, p_{1*}), \quad B_b^U \sim ER(2, h, p_{1*}) \quad \text{and} \quad (B_a^U, B_b^U) \mid \mathcal{E}_a(U) \sim ER(2, h, p),$$

where $B_a^U$ and $B_b^U$ are as defined in Definition 13.
**Proof:** Recall that, by definition, \( B_a^U = G_a[U, w_a^U] \) and \( 1 \{ (u, j) \in E( B_a^U ) \} = 1 \{ \{ u, w_{a,j} \} \in E(G_a) \} \). We will show that despite being defined using \( w_a^U \), the random variable \( B_a^U \) is independent of the random variable \( w_a^U \). Observe that \( B_a^U = G_a[U, w_a^U] \) is independent of \( G_a[V \setminus U] \) because they have no edge random variables in common. Because \( w_a^U = f_h(G_a[V \setminus U]) \), \( B_a^U \) is independent of \( w_a^U \) as well.

Similarly, \( B_b^U \) is independent of \( w_b^U \) and \( 1 \{ (u, j) \in E( B_b^U ) \} = 1 \{ \{ u, w_{b,j} \} \in E(G_b) \} \). As long as \( w_a^U = w_b^U \) holds, \( 1 \{ (u, j) \in E( B_b^U ) \} \) and \( 1 \{ (u, j) \in E( B_b^U ) \} \) have the joint distribution of a pair of corresponding edges in the correlated Erdős-Rényi model.

This result may be counterintuitive because we are selecting the right vertex set of \( B_a^U \) using high degree vertices, but there the edge density of \( B_a^U \) is the same as \( G_a \). For a fixed \( (u, j) \in U \times [h] \), the random variable \( 1 \{ (u, j) \in E( B_a^U ) \} \) is not determined by any single edge random variable from \( G_a \), but is a mixture of \( 1 \{ \{ u, v \} \in E(G_a) \} \) over all \( v \in V \setminus U \) because \( w_b^U \) is random. It is helpful to compare with \( G_a[U \setminus \{ u_1, u_2 \} \), where \( U \setminus \{ u_1, u_2 \} \) is a uniformly random subset of \( V \setminus H_a \). This bipartite graph is not distributed as \( ER(n, p_{1*}) \) because edges of \( G_a \) are slightly more likely to be sampled than non-edges.

Recall from Definition 8 that \( \mathcal{E}_a^S \) is defined as the event that \( \delta_{a,i} > \delta_{a,i+1} + 2 \) for all \( i \in [h] \) and \( \mathcal{E}_b^S \) is the corresponding event for \( w_b \) and \( G_b \).

**Lemma 15.** The event \( \mathcal{E}_a^S \) implies \( w_a = w_a^U \) for all \( U \subseteq V \) pair of vertices that do not include any from \( w_a \).

Similarly \( \mathcal{E}_b^S \) implies \( w_b = w_b^U \).

**Proof:** For any \( v \in V \), the degree of \( v \) in \( G_a \) differs by at most 2 from the degree of \( v \) in \( G_a[V \setminus U] \). The same holds for \( G_b \).

Finally we prove our main theorem:

**Theorem 3.** Let \( G_a = (V, E_a) \) and \( G_b = (V, E_b) \) such that \((G_a, G_b) \sim ER(n, p)\) where \( p \) is a function of \( n \) such that \( p_{11} \leq o(1) \).

\[
p_{11} \geq \omega \left( \frac{\log^{7/5} n}{n^{1/5}} \right) \text{ and } p_{01} + p_{10} \leq o \left( \frac{p_{11}^5}{\log^6 n} \right).
\]

Then Algorithm 1 with parameter \( h \) such that \( \frac{\log n + o(1)}{p_{11}} \leq h \leq O \left( \frac{\log n}{p_{11}} \right) \) exactly recovers the matching between the vertex sets of \( G_a \) and \( G_b \) with probability \( 1 - o(1) \).

