De-anonymizability of Social Network: Through the Lens of Symmetry

ABSTRACT

Social network de-anonymization, which refers to re-identifying users by mapping their anonymized network to a correlated, unanonymized cross-domain network, is an important problem that has received intensive study in network science. However, it remains less understood how network structural features intrinsically affect whether or not the network can be successfully de-anonymized. To find the answer, this paper offers the first study on the relation between de-anonymizability and network symmetry. To this end, we propose to capture the symmetry of a graph by concepts in abstract algebra such as automorphism and homomorphism. By defining the matching probability matrix, we are able to characterize the de-anonymizability, i.e., the expected number of correctly matched nodes. Specifically, we show that for a graph pair with arbitrary topology, the de-anonymizability is equal to the maximal diagonal sum of the matching probability matrix, which is generated from automorphisms/homomorphisms, depending on whether the graph pair results from a full or partial sampling of the underlying ground truth. Due to the prohibitive cost of enumerating all possible homomorphisms, we further propose an equivalent characterization of deanonymizability, and accordingly design a sampling algorithm for approximately estimating the de-anonymizability, which significantly reduces the computational cost. Such a general result allows us to theoretically obtain the de-anonymizability of any networks with more specific topology structure. For example, for any classic Erdős-Rènyi graph with designated n and p, we can represent its de-anonymizability numerically by calculating the local symmetric structure that it contains. Extensive experiments are also performed to validated all our findings. To our best knowledge, this is the first work that rigorously quantifies the relationship between the de-anonymizability and the symmetry property of general networks in a non-asymptotic manner, and thus sheds light on enhancing privacy for real networks design.

1 INTRODUCTION

As the popularity of social networks increases, the privacy of personal information in social networks becomes an issue of great concern. Concealing the personal identity in social network is one of the commonest methods to protect personal information, but it is insufficient for privacy protection since adversaries may use correlated side information, e.g., the information across multiple networks, to uncover the identity of anonymous user. Such re-identification process using auxiliary correlated information is called *Social Network De-anonymization*. The problem is initially proposed by Narayanan and Shimatikov [17]. In the past decades, a large amount of work [17] [20][14] [11] [3] [13][9] [19] [25] [4]

[22] emerges focusing on the de-anonymization problem with different aspect.

In this work, our focus is on a significant branch of deanonymization problem: seedless de-anonymization. In seedless de-anonymization, the attacker needs to re-identify the user identity in a published network using an auxiliary network with full identity information. The published network is completely anonymous, where no pre-identified nodes (i.e. the so-called seeds) are given. The correlation between two networks only lies in the similarity in their topology, since these two networks are supposed to be from the same underlying relationship network. The attacker aims to uncover the identities in this published anonymous network by matching the users in the published network to those in the auxiliary network. In this sense, seedless de-anonymization is analog to the classical graph matching problem, which aims to match the nodes between two graphs with a maximum number of edges overlap.

Various algorithms for seedless de-anonymization have been proposed [17] [20][14] [13] [9] [19] [25] [4]. Unfortunately, such algorithms may occasionally fail to perfectly de-anonymize the published network due to the natural characteristics of the network itself. Further, many works [3] [11] [9] have discussed that under some circumstances, **no algorithm** can successfully re-identify the users in the network. We thus use the term **de-anonymizability** to describe the accuracy with which a de-anonymization attack can (at most) achieve upon certain network.

However, it has not yet been well understood how network structural features intrinsically affect the de-anonymizability of the graph. First, all of the previous works were based on the assumption that the graphs are generated by classical network models, e.g. classical Erdős-Rènyi network [17] [20] [13] [9], correlated Erdős-Rènyi network model [19] [25] [4] and power law model [14], which may not represent real networks. Second, almost all of the previous studies [17] [20][14] [13] [9] [19] [25] [4] only focus on the asymptotic regime, i.e. the regime where the probability of successfully matching all nodes approaches either 1 or 0, as the number of nodes approaches infinity, while there are no non-asymptotic results on de-anonymizability yet. In short, there is a need for a more systematical, quantitative and non-asymptotic analysis on de-anonymizability.

Therefore, in this paper, we provide the first study that systematically analyzes how graph structure characteristics will affect the de-anonymizability, without the assumption on any network model. We will obtain the quantitative, non-asymptotic result on de-anonymizability, which is defined as the maximum number of nodes that one can expect to correctly match in the given network.

In particular, we are interested in how symmetry of a graph can affect the accuracy of de-anonymization. The idea of studying symmetry is intuitive, since attackers have no way to re-identify the symmetric nodes using only structural information. However, a thorough understanding on the relationship between symmetry and de-anonymizability remains elusive. In particular, how should we measure and describe the degree of symmetry of an arbitrary graph? What is the exact quantitative relationship between symmetry and de-anonymizability? In this paper, we aim to answer these two problems.

This paper borrows ideas from abstract algebra such as automorphism, homomorphism, etc. to define the degree of symmetry of a graph, which then allows us to build the relationship between symmetry and de-anonymizability in general graphs. This result enables us to predict the maximum expectation of the number of correctly-matched nodes when a de-anonymization problem is given. We implement a practical algorithm based on sampling, which overcomes the exponential time complexity of the original exact algorithm. Besides, we conduct a case study on Erdős-Rènyi network model to apply such general results to a more specific situation. We also conduct experiments to verify our result.

Our main contributions are:

- (1) We conduct the first theoretical study on de-anonymizability through the lens of symmetry. Learning from the way that symmetry is described in abstract algebra, we introduce concepts such as automorphisms, homomorphisms, etc., from abstract algebra to precisely capture the symmetry of a network. We further define intra-symmetry and inter-symmetry based on those concepts to describe the extent of symmetry within a graph and structural similarity between two social networks, respectively.
- (2) Based on these concepts, we proposed a method that quantitatively determines the de-anonymizability of given networks. Our method can find the maximum expectation number of correctly matched nodes, which is equal to the maximum diagonal sum of the matching probability matrix that we define. Then, by defining automorphism transition matrix and homomorphism transition matrix, we build the relationship between symmetry and de-anonymizability. Our method is systematic, general, and non-asymptotic. It can be applied to any general de-anonymization problem without depending on any specific network model.
- (3) To overcome the exponential time complexity of finding all homomorphisms, we propose an equivalent characterization of de-anonymizability by enumerating permutations instead of enumerating possible underlying networks, and accordingly design a practical approximating algorithm via sampling techniques, which overcomes the exponential time complexity, and can approximately estimate de-anonymizability by virtue of a well-designed sample selection strategy. Other techniques like orbit contracting are also used to reduce the complexity.

(4) We apply the general method to the analysis of classical network model. As a case study, we analyzed the deanonymizability of Erdős-Rènyi graph with any given parameters n and p. By enumerating the local symmetric structure in Erdős-Rènyi model, we obtain a numerical upper bound on de-anonymizability in Erdős-Rènyi graph. We also gave proof on the correctness by illustrating the fact that in the giant component of a supercritical Erdős-Rènyi graph, the number of symmetric nodes is of the order o(1). All the results above are verified by extensive experiment results.

The remainder of the paper is organized as follows: In Section 2, we survey previous work on the topic of deanonymization, de-anonymizability and symmetry. In Section 3, we introduce the model for de-anonymization and problem formulation for de-anonymizability, and also introduce some symmetry-related concepts. Section 4 demonstrates our main result, i.e., the method of obtaining the de-anonymizability on general graphs. In Section 5 we consider the algorithm aspect of de-anonymizability. In Section 6, we conduct a case study in which we extend our general method to obtain de-anonymizability of classical Erdős-Rènyi network model. Section 7 contains the experiment verification and result. We conclude with some discussion in Section 8.

2 RELATED WORK

2.1 De-anonymization Algorithms

Narayanan and Shimatikove [17] first proposed de-anonymization problem. They formulated this problem and proposed a generic algorithm based on network structure information with the help of seed nodes, i.e. pre-identified node pairs that are known to be correctly matched. However, in many situations, it is difficult to obtain such seed nodes due to the limited access to user profiles [9] [25]. Pedarsani and Grossglauer [20] first studied the seedless de-anonymization problem in the context of Erdős-Rènyi model, and they took the number of mismatched edge as the objective function. A different cost function based on Maximum a Posterior (MAP) was proposed in [18] and also used in [9] [25]. Recent works for correlated Erdős-Rènyi networks were reported in [22] [4]; Nitish and Silvio also proposed algorithm in [14] for the preferential attachment (PA) model.

2.2 De-anonymizability

Some networks are difficult to de-anonymize due to their inherent topoligical structure. Along with their problem formulation and algorithm, Pedarsani and Grossglauser [20] also approached the problem of finding theoretic conditions for successful de-anonymization. Cullina and Kiyavash [3] further investigated the conditions under which a pair of correlated Erdős-Rènyi graphs can be correctly matched. However, most of these studies focus on the asymptotic regime, i.e., when the probability of correctly matching all nodes goes to either 1 or 0, as the number of nodes approaches infinity. Further, they mostly base their studies on the assumption of classical network models such as Erdős-Rènyi [18][9] and preferential attachment[14].

The concept of de-anonymizability, was also proposed by Ji et al. [10] [11] [12], which is a metric to describe the accuracy that a de-anonymization attack can achieve. Although the original intention of our proposing de-anonymizability is the same, the de-anoymizability in our paper has a totally different definition from theirs. The metric that we consider here is the performance of de-anonymization algorithm in **non-asymptotic** situation. We aim to provide a quantitative characterization of de-anonymizability by obtaining the maximum expected number of correctly mapped nodes of a de-anonymization problem.

2.3 Symmetry and De-anonymization

Symmetry is a widely discussed topic in mathematics, especially in abstract algebra. Many concepts, like isomorphism, automorphism, homomorphism, etc., are used to describe different types of symmetry in algebra structure. Related contents can be found in any textbook on abstract algebra, and are beyond the scope of this work. In the context of graph, Graph Isomorphism, Graph Automorphism and Graph Homomorphism are also classical topics[2][6], which show potential to describe the degree of symmetry of graphs.

[26][15] have used symmetry to anonymize the network. They proposed some techniques to add symmetry to a network, in order to protect personal information from structural attack. However, no previous work has applied symmetry to the theoretical analysis of de-anonymization problem. To the best of our knowledge, this paper is the first to build the relationship between symmetry and de-anonymizability in general graphs.

3 PRELIMINARY DEFINITION AND CONCEPT

3.1 De-anonymization Problem

Let G = (V, E) be the underlying social network, where V is the set of nodes, E is the set of edges. The underlying network indicates the true relationship among all users V, but is invisible to the attacker. We further define $G_1 = (V_1, E_1)$ as the published network and $G_2 = (V_2, E_2)$ the auxiliary network. The published network is completely anonymous: no identity information is given of any node in G_1 . In contrast, in auxiliary network, each node in G_2 has a name label which is available to the attacker.