**Proof:** Theorem 9 provides the condition on the correlation of graphs required to successfully match a given number \( h \) of high-degree vertices. From the inequalities \( h \leq O \left( \frac{\log n}{p_{11}} \right) \), \( \log h \leq \log n \), and the conditions in the theorem statement, \( p_{11} \geq \omega \left( n^{-1/5} \log^{7/5} n \right) \) and \( p_{01} + p_{10} \leq o \left( \frac{p_{11}^5}{\log^6 n} \right) \), we have

\[
\max \left\{ (\log h)^2, n(p_{10} + p_{01}) \log h \right\} \leq o \left( \frac{n p_{11}^5 h^4 \log n}{h^4 \log n} \cdot \frac{p_{11}}{p_{1*}} \right).
\]

Thus \( P \left[ \mathcal{E}^H \land \mathcal{E}_a^S \land \mathcal{E}_b^S \right] \geq 1 - o(1) \), where \( \mathcal{E}^H \), \( \mathcal{E}_a^S \) and \( \mathcal{E}_b^S \) are events as defined in Definition 8. These events imply \( H_a = H_b = H \).

Recall the definition of \( \mathcal{E}^M(B_a, B_b) \) from Lemma 11 and \( \mathcal{E}^H(U) \) from Definition 13. Applying the union bound
to error events in the bipartite matching stage of the algorithm results in the following:

\[
P[\tilde{M} \neq M | \mathcal{E}^H \land \mathcal{E}_a^S \land \mathcal{E}_b^S] \leq \sum_{\{u_1,u_2\} \subseteq V \setminus H} P \left[ \mathcal{E}^M(G_a[U, w_a], G_b[U, w_b]) \land \mathcal{E}^H \land \mathcal{E}_a^S \land \mathcal{E}_b^S \right]
\]

\[
\leq \sum_{\{u_1,u_2\} \subseteq V \setminus H} P \left[ \mathcal{E}^M(B_a^U, B_b^U) \land \mathcal{E}^H(U) \right]
\]

\[
\leq \sum_{\{u_1,u_2\} \subseteq V} P \left[ \mathcal{E}^M(B_a^U, B_b^U) | \mathcal{E}^H(U) \right]
\]

\[
\leq \sum_{\{u_1,u_2\} \subseteq V} \exp(h \rho^2).
\]

In (a) is derived by applying Lemma 15 twice, which gives \(G_a[U, w_a] = B_a^U\), \(G_b[U, w_b] = B_b^U\), and \(w_a^U = w_b^U\). (Recall that the event \(\{w_a^U = w_b^U\}\) is denoted by \(\mathcal{E}^H(U)\).) In (b), we use \(P[\mathcal{E}^U] \leq 1\) and also extend the sum to include pairs \(\{u_1,u_2\}\) that include members of \(H\). Because \(u_1\) and \(u_2\) are now arbitrary vertices with no conditioning, from Lemma 14 we have that \((B_a^U, B_b^U) \sim ER(2, h, p)\). Observe that for any \(U = \{u_1, u_2\} \subseteq V \setminus H\), the signatures in Lemma 11 are the same as the signatures in Algorithm 1: \(\text{sig}_{G_a[U, w_a]}(u_i) = \text{sig}_{B_a^U}(u_i)\).

Finally, (c) follows from Lemma 11. Note that the final bound is the same as the one stated earlier in Remark 12.

We have

\[
\rho = \sqrt{p_{10}p_{11} + p_{10}p_{00} - p_{10}p_{00} + p_{01}p_{11}}
\]

\[
= \sqrt{p_{11}p_{00}} \left( \sqrt{2 + \frac{p_{10}}{p_{11}} + \frac{p_{01}}{p_{00}}} - \sqrt{2 + \frac{p_{01}p_{10}}{p_{11}p_{00}} + \frac{p_{10}}{p_{11}} + \frac{p_{01}}{p_{00}}} \right)
\]

\[
\geq \sqrt{2p_{11}} \left( 1 - O \left( \frac{1}{\log n} \right) \right)
\]

because \(\frac{p_{10}}{p_{11}} \leq o \left( \frac{1}{\log^2 n} \right)\) and \(\frac{p_{01}}{p_{00}} \leq o \left( \frac{1}{\log^2 n} \right)\). The logarithm of the probability of incorrect matching in \(V \setminus H\) is at most

\[
\log \left( n(n-1) \exp(h \rho^2) \right) \leq 2 \log n - \frac{\log n + \omega(1)}{p_{11}} \cdot 2p_{11} \left( 1 - O \left( \frac{1}{\log n} \right) \right)
\]

\[
\leq 2 \log n - 2 \log n + \mathcal{O}(1) - \omega(1) \left( 1 - O \left( \frac{1}{\log n} \right) \right) = -\omega(1).
\]

V. CONCLUSION

We studied the performance of a canonical graph matching algorithm under the correlated ER graph model and obtained the expression for the region where the algorithm succeeds. To do so we analyzed the two steps of the algorithm, comprised of a high-degree matching and a subsequent bipartite matching. The first step which identified the pairing between high-degree subset of vertices can provide an initial set of seed vertices which may be used for various seed-based matching approaches. In this work we used a particular bipartite matching algorithm based on signatures derived from connections of the remaining (i.e. unidentified) vertices to the high-degree vertices identified at the first step.

There are a number of possible directions in which this work can be extended. One would be removing the assumption of the current model that the two vertex sets have a one-to-one correspondence. This would allow the analysis of more realistic scenarios where both graphs can potentially contain many vertices that have no exact match in the other. In this case it is necessary to avoid matching such vertices by considering some measure of the strength of correspondence between matching candidates. Another direction to consider is the scenario where information offered by the graph structure is richer. This would be the case when the edges are directed or weighted. It could also be the case that adjacency relations are defined by more than 2 states, rather than our model where
the existence and absence of edges are the only 2 states. Another model with richer information would be the case of hypergraphs. Finally we note that some extensions to the algorithm, (such as considering highest-degree vertices at distance two rather than only immediate neighbor in the bipartite matching step) could provide considerable improvements to the region where the algorithm succeeds.

**Appendix I**

**Construction of FIG. 1**

The adversarial model is defined as follows: Consider a random graph $G_a = ER(n;p)$ and its modified copy $G_b$ obtained by the addition or deletion of at most $d$ edges by an adversary where $d \geq 2$ is a deterministic function of $n$.

Note that the parameters in this problem formulation relate to the correlated random graph problem through:

$$ p = p_1 = p_{11} + p_{10} = p_{11} (1 + o(1)) \quad \text{and} \quad d = (p_{10} + p_{01}) \left( \frac{n}{2} \right). \quad (6) $$

By Theorem 5.3 in [19], there exists an appropriate choice of parameter $h$ for which Algorithm 1 perfectly matches the vertex sets of the two graphs with probability at least $1 - o(1)$ as long as $p = \omega \left( d \log n \left( \frac{d^2}{n} \right)^{1/7} \right)$. By the equalities in [6] this condition is satisfied when

$$ \Omega \left( \frac{n^{-2}}{} \right) \leq (p_{01} + p_{10}) \frac{2}{7} \leq o \left( \frac{p_{11}}{\log n} n^{-17/7} \right). $$

Recall that the x-axis shows $\log_{\log n} p_{01}$ and the y-axis shows $\log_{\log n} p_{01}$. Taking the logarithm of both sides and dividing by $\log n$, in the symmetric case, results in the triangular region defined by the inequality

$$ -2 \leq \frac{9}{7} x \leq y - \frac{17}{7} - o(1). $$

Note that $d = o(1)$ for $p_{01} + p_{10} \leq o \left( \frac{n^{-2}}{17} \right)$, so the adversarial scenario with a fixed number of edge changes reduces to the graph isomorphism problem. The condition to guarantee successful matching for that problem, given in Theorem 3.17 in [23], is $p = \omega \left( n^{-1/5} \log n \right)$, which corresponds to the region where $y \geq -\frac{1}{5} + o(1)$ and $x \leq -2$.