Like in most previous work[11][9], we suppose G_1 and G_2 have the same node set with G. In the case that $V_1 \neq V_2$, we can make $V_1 = V_2$ by adding isolated nodes to the network with fewer nodes[11]. Further, we suppose the vertex in G as $V = \{1, 2, ..., n\}$ for the sake of convenience [3].

We suppose G_1 and G_2 are generated via independent samplings of G. By sampling we mean that the edges in G_1 and G_2 are sampled from G. We can model the sampling process from G to $G_i(i=1,2)$ as follows: For graph $G_i(i=1,2)$, each existing edge in G is sampled to G_i i.i.d. with a sampling rate s_i . That is, for each edge $e \in E$, we have

$$P(e \in E_i) = \begin{cases} s_i & \text{if } e \in E \\ 0 & \text{if } e \notin E \end{cases} \tag{1}$$

In this sense, the underlying network G is the only bridge between G_1 and G_2 , though it is invisible to the adversaries.

Given the published network G_1 and the auxiliary network G_2 , the problem of social network de-anonymization aims to match the node in G_1 to the nodes in G_2 using only the structural information of G_1 and G_2 as side information. Formally, we need to find a permutation $\sigma: V_1 \mapsto V_2$. For $v_1 \in V_1$ and $v_2 \in V_2$, $\sigma(v_1) = v_2$ means the node $v_1 \in V_1$ and the $v_2 \in V_2$ derive from the same node in the underlying network (and since we have the name label of v_2 in v_2 , we can then deduce the name label of v_1 in v_1).

Unlike most of the previous work, in this paper we do not assume that G is generated by some specific network model. Instead, we allow G to have arbitrary topology, and only assume the sampling rates s_1 , s_2 to be known. The assumption of known sampling rates is reasonable, since they can be obtained from statistical manners.

The parameters defined above can be simply denoted by a parameter set $\theta = (G_1, G_2, s_1, s_2)$, which we will use to state a de-anonymization problem. In the rest of the paper we may simply refer to a de-anonymization problem as a de-anonymization problem with parameter $\theta = (G_1, G_2, s_1, s_2)$ without causing ambiguity.

3.2 De-anonymizability

Predicated on Section 3.1, in the sequel we propose the concrete quantification of de-anonymization accuracy, denoted as **de-anonymizability** formally. Note that de-anonymizability will be the principal metric discussed in this paper, which measures the potential accuracy of a de-anonymization problem. To this end, we denote the true permutation between G_1 and G_2 as σ_0 . Note that σ_0 is a random variable due to the lack of ground truth information. In other words, although there is a unique true mapping, i.e., the true permutation between G_1 and G_2 , this true mapping is unknown to the attacker, who can only hypothetically choose among many similar seemingly true mappings. Counter-intuitive at the first sight, this claim can be illustrated by the following two examples:

- (a). Suppose $G = K_N$ (complete graph) and $G_1 = G_2 = G$. Given G_1 and G_2 , any permutation σ can be the true mapping since adversaries have no information other than their topology. More concretely, σ_0 is a random variable satisfying $P(\sigma_0 = \sigma) = \frac{1}{N!}$ for any permutation σ from V_1 to V_2 .
- (b). Suppose G_1 , G_2 are given in Figure 1. Two possible underlying networks G and G' are shown, and we cannot tell which to be the true underlying network. As a result, two totally different ways of matching from G_1 to G (or G') exist, and it is uncertain which one is true. We can see that even G_1 itself is asymmetric[7], the process of sampling will still bring uncertainty to the de-anonymization.

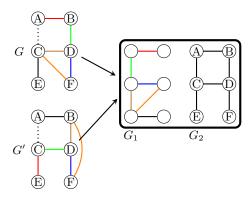


Figure 1: Uncertainty From Sampling. G_1 and G_2 are known, but multiple underlying networks (including G and G') is feasible, and can be the true underlying network.

To be more concrete, for any de-anonymization problem with parameter set $\theta = (G_1, G_2, s_1, s_2)$, let $\Pi = \pi$ denote all the permutations on V. For each de-anonymization problem, there exists a probability distribution of the true mapping σ_0 , denoted as $P(\sigma_0 = \pi | \theta)$ for all π in Π . Note that one of the main focus in the body part of this paper is how to obtain such probability distribution.

For any two permutations π_1, π_2 from V_1 to V_2 , we denote $N_{(\pi_1, \pi_2)}$ as the number of nodes in V_1 , each of which, under π_1 and π_2 , has the same image in V_2 . Formally, we have ¹

$$N_{(\pi_1, \pi_2)} = \sum_{v \in V, \pi_1(v) = \pi_2(v)} 1 \tag{2}$$

Then, the expectation of the number of correctly matched nodes for any permutation (as a solution attempting to solve the de-anonymization problem with parameter set θ) σ , denoted as $E_{\sigma|\theta}$, can be calculated by

$$E_{\sigma|\theta} = \sum_{\pi \in \Pi} P(\sigma_0 = \pi|\theta) N_{(\sigma,\pi)}$$

Under the circumstance without ambiguity, we use E_{σ} to refer to the expectation. Intuitively, E_{σ} is the expectation of the number of correctly mapped nodes when σ is exerted to the anonymous network G_1 .

Among all σ , a best permutation σ^* for a de-anonymization problem is such a permutation that maximizes the expectation of the number of correctly-mapped nodes, which can be expressed as

$$\sigma^* = \arg\max_{\sigma \in \Pi} E_{\sigma}$$

And the expectation E_{σ^*} is the maximum expectation of the number of successfully de-anonymized nodes. We define de-anonymizability of a de-anonymization problem as E_{σ^*} , which is a performance upper bound of any de-anonymization algorithm on this de-anonymization problem. To be concrete, we have the following definition:

Definition 3.1 (De-anonymizability). Given a de-anonymization problem with parameter $\theta = (G_1, G_2, s_1, s_2)$, the true mapping σ_0 is a random variable with probability distribution $P(\sigma_0 = \pi | \theta)$ for any π in Π , all the permutations on V. (One of) the best permutation σ^* is

$$\sigma^* = \arg\max_{\sigma} E_{\sigma} = \arg\max_{\sigma} \sum_{\pi \in \Pi} P(\sigma_0 = \pi | \theta) \sum_{v \in V, \sigma_0(v) = \pi(v)} 1$$

where σ is any permutation on V. The de-anonymizability of this problem is defined as E_{σ^*} . It reaches the maximum expectation of the number of correctly matched nodes over all permutation on V.

As mentioned, de-anonymizability will be our primary focus throughout the rest of the paper. Before we start our analysis, we further proceed to give out the definition of symmetry, which is the essence of de-anonymizability.

3.3 Definition of Symmetry

Intuitively, symmetry property determines de-anonymizability of the networks fundamentally. The symmetry property of networks consists of two perspectives: intra-symmetry and inter-symmetry. The intra-symmetry reflects the extent of symmetry of nodes inside a network, while the inter-symmetry measures the extent of structural similarity between two social networks. Here we formally define them with the help of concepts originated from abstract algebra.

First we define intra-symmetry, which uses the concept of (graph) automorphism.

Definition 3.2 (Automorphism and Intra-symmetry). For two graph $G_1 = (V_1, E_1)$ and $G_2 = (V_2, E_2)$, if a bijection $f: V_1 \to V_2$ such that $\forall (v_i, v_j) \in E_1 \leftrightarrow (f(v_i), f(v_j)) \in E_2$, then we say G_1 and G_2 are isomorphic, and f is an isomorphism of G_1 onto G_2 . If $G_1 = G_2 = G$, then f is an automorphism of G onto itself. The intra-symmetry of a graph, is measured by the whole set of distinct automorphism(s) of a graph.

Inter-symmetry, on the other hand, is the structural similarity across the graphs. To precisely define it we need the concept of (graph) bijective homomorphisms.

Definition 3.3 (Homomorphism and Inter-symmetry). For two graph $G_1 = (V_2, E_2)$ and $G_2 = (V_2, E_2)$, if a bijection $h: V_1 \to V_2$ such that $\forall (v_i, v_j) \in E_1 \to (f(v_i), f(v_j)) \in E_2$, then we say h is a bijective homomorphism from G_1 to G_2 . In this paper, we slightly abuse the term homomorphism to refer to the graph bijective homomorphism. For a specific underlying graph G, the published graph G_1 and the auxiliary graph G_2 , the inter-symmetry is measured by the set of distinct homomorphism(s) from G_1 to G and set of distinct homomorphism(s) from G_2 to G.

Since G is unknown, we see it as a random variable (we will describe the detail in Section 4.3), and thus the intersymmetry of a de-anonymization problem is also a random variable.

The notation $v \in V$ in the formula is equivalent to $v = 1, 2, \ldots, n$. At times, we interchange these two notations in this paper, especially in the subscript of summation notation.

4 DE-ANONYMIZABILITY IN GENERAL GRAPHS

In this part, we show our general method to determine the de-anonymizability of general de-anonymization problems. By 'general' we mean there is no constraint on graph topology. In doing so, we first demonstrate in Section 4.1 that de-anoymizability can be calculated as long as the probability distribution of the true mapping σ_0 is known. Then, in Sections 4.2 and 4.3, we obtain the probability distribution of σ_0 for the calculation of de-anonymization in fully sampled cases and partially sampled cases, respectively.

4.1 Introduction of Matching Probability Matrix

Let us define matching probability matrix. For each de-anonymization problem $\theta = (G_1, G_2, s_1, s_2)$ where $|V_1| = |V_2| = n$, the matching probability matrix of this problem (denoted as M) is an n-by-n matrix, each element of which is given by:

$$M_{ij} = \sum_{\pi \in \Pi} P(\sigma_0 = \pi | \theta) \mathbb{1} \{ \pi(i) = j \}$$
 (3)

Intuitively, the element M_{ij} is equal to the probability that node i in V_1 is mapped (by the true mapping) to node j in V_2 . However, in order to prove this claim, the concept of doubly stochastic matrix needs to be introduced.

A doubly stochastic matrix [23] is a square matrix with nonnegative real entries and the sum of the elements in each row and each column is equal to 1. Concretely, for an $n \times n$ matrix, it is a doubly stochastic matrix if it satisfies:

$$\begin{cases} A_{ij} \ge 0 \\ \sum_{j=1}^{n} A_{ij} = \sum_{j=1}^{n} A_{ji} = 1 \text{ for any } j = i, 2, \dots n \end{cases}$$

Proposition 4.1. A matching probability matrix is a doubly stochastic matrix.