The achievability region is derived similarly. Theorem 2 in [21] gives the following achievability condition as

$$ p_{11} \geq 2 \frac{\log n + \omega(1)}{n} \quad \text{and} \quad p_{01} p_{10} = o \left( p_{11} p_{00} \right), $$

which for $p_{00} = 1 - o(1)$ and $p_{10} = \Theta \left( p_{01} \right)$ corresponds to

$$ p_{11} = \Omega \left( \frac{\log n}{n} \right) \quad \text{and} \quad p_{01}^2 = o \left( p_{11} \right). $$

This gives the the region defined by $y \geq -1 + o(1)$ and $2x \leq y$.

**Appendix II**

**Derivations of Probability Generating Functions**

**A. Probability generating function of the degree separation beta**

Given the random graphs $(G_a, G_b) \sim ER(n;p)$ and for a given pair of vertices $u, v$, define $d^u_a = |N_a(u) \setminus \{v\}|$, $d^u_a = |N_a(v) \setminus \{u\}|$ and $d^u_b, d^v_b$ analogous for $G_b$. We seek to find $F_\beta = \mathbb{E} [ z^\beta | d_a, d_b]$. where $\beta = d_b(u) - d_b(v)$.

Let us denote the degree separation in $G_a$ as $\alpha = d_a(u) - d_a(v)$. Note that $d^u_a - d^u_a = d_a(u) - d_a(v) = \alpha$ and $d^u_b - d^v_b = d_b(u) - d_b(v) = \beta$. Let us denote the number edges of $x$ in $G_a \setminus \{u\}$ that are non-edges in $G_b$ (i.e. number of edges exclusive to $G_a$) as $e^u_a = |N_a(u) \setminus N_b(u) \setminus \{|v\}|$ and vice versa as $e^v_b = |N_b(u) \setminus N_a(u) \setminus \{|v\}|$.

It can be shown that $d^u_b = d^u_a - e^u_a + e^v_b$. Similarly define $e^u_b$ and $e^v_b$ by ignoring the edge $\{u, v\}$. We then have

$$ d^u_b - d^v_b = d^u_a - e^u_a + e^v_b. $$
or simply \( \beta = \alpha - e_{\alpha}^{u} + e_{\alpha}^{v} + e_{\alpha}^{b} - e_{\alpha}^{\bar{b}} \). Notice that given \( d_{\alpha}^{u} \) and \( d_{\alpha}^{\bar{b}} \), \( \alpha \) is deterministic. Also notice that the remaining terms \( e_{\alpha}^{u}, e_{\alpha}^{v}, e_{\alpha}^{b}, e_{\alpha}^{\bar{b}} \) are mutually independent binomially distributed random variables with distribution:

\[
e_{\alpha}^{u} \sim B \left( d_{\alpha}^{u}, \frac{p_{10}}{p_{1*}} \right), \quad e_{\alpha}^{v} \sim B \left( d_{\alpha}^{v}, \frac{p_{01}}{p_{0*}} \right), \quad e_{\alpha}^{b} \sim B \left( d_{\alpha}^{b}, \frac{p_{10}}{p_{1*}} \right), \quad e_{\alpha}^{\bar{b}} \sim B \left( d_{\alpha}^{\bar{b}}, \frac{p_{01}}{p_{0*}} \right)
\]

where \( d_{\alpha}^{u} = n - 2 - d_{\alpha}^{u} \) and \( d_{\alpha}^{\bar{b}} = n - 2 - d_{\alpha}^{\bar{b}} \). The probability generating function of a binomially distributed random variable \( X \sim \text{Bin}(n, p) \) is given by \([1 + p(z - 1)]^{n}\). Thus we get the probability generating function of \( \beta \) as

\[
F_{\beta}(z) = z^{\alpha} \left( 1 + \frac{p_{10}}{p_{1*}} (z - 1) \right)^{d_{\alpha}^{u}} \left( 1 + \frac{p_{01}}{p_{0*}} (z - 1) \right)^{d_{\alpha}^{v}} \left( 1 + \frac{p_{01}}{p_{0*}} (z - 1) \right)^{d_{\alpha}^{b}} \left( 1 + \frac{p_{01}}{p_{0*}} (z - 1) \right)^{d_{\alpha}^{\bar{b}}}
\]

### B. Probability generating function of the relative signature distance delta

Consider the random bipartite graphs \( B_{a} = (V, H; E_{a}), B_{b} = (V, H; E_{b}) \) distributed according to \( (B_{a}, B_{b}) \sim \text{ER}(h, n; p) \). For a given pair of vertices \( u, v \in V \) let us define the relative signature distance of \( u \) to \( v \) observed from \( G_{b} \) as \( \gamma(u, v) = |\text{sig}_{a}'(v) - \text{sig}_{b}'(u)| - |\text{sig}_{a}'(u) - \text{sig}_{b}'(u)| \).

\( \gamma(u, v) \) can be expressed as the sum of the contributions of each high-degree vertex \( w \in H \). The neighborhoods \( N_{a}(v), N_{a}(u) \) and \( N_{b}(u) \) partition the set of high-degree vertices in 8 disjoint sets as given in Fig. 2. Then we have

\[
\gamma(u, v) = \sum_{w \in H} \mathbb{1}\{w \in H_{3} \cup H_{4}\} - \mathbb{1}\{w \in H_{1} \cup H_{6}\}
\]

Notice that for any \( w \in H \), \( P[w \in H_{3} \cup H_{4}] = p_{00}p_{1*} + p_{11}p_{0*} \) and \( P[w \in H_{1} \cup H_{6}] = p_{10}p_{0*} + p_{01}p_{1*} \).

In fact the random variables \( \{\mathbb{1}\{w \in H_{3} \cup H_{4}\} - \mathbb{1}\{w \in H_{1} \cup H_{6}\}\}_{w \in H} \) are mutually independent and identically distributed. Let us define \( q_{0} = p_{00}p_{1*} + p_{11}p_{0*} \) and \( q_{1} = p_{10}p_{0*} + p_{01}p_{1*} \). This gives us the following generating function

\[
F_{\gamma}(z) = \mathbb{E} \left[ z^{\gamma(u,v)} \right] = [1 + q_{0} (z - 1) + q_{1} (z - 1)]^{h}.
\]

### APPENDIX III

**PROOF OF COROLLARY 5**

**Corollary 5.** Let \( (G_{a}, G_{b}) \sim \text{ER}(n; p) \) where \( G_{a} = (V; E_{a}) \) and \( G_{b} = (V; E_{b}) \). Define \( \rho \triangleq \frac{\Delta(G_{a})}{\Delta p_{1*}} + \frac{\Delta(G_{b})}{\Delta p_{0*}} \) and \( \varepsilon \triangleq \frac{p_{01}}{p_{1*}} + \frac{p_{01}}{p_{0*}} \). Let \( h \in [n] \) and \( \eta \) be functions of \( n \). Let \( s \) be an integer such that \( s \geq h + \frac{1}{\sqrt{n}} \log \left( \frac{n}{\eta} \right) + 1 \). If

\[
\forall i \in [s], \quad \delta_{a,i} - \delta_{a,i+1} \geq (1 - \varepsilon)^{-1} \left( k + 4 \max \{\eta, \sqrt{\rho \cdot \eta}\} \right)
\]

then, with probability at least

\[
1 - (2h + 1) e^{-\eta} / (1 - e^{-\eta}),
\]

\( f_{h}(G_{a}) = f_{h}(G_{b}) \) and \( \delta_{b,i} - \delta_{b,i+1} > k \) for any \( i \in [h] \).

**Proof:** Let \( H_{a} \) and \( S_{a} \) be the set of \( h \) and \( s \) highest-degree vertices in \( G_{a} \) respectively and define \( H_{b} \) analogously for \( G_{b} \). The following two events collectively imply \( f_{h}(G_{a}) = f_{h}(G_{b}) \) and \( \delta_{b,i} - \delta_{b,i+1} > k \) for any \( i \in [h] \).