PROOF. Obviously each element in M is nonnegative. On the other hand,

$$\sum_{j=1}^{n} M_{ij} = \sum_{j=1}^{n} \sum_{\pi \in \Pi} P(\sigma_0 = \pi) \mathbb{1} \{ \pi(i) = j \}$$

$$= \sum_{\pi \in \Pi} P(\sigma_0 = \pi) \sum_{j=1}^{n} \mathbb{1} \{ \pi(i) = j \} = \sum_{\pi \in \Pi} P(\sigma_0 = \pi) = 1$$

Therefore, the summation of the elements in each row is equal to 1. Similarly, the summation of the elements in each row sum is also equal to 1. The result follows. \Box

For a doubly stochastic matrix M, the diagonal sum of M corresponding to a permutation σ on $1, 2, \ldots, n$ is defined as $\sum_{i=1}^{n} M_{i\sigma(i)}$. We now demonstrate that, the expected number of correctly matched nodes of a permutation σ is equal to the diagonal sum of M corresponding to σ .

Theorem 4.2. Given a de-anonymization problem with θ , the matching probability matrix of which is M. For any permutation σ from V_1 to V_2 , the expectation of the number of correctly matched nodes of a permutation σ is equal to the diagonal sum of M corresponding to σ .

PROOF. By definition of the expectation of the number of correctly matched nodes of a permutation σ , we have

$$E_{\sigma|\theta} = \sum_{\pi \in \Pi} P(\sigma_0 = \pi) \sum_{v \in V, \sigma(v) = \pi(v)} 1$$

$$= \sum_{\pi \in \Pi} P(\sigma_0 = \pi) \sum_{i=1}^n \mathbb{1} \{ \sigma(i) = \pi(i) \}$$

$$= \sum_{i=1}^n \sum_{\pi \in \Pi} P(\sigma_0 = \pi) \mathbb{1} \{ \pi(i) = \sigma(i) \}$$

$$= \sum_{i=1}^n M_{i\sigma(i)}$$

Consequently, obtaining the maximum expectation (i.e. obtaining the de-anonymizability) is equivalent to finding the maximum diagonal sum [23] of the matching probability matrix M. We denote h(M) as the maximum diagonal sum of a doubly stochastic matrix M. Therefore, we come to the conclusion that we can obtain the de-anonymizability when the probability distribution of σ_0 is known.

In the following, we aim to find the probability distribution of σ_0 in both fully sampled cases and partially sampled cases, and then generate the corresponding matching probability matrix for further obtaining the de-anonymizability these two cases, respectively.

4.2 Fully Sampled Case

We first study the fully sampled cases, where the sampling rate $s_1 = s_2 = 1$. In this way, any edge in G also exists in both G_1 and G_2 . By relabeling the nodes, we can assume that $G_1 = G_2 = G$ without loss of generality. We now strive to obtain the de-anoymizability of a fully-sampled de-anonymization problem in terms of the intra-symmetry of G. Obviously we do not need to consider inter-symmetry in fully sampled

A true mapping in the fully sampled case must keep existence and non-existence of all edges. That means a true mapping can be obtained with non-zero probability *iff* it is an automorphism of G. Proposition 4.3 claims that, all the automorphisms have the same probability to be the true mapping.

Proposition 4.3. For a de-anonymization problem with parameter set $\theta = (G_1, G_2, s_1, s_2)$ where $s_1 = s_2 = 1$ and $G_1 = G_2 = G$, the probability distribution of the true mapping is

$$P(\sigma_0 = \pi | \theta) = \begin{cases} \frac{1}{|Aut(G)|} & \pi \in Aut(G) \\ 0 & otherwise \end{cases}$$

where Aut(G) is the set of all the automorphisms of G, and |Aut(G)| is its cardinality .

PROOF. For a permutation π , if it is not an automorphism of G the probability that it is the true mapping is 0, since it did not keep all existence and absence of edges in graph G, which is impossible for a true mapping in fully sampled cases. Then we consider the situation where π is an automorphism

of G. Notice that when de-anonymizing the only side information we know is structure information, and therefore it does not affect the result when we arbitrarily interchange the label of nodes in the published network G_1 . Suppose there is another automorphism π' of G which has a larger probability than π , then we can interchange the label of the nodes in V_1 such that π and π' interchange with each other after the relabeling, which makes the probability of π' become smaller than π . It yields a contradiction. Therefore, all the automorphisms have the same probability to be the true mapping, that is, $\frac{1}{|Orb(G)|}$.

After obtaining the probability distribution of the true mapping σ_0 , we use Equation (3) to generate the matching probability matrix. However, for the sake of clarity in expression, it is worthwhile to introduce another important concept orbit, which also originates from abstract algebra [5]. Instead of directly adopting the original concept of orbit, here we redefine the concept of orbit in the context of graph theory to fit in with our study.

Definition 4.4 (Orbit). For a graph G = (V, E), two nodes v_1, v_2 are symmetric (automorphically equivalent) [24] (denoted as $v_1 \sim v_2$) if there exists an automorphism f of G such that $f(v_1) = v_2$. An orbit is a subset of nodes. The orbit that a certain node v belongs to contains all the nodes that are symmetric to v. Precisely, an orbit $\mathcal{O} = \{v_1, v_2, \dots, v_i\}$ satisfies: if $v \in \mathcal{O}$, then for any $v' \sim v, v' \in \mathcal{O}$,

Based on Definition 4.4, intuitively, an orbit is a subset of node set, in which all nodes are internally symmetric. Lemmas

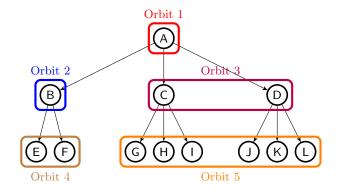


Figure 2: An Illustration of Orbit

4.5 and 4.6 present some further properties regarding the

Lemma 4.5. [5] A graph G can be partitioned by several orbits. That is, there exists a partition $\{\mathcal{O}_1, \mathcal{O}_2, \dots, \mathcal{O}_k\}$ of V such at for each i = 1, 2, ..., k, \mathcal{O}_i is an orbit in V.

the cardinality of set of all its automorphisms is

$$|Aut(G)| = \prod_{i=1}^{k} |\mathcal{O}_i|!$$

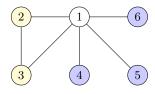
Note that Lemma 4.5 is a variant of the classical theorem in abstract algebra [5]. Here we rewrite it in the context of graph theory to fit in with our study. The detailed proofs of both Lemmas 4.5 and 4.6, due to space limitations, are available in Appendix A.1

Based on the above lemmas, for a node v, we define $\mathcal{O}(v)$ as the orbit containing node v. For a graph G, we define $Orb(G) = \{ \mathcal{O}_1, \mathcal{O}_2, \dots, \mathcal{O}_k \}$ as the orbits of G, where |Orb(G)| = k as the number of orbits that G contains. Using the concept of orbit, we can quantify the intra-symmetry, by organizing all the automorphisms into a matrix structure, as given formally in Definition 4.7:

Definition 4.7 (Automorphism transition matrix). For a graph G, the automorphism transition matrix A(G) is defined

$$A_{ij} = \begin{cases} \frac{1}{|Orb(i)|} & j \in Orb(i) \\ 0 & otherwise \end{cases}$$

Note that A is a symmetric matrix, since for any two nodes $i, j \in V$, $i \in Orb(j)$ is equivalent to $j \in Orb(i)$, which implies |Orb(i)| = |Orb(j)|. Particularly, we denote $A_1 = A(G_1), A_2 = A(G_2)$ as the automorphism transition matrix of A_1 and A_2 , respectively. Figure ?? is an illustration of automorphism matrix.



sents an orbit

(a) A graph with three orbits, each color repre-

Γ1	0	0	0	0	0
$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\frac{1}{2}$	$\frac{1}{2}$	0	0	0
0	$\frac{\frac{1}{2}}{\frac{1}{2}}$	$\frac{\frac{1}{2}}{\frac{1}{2}}$	0	0	0
$\begin{vmatrix} 0 \\ 0 \end{vmatrix}$	Õ	Õ	$\frac{1}{3}$	$\frac{1}{3}$	$\frac{1}{3}$
0	0	0	$\frac{1}{3}$	$\frac{1}{3}$	$\frac{1}{3}$
o	0	0	0 $\frac{1}{3}$ $\frac{1}{3}$ $\frac{1}{3}$	$0 \\ \frac{1}{3} \\ \frac{1}{3} \\ \frac{1}{3}$	$0 \\ \frac{1}{3} \\ \frac{1}{3} \\ \frac{1}{3} \\ -$

(b) The automorphism transition matrix of the graph on the left

Figure 3: An illustration of automorphism

The following theorem builds the relationship between symmetry and de-anonymization by claiming that, in a fullysampled de-anonymization problem, its matching probability matrix is exactly equal to the automorphism transition matrix of G.

Theorem 4.8. For a de-anonymization problem with parameter set $\theta = (G_1, G_2, s_1, s_2)$ where $s_1 = s_2 = 1$ and $G_1 = G_2 = G$, its matching probability matrix M is equal to the automorphism transition matrix of G, i.e. M = A(G).

The proof is completed by a direct calculation of matching probability matrix using its definition (equation 3) via the probability distribution obtained in Proposition 4.3. The readers can see Appendix A.2 for more details. .

According to Theorem 4.8, the de-anonymizability is con-LEMMA 4.6. For a graph G partitioned by orbits $\{\mathscr{O}_1, \mathscr{O}_2, \ldots, \mathscr{O}_k\}$ sequently the max diagonal sum of A(G). In the following we see cardinality of set of all its automorphisms is

> Proposition 4.9. For a fully sampled de-anonymization problem $\theta = (G_1, G_2, s_1, s_2)$ where $s_1 = s_2 = 1$ and $G_1 =$ $G_2 = G, E_{\sigma^*} = |Orb(G)|.$

PROOF. We only need to prove that the maximum diagonal sum of A (i.e. h(A)), is equal to |Orb(G)|.

On one hand, $h(A) \leq \sum_{i=1}^{n} \max_{j=1}^{n} A_{ij} = \sum_{i=1}^{n} \frac{1}{|Orb(i)|} = \sum_{v \in V} \frac{1}{|Orb(v)|}$. For each orbit $\mathcal{O}_i = \{v_{i1}, v_{i2}, \dots, v_{ip}\}$ in G, $\sum_{v \in \mathcal{O}_i} = p * \frac{1}{|Orb(v)|} = p * \frac{1}{p} = 1$. That means the summation over $v \in V$ equals to the orbit number of G.

On the other hand, such a h(A) is reachable. For any automorphism σ of G, the diagonal sum corresponding to σ is equal to h(A).

This result is surprisingly simple, but useful. As an example, consider the complete graph illustrated in Figure 4a. It can be seen that, all the nodes are in the same orbit, thus the de-anonymizability is 1, which accords with the previous calculation. On the other hand, Figure 4b shows an asymmetric graph, which has no non-trivial automorphism. The de-anonymizability is 6, since each node owns an orbit containing no other nodes. That means we can expect a $\sigma^* = \sigma_0$ which matches all the nodes correctly.



(a) A Symmetric Graph (|Orb|=1)

(b) An Asymmetric Graph (|Orb|=6)

Figure 4: Symmetric Graph and Asymmetric Graph

Therefore, to obtain the de-anonymizability in the fully sampled case, we only need to calculate the number of orbits in a graph, as summarized in Algorithm 1.

Algorithm 1: Getting De-anonymizability in Fully Sampled Case

input : Graph G=(V,E)

output: De-anonymizability of G

1 Orb \leftarrow get_orbit (G);

2 return number_of_orbit (Orb);

4.3 Partially Sampled Case

Next we consider the partially sampled case where at least one of s_1 , s_2 is less than one. Due to compactness, all the technical details are provided in Appendix B.

4.3.1 The probability distribution of underlying network. Recall that for a de-anonymization problem, the only information we know is $\theta = (G_1, G_2, s_1, s_2)$, while the underlying network G is unavailable in de-anonymization. On the other hand, the primary connection between G_1 and G_2 is, however, G. Due to the lack of ground truth of G, we again consider G to be a random variable. We denote \mathcal{G} to be all $2^{\binom{n}{2}}$ possible graphs with |V| = n, and denote $P(G|\theta)$ to be the probability distribution of G being the true underlying network. In this subsection, we study the probability distribution of every possible underlying network G and its effect on the de-anonymization process. For general de-anonymization

problems, we make our only assumption that there is no preference on the underlying network G. In other words, each graph has the same prior probability. However, due to the existence of θ , each G has different posterior probabilities to be the ground truth underlying network. The following proposition shows the probability distribution of the underlying network G from a Bayesian perspective.

PROPOSITION 4.10. Given parameter $\theta = (G_1, G_2, s_1, s_2)$ of a de-anonymization problem, for any graph G = (V, E), the probability of its being the ground truth underlying network is propositional to $\text{hom}(G_1, G) \text{hom}(G_2, G)((1 - s_1)(1 - s_2))^{|E|}$, where hom(F, G) is the bijective homomorphism counting from F to G. More precisely,

$$P(G|\theta) = H \operatorname{hom}(G_1, G) \operatorname{hom}(G_2, G) ((1 - s_1)(1 - s_2))^{|E|}$$

where $H = \sum_{G \in \mathcal{G}} \text{hom}(G_1, G) \text{hom}(G_2, G)((1-s_1)(1-s_2))^{|E|}$ is a normalization parameter.

PROOF. The proof is based on Bayes' Rule and our assumption. The detail is given in Appendix B.1 \Box

The probability distribution of the true mapping σ_0 can be expressed by a total probability formula with known probability of G, which is

$$P(\sigma_0 = \pi | \theta) = \sum_{G \in \mathcal{G}} P(G|\theta) P(\sigma_0 = \pi | \theta, G)$$

Consequently, for the matching probability matrix M, it can also be expressed by a total probability formula,

$$M = \sum_{G \in \mathscr{G}} P(G|\theta) M_G$$

$$= \sum_{G \in \mathscr{G}} \sum_{\pi \in \Pi} P(G|\theta) P(\sigma_0 = \pi|\theta, G) \mathbb{1}\{\pi(i) = j\}$$
(4)

where M_G is the matching probability matrix when G is given as known.

In the following subsection, we focus on how to calculate the probability distribution of the true mapping σ_0 when G is known, i.e. the term $P(\sigma_0 = \pi | \theta, G)$

4.3.2 The distribution of true mapping. Due to the existence of the underlying network G, the permutation from G_1 to G_2 is not enough for our analysis. Therefore, we analyze the problem via matching G_1 and G_2 , respectively, to G. The final mapping from G_1 to G_2 is a **composition** of these two mappings. Since $G_i(i=1,2)$ is sampled from G, an feasible mapping (from G_i to G) only needs to keep the edge existence, but not the non-existence. In other words, the feasible mapping from $G_i(i=1,2)$ to G should be a (graph bijective) homomorphism from $G_i(i=1,2)$ to G. In contrast to the fully sampled case where intra-symmetry plays a primary role because of automorphism, the homomorphism property suggests that in the partially sampled case we need to study the relationship between inter-symmetry and deanonymizability.

We define the true mapping from G_1 to G as f_0 , and the mapping from G_2 to G h_0 . Then we have $\sigma_0 = f_0 \circ h_0^{-1}$. For the same reason with σ_0 , f_0 and h_0 are all random variables. Also, We define $F_G = \{f_1, f_2, \ldots, f_{k1_G}\}$ as all the homomorphisms from G_1 to G, and $H_G = \{h_1, h_2, \ldots, h_{k2_G}\}$ the homomorphisms from G_2 to G. Here $k1_G = \text{hom}(G_1, G), k2_G = \text{hom}(G_2, G)$ represent the number of homomorphisms from G_1 and G_2 , respectively, to G. Notice that here F_G , H_G , $k1_G$, $k2_G$ are variant among different G.

Proposition 4.11 claims that each homomorphism has the same probability to be the true permutation from G_1 and G_2 , respectively, to G.

PROPOSITION 4.11. Given underlying network G and parameter θ of a de-anonymization problem, each homomorphism mapping f_i from G_1 to G has the probability of $\frac{1}{\hom(G_1,G)}$ to be the true mapping from G_1 to G. Similarly, each h_i has the probability of $\frac{1}{\hom(G_2,G)}$ to be the true mapping from G_2 to G.

PROOF. Again, determining which permutation to be the true one is an inference process, so it is reasonable to use Bayes' Law in determining the probability of the true permutation. The detail of the proof is given in Appendix B.2. \Box

Similar to the fully sampled case, we define the homomorphism transition matrix from G_1 to G as follows:

Definition 4.12 (Homomorphism Transition Matrix). For a de-anonymization problem θ and a given underlying network G, the homomorphism transition matrix from G_1 to G is

$$C_G = \frac{1}{k1_G} \begin{bmatrix} c_{11} & c_{12} & \dots & c_{1n} \\ c_{21} & c_{22} & \dots & c_{2n} \\ \dots & \dots & \dots & \vdots \\ c_{n1} & c_{n2} & \dots & c_{nn} \end{bmatrix}$$

where c_{ij} is the number of homomorphisms from G_1 to G that matches the node i in G_1 to the node j in G. Formally, $(C_G)_{ij} = c_{ij} = \sum_{f \in F_G} \mathbb{1}(f(i) = j)$. Similarly, for G_2 , the homomorphism transition matrix from G_2 to G is

$$D_G = \frac{1}{k2_G} \begin{bmatrix} d_{11} & d_{12} & \dots & d_{1n} \\ d_{21} & d_{22} & \dots & d_{2n} \\ \dots & \dots & \dots & \dots \\ d_{n1} & d_{n2} & \dots & d_{nn} \end{bmatrix}$$

where $(D_G)_{ij} = d_{ij} = \sum_{h \in H_G} \mathbb{1}(h(i) = j).$

Intuitively, the element C_{ij} (resp. D_{ij}) in homomorphism transition matrix indicates the probability that node i in G_1 (resp. G_2) is mapped to node j in G by the true mapping.

Now we can calculate the probability distribution of the true mapping σ_0 . Although it can be explicitly expressed by the distribution of f_0 and h_0 , we here directly calculate the matching probability matrix given G (i.e. M_G), and consequently M, in terms of C_G and D_G .

Theorem 4.13. For a de-anonymization problem θ with a given underlying network G, $M_G = C_G D_G^T$. Further, $M = \sum_{G \in \mathscr{G}} P(G|\theta) C_G D_G^T$

PROOF. For each element in M_G , we have

$$(M_G)_{ij} = \sum_{\pi \in \Pi} P(\sigma_0 = \pi | \theta, G) \mathbb{1} \{ \pi(i) = j \}$$

$$\stackrel{(0)}{=} \mathbb{E}(P(\sigma_0 = \pi | \theta, G) \mathbb{1} \{ \pi(i) = j \})$$

$$\stackrel{(1)}{=} P(\sigma_0(i) = j | \theta, G)$$

$$\stackrel{(2)}{=} \sum_{k=1}^n P(f_0(i) = k, h_0(j) = k | \theta, G)$$

$$\stackrel{(3)}{=} \sum_{k=1}^n P(f_0(i) = k | \theta, G) P(h_0(j) = k | \theta, G)$$

$$\stackrel{(4)}{=} \sum_{k=1}^n (C_G)_{ik} (D_G)_{jk} = (C_G D_G^T)_{ij}$$

In this formula, (0) holds due to the definition of expectation, (1) holds due to the fact that the expectation of an indicator function is equal to its probability, (2) holds due to the fact that σ_0 is the composition of f_0 and h_0^{-1} , (3) holds due to the fact that G_1 and G_2 are independent samplings from G, (4) holds due to the probability distribution we obtained in Proposition 4.11.

Therefore, each element in M_G is equal to the corresponding element in $C_G D_G^T$, completing our proof.

So far, we have already proposed our method to determine the matching probability matrix of a de-anonymization problem. However, it is obvious that this method is costly in terms of time complexity. The reason is two-folded: (1) the method involves enumerating common supergraph, which is exponentially expensive; (2)finding graph bijective homomorphisms is proved to be NP-Complete in general case[8]. The prohibitive cost drives the necessity of proposing more efficient approximate algorithms. To this end, in the sequel (Sections 4.3.3 and 4.3.4) we will try to explore a bit more deeper into more properties of the de-anonymizabilit, which are helpful in our later approximate algorithm design.

4.3.3 The relationship between inter-symmetry and intra-symmetry. The first property that we want to explore is the relationship between inter-symmetry and intra-symmetry. The following theorem shows that, intra-symmetry can be 'factored out' from inter-symmetry, and intra-symmetry can determine the upper bound of de-anonymizability.

Theorem 4.14. Given problem θ and an presumed underlying network G, let A_1,A_2 be their automorphism transition matrices (defined in Section 4.2) of G_1,G_2 , respectively. Let C_G , D_G be the homomorphism transition matrix from G_1 and G_2 , respectively, to G. Then each homomorphism transition

²For a permutation f, the inverse of f, denoted as f^{-1} , is a permutation that satisfies: for each v, $f^{-1}(f(v)) = v$

matrix keeps invariant under the multiplication of corresponding automorphism transition matrix. Precisely,

$$C_G = A_1 C_G$$
$$D_G = A_2 D_G$$

COROLLARY 4.15. The matching probability matrix M can be represented as: $M = A_1 M A_2$.

PROOF. M is a linear combination of M_G , and for each M_G , $M_G = C_G D_G = A_1 C_G D_G A_2$. Since A_1 and A_2 are constant matrices within a de-anonymization problem, the result follows.

After building the relationship between intra-symmetry and inter-symmetry, we strive to bound the de-anonymizability by the intra-symmetry in G_1 or G_2 . Recall that A_1 , M, A_2 are all doubly stochastic matrix³. Then Theorem 4.16 shows that the maximum diagonal sum of the product of two doubly stochastic matrices is no greater than that of any one of them.