- Let \( E_{\text{high}} \) be the event that vertices in \( H_{a} \) have the same degree ordering in \( G_{a} \) and in \( G_{b} \) as well as a minimum degree separation larger than \( k \) in \( G_{b} \). Note that this does not guarantee \( H_{a} = H_{b} \).
- Let \( E_{\text{low}} \) be the event that all vertices in \( V \setminus H_{a} \) have degree less than \( \delta_{b,h} - k \) in \( G_{b} \), i.e. no vertex from \( V \setminus H_{a} \) and \( H_{a} \) all have a sufficiently large degree separation with the \( h \)-th highest-degree vertex.

First we consider \( E_{\text{high}} \), i.e. the event where \( \delta_{b,i} - \delta_{b,j} > k \) for any \( i < j \) with \( i, j \in [h] \). Notice that it is sufficient to check this condition for consecutive pairs of vertices in the degree sequence. Because we have the condition \( \delta_{b,i} - \delta_{b,i+1} > k \) in \( G_{b} \) have the same degree ordering as well as a degree separation larger than \( k \) with probability at least \( e^{-\eta} \). Thus, by the union bound, we get

\[
P \left[ E_{\text{high}} \right] \leq 1 - he^{-\eta}.
\]
Second we consider \( \mathcal{E}^{\text{low}} \), i.e. the event where \( \delta_{b,h} - \delta_{b,i} > k \) for any \( i \in [n] \setminus [h] \). By the condition in (8) we have

\[
\forall i \in [s] \setminus [h], \quad \delta_{i,h} - \delta_{i,i} \geq (i - h)(k + 4 \max \{ \eta, \sqrt{\rho \cdot \eta} \}) (1 - \varepsilon)^{-1} \\
\geq \left( k + 4 \max \{ (i - h)\eta, \sqrt{(i - h)\rho \cdot \eta} \} \right) (1 - \varepsilon)^{-1} \\
\forall i \in [n] \setminus [s], \quad \delta_{i,h} - \delta_{i,i} \geq (s + 1 - h)(k + 4t \max \{ \eta, \sqrt{\rho \cdot \eta} \}) (1 - \varepsilon)^{-1} \\
\geq \left( k + 4 \max \{ (s + 1 - h)\eta, \sqrt{(s + 1 - h)\rho \cdot \eta} \} \right) (1 - \varepsilon)^{-1}.
\]

By Lemma 4 we then have \( P[\delta_{a,h} - \delta_{a,i} \leq k] \leq \exp(-\eta \min\{i - h, s + 1 - h\}) \). Then, by the union bound,

\[
P[\mathcal{E}^{\text{low}}] \leq \sum_{i=h+1}^{s} e^{-\eta(i-h)} + \sum_{i=s+1}^{n} e^{-\eta(s+1-h)} \\
\leq \frac{e^{-\eta}}{1 - e^{-\eta}} + \frac{(n - s)^{h} e^{-\eta}}{n}
\]

Applying the union bound again we obtain

\[
P[\mathcal{E}^{\text{high}} \lor \mathcal{E}^{\text{low}}] \leq (2h + 1) e^{-\eta} / (1 - e^{-\eta}).
\]