Theorem 4.16 (Theorem 4.1 in [23]). For two n- \times -n doubly stochastic matrices A and B, $h(AB) \leq \min(h(A), h(B))$.

COROLLARY 4.17. For any G, $h(M) = h(A_1MA_2) \le h(A_1) = |Orb(G_1)|$. Similarly $h(M) \le |Orb(G_2)|$.

Corollary 4.17 indicates that intra-symmetry in G_1 or G_2 can determine the upper bound of the de-anonymizability of the de-anonymization problem. Given G_1 , G_2 , the de-anonymizability of the problem can not exceed the orbit numbers of G_1 and G_2 . In other words, as long as one of the G_1 and G_2 are highly symmetric, we cannot expect too many nodes to be correctly de-anonymized. Notice that, in this subsection we do not rely on the assumption of the prior probability of G.

4.3.4 An equivalent approach to obtain the probability distribution of σ_0 . In this subsection we propose a different approach to work out the probability distribution of the true mapping. This approach can reach the equivalent result to the de-anonymizability presented in our main result in Section 4.3.2, but it is much more useful in the approximating process. We refer to this approach as the equivalent approach hereinafter with contrast to the approach proposed in Section 4.3.2 (referred to as original approach). The equivalent approach contains the following process:

In the equivalent method, instead of enumerating all possible underlying network G, we alternatively **enumerate all permutation** π from G_1 to G_2 , and **calculate the probability** of each π becoming the true mapping.

For a certain permutation π , we define the union graph of G_1 and G_2 under permutation π as the minimum graph which guarantees the existence of edges from both the G'_1 and G_2 , where G'_1 is the relabeled G_1 by permutation π .

Definition 4.18 (Union graph under given permutation). For two graphs $G_1 = (V_1, E_1)$, $G_2 = (V_2, E_2)$ with $V_1 = V_2 = V$ under given permutation π is construct as follow: first relabel G_1 with π so that the node i in G_1 is labeled by $\pi(i)$. We denote this relabeled graph as $G'_1 = (V_1, E'_1)$. Then union graph $G = (V, E'_1 \cup E_2)$.

The union graph of G_1 and G_2 under given permutation π is the minimal⁴ feasible underlying network, since it must keep the existence of edges from both G_1 and G_2 . All the spanning supergraphs of the union graph can be candidates of feasible underlying network. The probability of a permutation to be the true mapping, consequently, is proportional to the sum of probability of all possible underlying networks of π . Theorem 4.19, which is the core of equivalent approach, states this idea in detail. The proof is given in Appendix B.4.

Theorem 4.19. Given a de-anonymization problem with parameter $\theta = (G_1, G_2, s_1, s_2)$, let Π be all the permutations from V_1 to V_2 (i.e. all the permutations on V). Then matching probability matrix M can be calculated by

$$M_{ij} = Z \sum_{\pi \in \Pi} \mathbb{1}\{\pi(i) = j\} \left(\frac{\bar{s_1}\bar{s_2}}{1 + \bar{s_1}\bar{s_2}}\right)^{|E_{\pi}|}$$
 (5)

In this formula, $\bar{s_1} = 1 - s_1$, $\bar{s_2} = 1 - s_2$, $|E_{\pi}|$ is the edge number of the union of G_1 and G_2 under permutation π , Z is a normalization parameter which is identical among all elements in M. In particular

$$Z = \sum_{\pi \in \Pi} \left(\frac{\bar{s_1} \bar{s_2}}{1 + \bar{s_1} \bar{s_2}} \right)^{|E_{\pi}|}$$

Note that here we calculate the overall probability transition matrix in a totally different prospective. Recall that in the main result, we enumerate all possible underlying networks, and find all the homomorphisms from both graphs to underlying networks, both of which are time-consuming. In contrast, in this equivalent expression, we alternatively enumerate all the permutations, and calculate the probability that each permutation becomes the true mapping. Although this proposed equivalent process still incurs exponential time complexity, it will facilitate our design of a smart sampling technique that overcomes such huge complexity as well as a more practical approximate algorithm, as we will shortly present in next section.

5 ALGORITHM DESIGN OF DE-ANONYMIZABILITY

In this section we consider the algorithmic aspect of deanonymizability. Notice that we are not focusing on 'deanonymization algorithm', which aims to correctly map the nodes between the anonymous graph and the auxiliary graph. Instead, here we put forward algorithms that takes a parameter set $\theta = (G_1, G_2, s_1, s_2)$ as input and then outputs the de-anonymizability of the corresponding de-anonymization problem. For the fully sampled cases, we have already given out an algorithm that simply counts the orbit number of a

 $^{^3}$ We have proved previously that M is a doubly stochastic matrix. For A_1 and A_2 , the result can be proved easily by the definition of automorphism transition matrix

⁴by 'minimal' we mean the minimal number of edges

graph in Section 4.2. Therefore, here we only focus on the algorithm in partially sampled case.

As noted earlier, the method we have proposed to obtain the de-anonymizability in the partially sampled case, both the original one and the equivalent one, has an exponentially increasing time complexity. In this part, we design a practical algorithm based on the equivalent method that we propose in Section 4.3.4. The main idea in this algorithm is to enumerate a subset of all permutations by sampling.

Basically, the algorithm samples some of the permutations, and calculates the probability of these permutations. The probability transition matrix M is calculated according to the method stated in Theorem 4.19, but only the sampled permutations are taken into account.

In each sampling, a permutation is randomly sampled or artificially selected (we will discuss the selection strategy later), the union of G_1 and G_2 under this permutation is generated, and the probability of this permutation is calculated. Then, the matching probability matrix M is updated term by term according to Theorem 4.19. When the sampling process ceases, a normalization factor is also multiplied to each term of M, but the normalization factor here is the summation over the sampled permutations only.

It is easy to see the time complexity of this algorithm is $O(K(|E|+n^2))$, where K is the number of samples, |E| is the number of edges in union graph G, and the n^2 term is due to updating each term after each sampling.

However, a practical number of samplings are sure to be much less than the total number of all permutations (i.e. n!), which may degrade the performance of accuracy. Therefore, in the sequel we further propose some refinement this algorithm.

5.1 The Effect of Intra-symmetry and Orbit Contracting

According to Theorem 4.15, the matching probability matrix M can be represented as A_1MA_2 . Therefore, we can multiply M by A_1 (on the left) and A_2 (on the right) to incorporate the effect of intra-symmetry on de-anonymizability. This step requires solving two graph automorphism problems, the time complexity of which are considered to be higher than P but lower than NP-Complete. Also, finding the automorphisms of many networks requires relatively shorter time, meaning that this is a practical process to increase the precision of the de-anonymizability.

Consequently, since the intra-symmetry effect has been factored out, we do not need to consider intra-symmetry in the sampling process. Then we propose a new technique, which we call orbit contracting for further reducing the sampling space. The underlying principle of the orbit contracting is that when a permutation is sampled, then all the permutations that keep invariant under the automorphisms of G_1 and G_2 do not need to be sampled. When implementing orbit contracting, we can relabel the nodes within an orbit with the same label (but with multiple instances). This technique can greatly reduce the sampling space when the graph is highly symmetric, but its effect is not significant when the graph is asymmetric.

5.2 Sampling Selection Strategy

To get a good approximation of de-anonymizability within a finite number of samplings, we now discuss how to efficiently select the samplings of permutation.

Theorem 4.19 implies that the probability of a permutation monotonically decreases when the number of edges of the union graph increases. Intuitively, a permutation with a larger probability will have a larger impact on the probability transition matrix. Therefore, we try to find some permutations such that the number of edges of the union graph is as small as possible. This is actually consistent with the goal of **graph matching problem**. For this reason, we borrow the idea of some state-of-the-art graph matching algorithms, and take their outputs as the permutations we sampled. Also, we interchange a small number of nodes in these permutations to enlarge the number of samplings.

5.3 Finding the Maximum Diagonal Sum of Doubly Stochastic Matrices

A remaining consideration is how to obtain the maximum diagonal sum of the matching probability matrix. In fact, finding the maximum diagonal sum of a doubly stochastic matrix is NP-Complete, since it can be polynomially reduced to a $\{0,1\}$ programming problem.

Therefore, here we can have the following alternative solutions: (1) we sum up the maximum element in each row/column vector of this matrix, obtaining an upper bound of maximum diagonal sum; (2) we use heuristic algorithms to get a sub-optimal solution of maximum diagonal sum, obtaining a lower bound. After obtaining the bound of maximum diagonal sum of matching probability matrix, we finally obtain the de-anonymizability of a given de-anonymization problem.

To sum up, Algorithm 2 shows the pseudo-code of our designed algorithm.

Algorithm 2: Getting De-anonymizability in Partially Sampled Case

```
input: De-anonymization problem with
            \theta = (G_1, G_2, s_1, s_2), the number of samplings
  output: De-anonymizability of \theta
1 M \leftarrow zeros(n,n); /* Get a n-by-n zero matrix
  */
2 for i = 1 \dots k-sample do
      \pi \leftarrow \text{getSample}(); /* Get a permutation by
      random shuffling or via selection
      strategy */
      G \leftarrow \text{union}(G_1, G_2, \pi); |E| \leftarrow \text{G.edgeNumber}();
      prob \leftarrow [(1-s_1)(1-s_2)/(1+(1-s_1)(1-s_2))^{|E|};
      for k = 1 \dots n do
5
          M[i, \pi(i)] \leftarrow M[i, \pi(i)] + prob;
6
      end
7 end
8 M \leftarrow M/|M|; return max_diagonal_sum (M)
```

6 A CASE STUDY : DE-ANONYMIZABILITY IN ERDŐS-RÈNYI RANDOM GRAPHS

In this part, we conduct a case study on obtaining deanonymizability in the context of Erdős-Rènyi network. An Erdős-Rènyi network is characterized by two parameters n, p, representing the number of nodes, and the probability that any node pair has an edge in between, independently of each other. The de-anonymizability here refers to **the expectation of de-anonymizability of all instances** of graph generated by Erdős-Rènyi model. Since our method focuses on the automorphism and homomorphism of a graph, then the question comes that how to theoretically analyze the automorphism and homomorphism of an instance generated by Erdős-Rènyi model. We will study the fully sampled case in detail, and then briefly demonstrate how we deal with the partially sampled case based on the result from the fully sample case.

As [15] has mentioned, the symmetric structure in real-world network is more likely to be 'local'. Inspired by this phenomenon, we enumerate some locally symmetric structures Erdős-Rènyi graph, calculate the expected times of appearance of each of them, and calculate the number of orbits they contract.

6.1 Fully Sampled Case

In fully sampled cases we only need to count the orbits of the graph to get the de-anonymizability. In doing so, we introduce the concept of motif to express the locally symmetric structure.

Definition 6.1. For a graph G = (V, E), a motif is denoted by $V_s \subset V$, and we define $T(V_s) = |V_s| - |Orb(V_s)|$, where $|Orb(V_s)|$ is the number of orbits in the graph G that contains all the nodes in V_s . Notice that, $T(V_s)$ means the number of orbits that V_s 'contracts'.

Here we count up two commonest kinds of motif that have been verified to exist in many complex networks [15]:

- Fruits in cherry-like structure: The cherry-like motif is illustrated in Figure 10. Precisely, a set of k nodes forms a 'k-fruit cherry-like' motif(in short 'k-fruit) if and only if: (1) the degree of each of them is one; (2) they are connected to the same node. Proposition 6.2 shows the effect of cherry-like structures via the expected number of orbits contracted.
- (2) Small connected components: A small connected component in a graph is simply a connected component whose size is less than a threshold k. For small connected components, since different values of k will lead to different types of components, here we choose the threshold k = 7, of which the detailed illustration of all these 13 types of components are available in Figure 10 in Appendix C. Table 2 lists the number of orbits contracted by each type of connected components T(ci), and Proposition 6.3 shows the effect of small connect components.

Proposition 6.2. The number of orbits contracted by cherry-like structures (in expectation) is:

$$T(S) = \sum_{V_s \in S} T(V_s) = \sum_{k=2}^{n} (-1)^k \binom{n}{k} (n-k) p^k (1-p)^{k(n-k-1)} * p^{\binom{k}{2}}$$

Table 1: $T(s2_k)$ for each kind of motifs

i	$E(c_i)$	$T(c_i)$
1	$n(1-p)^{n-1}$	$2*E(c_1)-1$
2	$\binom{n}{2}p(1-p)^{2(n-2)}$	$2*E(c_2)-1$
3	$\binom{n}{3} \frac{3!}{2} p^2 (1-p)^{3(n-3)+1}$	$2*E(c_3)-1$
4	$\binom{n}{4} \frac{4!}{2} p^3 (1-p)^{4(n-4)+3}$	$2*E(c_4)-2$
5	$\binom{n}{4} \frac{4!}{3!} p^3 (1-p)^{4(n-4)+3}$	$4*E(c_5)-2$
6	$\binom{n}{5} \frac{5!}{2} p^4 (1-p)^{5(n-5)+6}$	$5*E(c_6)-3$
7	$\binom{n}{5} \frac{5!}{2} p^4 (1-p)^{5(n-5)+6}$	$4*E(c_7)-4$
8	$\binom{n}{5} \frac{5!}{4!} p^4 (1-p)^{5(n-5)+6}$	$2*E(c_8)-1$
9	$\binom{n}{6} \frac{6!}{2} p^5 (1-p)^{6(n-6)+10}$	$6*E(c_9)-2$
10	$\binom{n}{6} \frac{6!}{2} p^5 (1-p)^{6(n-6)+10}$	$6*E(c_9)-4$
11	$\binom{n}{6} \frac{6!}{2} p^5 (1-p)^{6(n-6)+10}$	$6*E(c_10)-4$
12	$\binom{n}{6} \frac{6!}{3!} p^5 (1-p)^{6(n-6)+10}$	$4*E(c_11)-4$
13	$\binom{n}{6} \frac{6!}{8} p^5 (1-p)^{6(n-6)+10}$	$4*E(c_12)-2$

PROPOSITION 6.3. The total number of orbits contracted by small connected components are $\sum_i T(c_i)$.

Considering the overall effect of both types of motifs, Proposition 6.4 characterizes the de-anonymizability of a Erdős-Rènyi model.

Proposition 6.4. The expected number of orbits (i.e. deanonymizability) of a graph generated from Erdős-Rènyi model G(n,p) is $E_{\sigma^*} = E[Orb(G)] = n - T(S) - T(C)$

Notice that in the above formula, the right hand side is a expression of n and p. Substituting (n,p) in this formula with specified values, we can get an approximation of the de-anonymizability of G.

For ease of understanding, let us now take an ER graph with n=1000, p=1/500 as an example. After some calculation we can get

$$T(S) = 33.69, T(C) = 181.49$$

 $E_{\sigma^*} = n - T(S) - T(C) = 784.82$

which means in an Erdős-Rènyi graph generated by G(1000, 1/500), more than 3/4 nodes can be (expected to be) de-anonymized.

6.2 Partially Sampled Case

In partially sampled case, for the problem $\theta = (G_1, G_2, s_1, s_2)$ where the underlying network is generated by Erdős-Rènyi model G(n,p), we calculate the de-anonymizability of $G(n,ps_1)$ and $G(n,ps_2)$ respectively, using the method proposed in Section 6.1. Then we take the smaller one as the upper bound of the de-anonymizability of the problem.

7 EXPERIMENT EVALUATION

7.1 Experiments on Real Dataset

We perform experiments on real-world network to verify our theorem. The dataset we use is a portion of Gnutella peer-to-peer network [16] that represents the underlying network. We sample this network according to different sampling rates. Three state-of-the-art de-anonymization algorithms are used as baseline algorithms. Specifically, Anchor [4] is a matching algorithm via finding anchor nodes in a network. Degree is a naive algorithm based on degree distribution. Similariy is an algorithm which recursively finds the node pair with the maximum similarity.

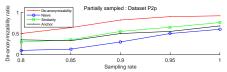


Figure 5: Validation on real data set.

7.2 Experiments on Erdős-Rènyi graph

To verify our result in the case study in Section 6, we conduct experiments on Erdős-Rènyi graph to testify our theoretical results, in the context of both fully sampled cases and partially sampled cases.

Fully sampled case. We choose N = 500, 2000, 5000, 10000as the representative of small-size network and large-size network, respectively. Using the method in Section 6, we calculate the expected de-anonymizability of the Erdős-Rènyi graph with different parameter. To compare the theoretical result with the experimental one, we generate a number of graphs generated by the given model, and count the orbit number as the experimental result. In this experiment, we use nauty [15], an efficient automorphism-related toolkit, to obtain the orbit number of a graph. For each model G(n, p), we generate 10 independent samples of Erdős-Rènyi graph and take the average of their orbit numbers. Figure 5 demonstrates the high consistency of our theoretical result with the experimental result. Also, the result accords with a wellknown classic conclusion [1] that the Erdős-Rènyi network tends to be asymmetric when c = np exceeds the threshold $\log(n)$.

Partially sampled cases. In partially sampled cases, the model is equivalent to the correlated $Erd \~os$ - $R\`enyi$ model. Recall that we use the minimum de-anonymizability of G_1 and G_2 . However, we have no way to directly verify our result due to the exponential time complexity of enumerating underlying networks or enumerating permutations. Therefore, we verify the result by (1) comparing the result with the performance of state-of-the-art de-anonymization algorithms (2) applying the method in Section 4.3 to get the de-anonymizability (which is merely an approximation, since the prior probability of G is not uniform among different underlying networks).

We choose G(2000, 0.5) to represent the underlying network. The parameters satisfy $np >> \log(n)$, which is a threshold value related to the symmetry of Erdős-Rènyi graphs. We

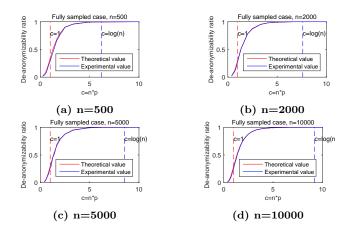


Figure 6: Experiments on fully sampled Erdős-Rènyi graph

choose $s_1 = s_2$ for simplicity. We also use three matching algorithms mentioned above as references. The result is shown in Figure 7.

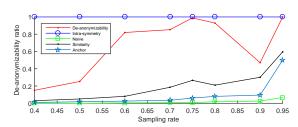


Figure 7: Validation on Partially Sampled Erdős-Rènyi network.

In this figure, De-anonymizability is the result applying the method in Section 4.3, and Intra-symmetry is expected number of orbits in G_1 and G_2 . Naive, Similarity and Anchor represent the performance of three aforementioned algorithms respectively. From the result, we can see that although the sampling algorithm may suffer from oscillation, we indeed obtain an upper bound of the performance of deanonymization algorithms. Since no similar previous work has been done, there is little reference that we can compare with. However, we show that there remains a large gap between the best state-of-the-art algorithm and the theoretical de-anonymizability for partially-sampled de-anonymization problems.

8 CONCLUSIONS

The past decades witnessed the advancement of the study on de-anonymization problem problem. Many algorithms are proposed, but systematic analysis on the accuracy of de-anonymization remains few. We proposed a quantitative method to determine the de-anonymizability of a non-asymptotic de-anonymization problems through the lens of symmetry. Our work is fundamental, and will provide useful guidelines to real network design.

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A PROOF DETAILS IN SECTION 4.2

A.1 Proof of Lemma 4.5 and Lemma 4.6

We first introduce the product of two permutations [5].

Definition A.1. If σ_1, σ_2 are two permutations on V, then σ_p is the product of σ_1 and σ_2 , if $\sigma_p(v) = \sigma_2(\sigma_1(v))$, for any $v \in V$.

Clearly the product of two permutations (on the same domain) is also a permutation.

A proposition about the transitivity property of automorphism follows.

PROPOSITION A.2. If two permutations σ_1, σ_2 are both automorphisms on G, then the product of σ_1 and σ_2, σ_p , is also an automorphism on G = (V, E).

PROOF. First, σ_p is also a permutation. Since σ_1 , σ_2 are both automorphisms of G, by definition

$$\forall (v_i, v_j) \in E \leftrightarrow (\sigma_1(v_i), \sigma_1(v_j)) \in E$$

$$\forall (v_i, v_j) \in E \leftrightarrow (\sigma_2(v_i), \sigma_2(v_j)) \in E$$

 σ_p , the product of σ_1, σ_2 , is a permutation that maps any v to $\sigma_2(\sigma_1(v))$ in node set. And by the two formula above, we can see

$$\forall (v_i, v_j) \in E \leftrightarrow \sigma_2(\sigma_1(v_i)), \sigma_2(\sigma_1(v_j)) \in E$$

It shows that σ_p is also an automorphism on G.

Now comes the proof of Lemma 4.5.

PROOF OF LEMMA 4.5. Clearly for each node v there exists an orbit containing v, for an nontrivial automorphism (which maps each node to itself) will map v to itself. Then the only thing we need to prove is that any two orbits are disjointed.

Actually that is easy to prove. Suppose there exists two different orbits \mathcal{O}_1 , \mathcal{O}_2 containing a common node v, we try to yield a contradiction. Consider an arbitrary node v_1 in \mathcal{O}_1 , and v_2 in \mathcal{O}_2 . Since v and v_1 are in the same orbit, there exists an automorphism σ_1 such that $v = \sigma_1(v_1)$. For the same reason, we have an automorphism σ_2 such that $v_2 = \sigma_2(v)$.