REFERENCES

[1] Y. Tian and J. Patel, “TALE: A Tool for Approximate Large Graph Matching,” Data Engineering, International Conference on, vol. 0, pp. 963–972, 2008.
[2] S. Zhang, J. Yang, and W. Jin, “SAPPER: Subgraph Indexing and Approximate Matching in Large Graphs,” PVLDB, vol. 3, no. 1, pp. 1185–1198, 2010.
[3] L. Backstrom, C. Dwork, and J. Kleinberg, “Wherefore art thou r3579x?,” Communications of the ACM, vol. 54, p. 133, dec 2011.
[4] F. Shirani, S. Garg, and E. Erkip, “An information theoretic framework for active de-anonymization in social networks based on group memberships,” 2017.
[5] E. Onaran, S. Garg, and E. Erkip, “Optimal de-anonymization in random graphs with community structure,” in 2016 IEEE 37th Sarnoff Symposium, IEEE, sep 2016.
[6] L. Fu, X. Fu, Z. Hu, Z. Xu, and X. Wang, “De-anonymization of social networks with communities: When quantifications meet algorithms,” 2017.
[7] S. Ji, W. Li, N. Z. Gong, P. Mittal, and R. Beyah, “On your social network de-anonymizability: Quantification and large scale evaluation with seed knowledge,” in Proceedings 2015 Network and Distributed System Security Symposium, Internet Society, 2015.
[8] A. Narayanan and V. Shmatikov, “Robust de-anonymization of large sparse datasets,” in 2008 IEEE Symposium on Security and Privacy (sp 2008), IEEE, may 2008.
[9] N. Korula and S. Lattanzi, “An efficient reconciliation algorithm for social networks,” Proceedings of the VLDB Endowment, vol. 7, pp. 377–388, jan 2014.
[10] L. Yartseva and M. Grossglauser, “On the performance of percolation graph matching,” in Proceedings of the first ACM conference on Online social networks - COSN 2013, ACM Press, 2013.
[11] E. Kazemi, S. H. Hassani, and M. Grossglauser, “Growing a graph matching from a handful of seeds,” Proceedings of the VLDB Endowment, vol. 8, pp. 1010–1021, jun 2015.
[12] R. Singh, J. Xu, and B. Berger, “Global alignment of multiple protein interaction networks with application to functional orthology detection,” Proceedings of the National Academy of Sciences, vol. 105, no. 35, pp. 12763–12768, 2008.
[13] O. Kuchaiev, T. Milenković, V. Memišević, W. Hayes, and N. Pržulj, “Topological network alignment uncovers biological function and phylogeny,” Journal of the Royal Society Interface, pp. 1341–1354, 2010.
[14] N. Malod-Dognin and N. Pržulj, “L-GRAAL: Lagrangian graphlet-based network aligner,” Bioinformatics, vol. 31, no. 13, pp. 2182–2189, 2015.
[15] V. Saraph and T. Milenković, “Magna: Maximizing accuracy in global network alignment,” Bioinformatics, vol. 30, no. 20, pp. 2931–2940, 2014.
[16] A. E. Aladag and C. Erten, “SPINAL: scalable protein interaction network alignment,” Bioinformatics, vol. 29, no. 7, pp. 917–924, 2013.
[17] K. Henderson, B. Gallagher, L. Li, L. Akoglu, T. Eliassi-Rad, H. Tong, and C. Faloutsos, “It’s who you know,” in Proceedings of the 17th ACM SIGKDD international conference on Knowledge discovery and data mining - KDD 2011, ACM Press, 2011.
[18] P. Pedarsani, D. R. Figueiredo, and M. Grossglauser, “A bayesian method for matching two similar graphs without seeds,” in Communication, Control, and Computing (Allerton), 2013 51st Annual Allerton Conference on, pp. 1598–1607, IEEE, 2013.
[19] M. Mitzenmacher and T. Morgan, “Reconciling graphs and sets of sets,” 2017.
[20] P. Pedarsani and M. Grossglauser, “On the privacy of anonymized networks,” in Proceedings of the 17th ACM SIGKDD international conference on Knowledge discovery and data mining - KDD 2011, ACM Press, 2011.
[21] D. Cullina and N. Kiyavash, “Improved achievability and converse bounds for erdos-renyi graph matching,” in Proceedings of the 2016 ACM SIGMETRICS International Conference on Measurement and Modeling of Computer Science - SIGMETRICS 2016, ACM Press, 2016.

[22] L. Babai, P. Erdo’s, and S. M. Selkow, “Random graph isomorphism,” SIAM Journal on Computing, vol. 9, pp. 628–635, aug 1980.

[23] B. Bollobas, Random Graphs. Cambridge University Press, 2001.