Then we denote σ_p as the product of σ_1 and σ_2 , that is, for each node v, $\sigma_p(v) = \sigma_2(\sigma_1(v))$. By the theorem above, σ_p is also an automorphism of G. Notice $\sigma_p(v_1) = \sigma_2(\sigma_1(v_1)) = v_2$, which means shows σ_p will map v_2 to v_1 . Since our v_1 and v_2 are chosen arbitrarily, we can deduce that $v_1 \in \mathcal{O}_2$ and $v_2 \in \mathcal{O}_1$. Again, since the arbitrary choice of v_1 and v_2 , we can claim that \mathcal{O}_1 and \mathcal{O}_2 contains the same nodes. That

means they are actually the same orbit. That completes the proof of disjoint property. \Box

The proof of Lemma 4.6 is a straightforward one. Having known all the orbits of a graph, constructing an automorphism of a graph can be seen as deciding a permutation within each orbit, and then combining them. There are $|Orb_i|!$ permutations within the orbit i. Applying the multiplication principle, we can obtain that $|Aut(G)| = \prod_{i=1}^k |\mathcal{O}_i|!$.

A.2 Proof of Theorem 4.8

We only need to prove that, for each element M_{ij} in matching probability matrix M, we have $M_{ij} = \frac{1}{|Orb(i)|}$. By definition

$$\begin{split} M_{ij} &= \sum_{\pi \in \Pi} P(\sigma_0 = \pi | \theta) \mathbb{1} \{ \pi(i) = j \} \\ &\stackrel{(0)}{=} \sum_{\pi \in Aut(G)} \frac{1}{|Aut(G)|} \mathbb{1} \{ \pi(i) = j \} \\ &= \frac{1}{|Aut(G)|} \sum_{\pi \in Aut(G)} \mathbb{1} \{ \pi(i) = j \} \\ &\stackrel{(1)}{=} \frac{1}{|Aut(G)|} \frac{|Aut(G)|}{|Orb(i)|} \\ &= \frac{1}{|Orb(i)|} \end{split}$$

In this formula, (0) holds due to the probability distribution we have obtained in Proposition 4.3. For equality (1) it is equivalent to count the number of distinct automorphisms which mapped i to j. Suppose i and j are in the orbit \mathscr{O}_q , then the number is equal to $\prod_{i=1}^{k,i\neq q} |\mathscr{O}_i|!*(|\mathscr{O}_q|-1)!$, which is equal to $\frac{|Aut(G)|}{|Orb(i)|}$ according to Lemma 4.6.

B PROOF DETAILS IN SECTION 4.3

B.1 Proof of Proposition 4.10

PROOF. Determining which graph to be the underlying network is like an inferencing process, so it is reasonable to use Bayes' Rule to deal with the probability. By Bayes' Rule we can write the probability of G given G_1, G_2 as:

$$P(G|G_1, G_2) = \frac{P(G_1, G_2|G)P(G)}{P(G_1, G_2)}$$

On the right side, (a) P(G) is a constant since we have no preference on underlying network; (b) $P(G_1, G_2)$ is a normalized factor and is identical among different G. Thus we have

$$\begin{split} P(G|G_1,G_2) &\propto & P(G_1,G_2|G) \\ &\stackrel{(0)}{=} P(G_1|G)(G_2|G) \\ &\stackrel{(1)}{=} \hom(G_1,G)s_1^{|E_1|}(1-s_1)^{|E|-|E_1|} \\ & \hom(G_2,G)s_2^{|E_2|}(1-s_2)^{|E|-|E_2|} \\ &\propto \hom(G_1,G) \hom(G_2,G)((1-s_1)(1-s_2))^{|E|} \end{split}$$

In formula, (0) holds because G_1 and G_2 are independent samplings from G. (1) holds because there are $hom(G_i, G)$ ways to sample G to get G_i .

B.2 Proof of Proposition 4.11

We only prove the proposition for G_1 . For G_2 the proof is the same.

Given G_1 and G, if a permutation f_i is proved to be the true mapping f_0 , then: (1) f_i is a (graph bijective) homomorphism from G_1 to G (otherwise G_1 cannot be sampled from G) (2) In the sampling process, for the edges in G, all the edges that exist in G_1 are 'sampled in', while all other edges that are absent from G_1 are 'sampled out'.

By Bayes' Law we can write that for any homomorphism f_i from G_1 to G, the probability that f is the true mapping f_0 is:

$$P(f_0 = f_i | G_1, G) = \frac{P(G_1 | f_0 = f_i, G) P(f_0 = f_i | G)}{P(G_1 | G)}$$

here, (a) $P(f_0 = f_i|G)$ is a constant since we have no preference for any specific mapping; (b) $P(G_1|G)$ is a normalized factor and is identical among different f_i ; (c) $P(G_1|f_0 = f_i, G) = (1 - s_1)^{|E| - |E_1|} s_1^{|E_1|}$ is constant since the edge number of G and both G_i are determined.

Therefore, each homomorphism f_i has the same probability $\frac{1}{\text{hom}(G_1,G)}$ to be the true mapping when G is given. Similar for G_2 .

B.3 Proof of Proposition 4.14

We only prove the result of G_1 , i.e. $C_G = A_1 C_G$. The proof for G_2 is completely the same. Let $C' = A_1 C_G$. Then

$$C'_{ij} = \sum_{k \in V} (A_1)_{ik} (C_G)_{kj}$$
$$= \sum_{k \in V} \frac{1}{|Orb_{G_1}(i)|} C_{kj}$$

Here $Orb_{G_1}(i)$ represents the orbit in G_1 that contains i. We can see from the formula that the theorem holds if $(C_G)_{kj} = (C_G)_{ij}$ for any $k \in Orb_{G_1}(i)$. In fact, the latter can be proved as follows:

Suppose i and k are in the same orbit (of G_1). That indicates that there exists an automorphism f (on G_1) that maps i to k (f(i) = k).

Then for each homomorphism σ from i (in G_1) to j (in G), there exists a permutation $\sigma' = f \circ \sigma$. On one hand, σ' is a homomorphism, since G_1 keeps invariant under the action of f. On the other hand, σ' maps k to j. This suggests that for each homomorphism that maps i(in G_1) to j(in G), there also exists a homomorphism mapping k(in G_1) to j(in G), and vice versa. Therefore, the number of homomorphisms that map i to j and map k to j is equal.

Recall that $(C_G)_{ij} = \frac{1}{k_1}c_{ij}$, which is determined by the number of homomorphisms that match i (in G_1) to j (in G). Thus $(C_G)_{ij} = (C_G)_{kj}$ for any i,k in the same orbit. Therefore, $C_G = A_1C_G$. Similarly $D_G = A_2D_G$.

B.4 Proof of Theorem 4.19

We denote the matrix calculated by Equation 5 as M', and the matching probability matrix calculated via the original

method as M. Then we need to prove that M' = M. First, it is easy to see that M' is also a doubly stochastic matrix. Therefore, we only need to prove that, the corresponding elements in M and M' are in proportion. Starting from Equation 4, we have

$$\begin{split} M_{ij} &= \sum_{G \in \mathscr{G}} \sum_{\pi \in \Pi} P(G|\theta) P(\sigma_0 = \pi|\theta, G) \mathbb{1}\{\pi(i) = j\} \\ &= \sum_{\pi \in \Pi} \sum_{G \in \mathscr{G}} P(G|\theta) P(\sigma_0 = \pi|\theta, G) \mathbb{1}\{\pi(i) = j\} \\ &\stackrel{(0)}{=} \sum_{\pi \in \Pi} \sum_{G \in \mathscr{G}} \sum_{f \in \Pi} P(G|\theta) P(f|\theta, G) P(h|\theta, G)) \mathbb{1}\{\pi(i) = j\} \\ &\propto \sum_{\pi \in \Pi} \sum_{G \in \mathscr{G}} \sum_{f \in \Pi} (\bar{s_1} \bar{s_2})^{|E|} \operatorname{hom}(G_1, G) \operatorname{hom}(G_2, G) \\ &P(f|\theta, G) P(h|\theta, G) \mathbb{1}\{\pi(i) = j\} \\ &\propto \sum_{\pi \in \Pi} \mathbb{1}\{\pi(i) = j\} \sum_{G \in \mathscr{G}} (\bar{s_1} \bar{s_2})^{|E|} \sum_{f \in \Pi} \operatorname{hom}(G_1, G) \operatorname{hom}(G_2, G) \\ &P(f|\theta, G) P(h|\theta, G) \\ &= \sum_{\pi \in \Pi} \mathbb{1}\{\pi(i) = j\} \\ &\sum_{G \in \mathscr{G}} (\bar{s_1} \bar{s_2})^{|E|} \mathbb{1}\{\exists f : f(G_1) \subset G\} \mathbb{1}\{h(G_2) \subset G\} \end{split}$$

In this formula, $h = \pi^{-1} \circ f$ so that we can have $f \circ h^{-1} = \pi$. Therefore, for each permutation π , we count up all the graphs G whose edge set is a superset of both that of G_1 and G_2 . Obviously, the condition holds iff G is the spanning super graph of the union of G_1 and G_2 under permutation π . We denote the union of G_1 and G_2 under permutation π as $G_{\pi} = (V_{\pi}, E_{\pi})$, and denote $N = \binom{n}{2}$. We have,

$$\begin{split} M_{ij} &\propto \sum_{\pi \in \Pi} \mathbbm{1}\{\pi(i) = j\} \\ &\sum_{i=0}^{N-|E_{\pi}|} (\binom{N - |E_{\pi}|}{i}) \bar{s_1}^{|E_{\pi}| - |E_1| + i} \bar{s_2}^{|E_{\pi}| - |E_2| + i}) \\ &= \sum_{\pi \in \Pi} \mathbbm{1}\{\pi(i) = j\} \bar{s_1}^{|E_{\pi}| - |E_1|} \bar{s_2}^{|E_{\pi}| - |E_2|} \\ &\qquad (1 + (\bar{s_1}\bar{s_2}))^{N - |E_{\pi}|} \\ &\propto \sum_{\pi \in \Pi} \mathbbm{1}\{\pi(i) = j\} \bar{s_1}^{|E_{\pi}|} \bar{s_2}^{|E_{\pi}|} (1 + (\bar{s_1}\bar{s_2}))^{-|E_{\pi}|} \\ &= \sum_{\pi \in \Pi} \mathbbm{1}\{\pi(i) = j\} \frac{\bar{s_1}\bar{s_2}}{1 + \bar{s_1}\bar{s_2}}^{|E_{\pi}|} \propto M'_{ij} \end{split}$$

which completes the proof.

C A CASE STUDY : DE-ANONYMIZABILITY IN ERDŐS-RÈNYI RANDOM GRAPHS

This part provides the technique details in the case study of de-anonymizability in Erdős-Rènyi graph.

As [15] has mentioned, the symmetric structure in realworld network is more likely to be 'local'. The following graph can serve as an example to show the difference between an artificially constructed graph and a network-generated graph. The left one is the famous (artificially constructed) Petersen Graph, of which the symmetry structure is completely global(that is, we have to search the whole graph to assert the existence of automorphism in the graph). The right one is an instance generated by Erdős-Rènyi model G(n=10, p=0.2). The only symmetric node pair here is (15,18) and (19,20), and detecting both of them only requires local information. On the other hand, in instances of network model, large, complicated symmetric structures are unlikely to appear.

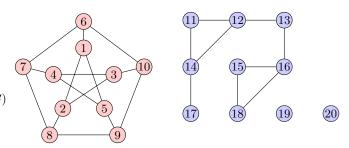


Figure 8: An comparison. The left is the (artificially constructed) Peterson Graph, in which detecting the automorphism requires searching all the nodes. The right is an instance from G(10,0.2). Only two node pairs, (15,18) and (19,20), are symmetric here.

From this phenomenon, we calculate the de-anonymizability via detecting some local automorphism structures in a network. This method is somehow like the *motif detection* [?]. We will study the fully sampled case in detail, and then briefly demonstrate how we deal with the partially sampled case based on the result from the fully sample case.

C.1 Fully Sampled Case

In fully sampled cases we only need to count the orbits of a graph to get its de-anonymizability. As we have said, we only focus on those local symmetric structures of a graph. Slightly abusing the concept, we also use motif to refer to those local subgraphs or patterns. In this section, a motif is merely a set of nodes with some specific pattern (especially the pattern in symmetry). In the analysis of Erdős-Rènyi graph, we will clearly specify which kind of patterns we consider. For a graph G = (V, E), a motif is denoted by $V_s \subset V$, and we define $T(V_s) = |V_s| - |Orb(V_s)|$, where $|Orb(V_s)|$ means the number of orbits in the graph G that contains all the nodes in V_s . Notice that, $T(V_s)$ means the number of orbits that V_s 'contracts'. The following theorem demonstrates an upper bound of the orbit number in a graph , which can be used to show the approximate de-anonymizability of a graph.

THEOREM C.1. Given a graph G = (V, E), suppose we have k motifs of G $V_{s1}, V_{s2}, \ldots, V_{sk}$. If any two motifs are vertex-disjoint, then we have $|Orb(G)| \leq |N| - \sum_{i=1}^{k} T(V_{si})$. The equality holds when:

 There does not exist a symmetric node pair across two motifs. That is, for any V_{si} and V_{sj}(i ≠ j), for any

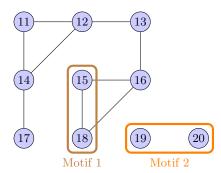


Figure 9: The instance from G(10,0.2). This picture is to show what a motif is.

 $v_i \in V_{si}$ and $v_j \in V_{sj}$, no automorphism of G will map v_i to v_j .

• All the motifs are found. That is, for any node v that does not belong to any of $V_{s1}, V_{s2}, \ldots, V_{sk}$, all the automorphism of G maps v to itself.

PROOF. The inequality is easy to prove by the definition of orbit. For the nodes that does not belong to any motif, it owns at most one orbit. Thus

$$|Orb(G)| \le |Orb(V - \bigcap_{i=1}^{k} V_{si})| + \sum_{i=1}^{k} |Orb(V_{si})|$$

$$\le |N| - \sum_{i=1}^{k} |V_{si}| + \sum_{i=1}^{k} |Orb(V_{si})|$$

$$= |N| - \sum_{i=1}^{k} T(V_{si})$$

The equality holds when no additional symmetric node pair exists, which can be expressed by the two given conditions.

We apply this theorem into the context of Erdős-Rènyi graph. We only consider the situation when $p \leq 0.5$, for a graph and its complement have the same automorphisms. We count up two commonest kinds of motifs in a graph:

- (1) The fruits in a cherry-like structure.
- (2) The small connected components.

In the sequel we discuss them respectively.

C.1.1 Cherry-like Motif. We first consider cherry-like motif, denoted as S. The cherry-like motif is shown above in Figure 10. Precisely, a set of k nodes forms a 'k-fruit cherry-like' motif(in short 'k-fruit') iff (1) the degrees of all of them are equal to one (2) all of them are connected to the same node. For a graph G, we define $S_k = \{V_{s_k}\}$ as the set of the all the 'k-fruit' of the G. We can obtain the expectation of how many times these type of structures appear. Specifically, for k nodes, the probability that all of them are merely connected to the same node is

$$P_{V_{s_k}} = (n-k)p^k(1-p)^{k(n-k-1)} * p^{\binom{k}{2}}$$

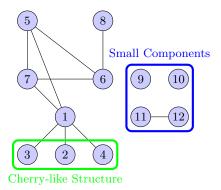


Figure 10: Two kinds of motifs we consider here.

The expectation appearance of 'k-fruit' over the whole graph is

$$E(|S_k|) = \binom{n}{k} P_{s_k} = \binom{n}{k} (n-k) p^k (1-p)^{k(n-k-1)} * p^{\binom{k}{2}}$$

And, since each 'k-fruit' obtains only one orbit,

$$\sum_{V_{s_k} \in S_k} T(V_{s_k}) = (k-1)|S_k|$$

We define $S = \bigcup_{k=2}^{n} S_k$ as the set of all cherry-like motifs in graph G. We cannot simply add the result above, since repeated counting appears. For example, a '3-fruit' structure also contains $C_3^2 = 3$ '2-fruit' structures. By the inclusive-exclusive principle, we have

$$T(S) = \sum_{V_s \in S} T(V_s) = \sum_{k=2}^{n} (-1)^k \binom{n}{k} (n-k) p^k (1-p)^{k(n-k-1)} * p^{\binom{k}{2}}$$

by which we can calculate the (expectation) number of 'cherry-like' motifs and the number of orbits they contract given any specific parameters n, p.

C.1.2 Small connected components. According to [1], it has been shown that in Erdős-Rènyi graph G(n, p) with np > 1 $\log(n)$, almost every graph generated by G(n,p) is asymmetric. On the other hand, when $np \leq \log(n)$, most graph generated by G(n, p) is not fully connected, and the existence of small connected components (with contrast to the giant component in Erdős-Rènyi graph) are likely to contain symmetric nodes. Therefore, we consider another type of motif: small connected components (denoted as C). Here we simply define that small connected components in a graph are all the connected components whose sizes are less than a threshold k. Notice that if two components share the same shape, not only the nodes within the motif may belong to the same motif (since most of the small components are symmetric), the corresponding nodes in different components will also belong to the same orbit. To reduce the number of components we have to enumerate, we use the fact that almost all the small components in Erdős-Rènyi graph are trees[1]. Therefore, we only enumerate all the trees with size less than k. As a tradeoff, a larger k will detect more automorphisms and improve

the accuracy the result, while exponentially increases the number of components that are necessary to enumerate. As an illustration, Figure 11 shows all 13 kinds of trees whose size is less than or equal to 6 [21].

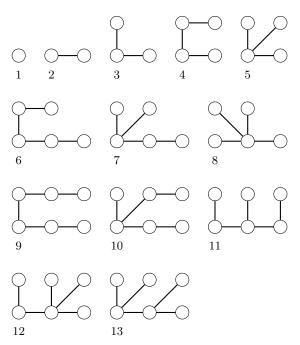


Figure 11: Different types of small components.

For each type, the expectation of times of its appearance is calculated in order to obtain the number of orbits it contracts. As an example, we show in detail how to calculate the expectation of C_1 (i.e. an isolated node). The probability that it is connected to none of the other points is

$$P(deq_i = 0) = (1 - p)^{n-1}$$

Then the expectation over the whole graph is equal to

$$E(c_1) = n(1-p)^{n-1}$$

which shows the number of C_1 motifs (i.e. isolated nodes) in G (in expectation).

For type 3,5,7,8,12,13, cherry-like structure exists in those components. Therefore, we only contract the orbit **across** the components. Take type 3 as an example, the expectation of appearance of type 3 components is:

$$E(c_3) = \binom{n}{3} \frac{3!}{Aut(c_3)} p^2 (1-p)^{3(n-3)+1}$$

It is easy to observe that, the orbit number, after contraction in C, is 2. However, in each type-3 component (i.e. C_3), the two 'fruit' nodes have already been contracted into one orbit after the analysis Section C.1.1, and therefore, only $2*E(c_3)-2$ (rather than $3*E(c_3)-2$) orbits are contracted. We list the results of each type in the Table 2.

Consequently, $T(C) = \sum_{i} T(c_i)$ represents the total number of orbits contracted by small connected components. In

Table 2: T(C) for each kind of motifs

i	$E(c_i)$	$T(c_i)$
1	$n(1-p)^{n-1}$	$2*E(c_1)-1$
2	$\binom{n}{2}p(1-p)^{2(n-2)}$	$2*E(c_2)-1$
3	$\binom{n}{3} \frac{3!}{2} p^2 (1-p)^{3(n-3)+1}$	$2*E(c_3)-1$
4	$\binom{n}{4} \frac{4!}{2} p^3 (1-p)^{4(n-4)+3}$	$2*E(c_4)-2$
5	$\binom{n}{4} \frac{4!}{3} p^3 (1-p)^{4(n-4)+3}$	$4*E(c_5)-2$
6	$\binom{n}{5} \frac{5!}{2} p^4 (1-p)^{5(n-5)+6}$	$5*E(c_6)-3$
7	$\binom{n}{5} \frac{5!}{2} p^4 (1-p)^{5(n-5)+6}$	$4*E(c_7)-4$
8	$\binom{n}{5} \frac{5!}{4!} p^4 (1-p)^{5(n-5)+6}$	$2*E(c_8)-1$
9	$\binom{n}{6} \frac{6!}{2} p^5 (1-p)^{6(n-6)+10}$	$6*E(c_9)-2$
10	$\binom{n}{6} \frac{6!}{2} p^5 (1-p)^{6(n-6)+10}$	$6*E(c_9)-4$
11	$\binom{n}{6} \frac{6!}{2} p^5 (1-p)^{6(n-6)+10}$	$6*E(c_10)-4$
12	$\binom{\tilde{n}}{c} \frac{\tilde{6}!}{2!} p^5 (1-p)^{6(n-6)+10}$	$4*E(c_11)-4$
13	$\binom{n}{6} \frac{6!}{8!} p^5 (1-p)^{6(n-6)+10}$	$4*E(c_12)-2$

fact, a larger component size threshold k can detect more small components, but when one motif does not exist, extra orbits are contracted wrongly. Therefore, we dynamically decide k when conducting our experiments. After analyzing those two kinds of motifs, the de-anonymizability of a graph G is then given by

$$E_{\sigma^*} = E[Orb(G)] = n - T(S) - T(C)$$

Notice that in the above formula, the right hand side is a expression of n and p. Substituting (n,p) in this formula with specified values, we can get an approximation of the de-anonymizability of G.

For ease of understanding, let us now take an ER graph with n=1000, p=1/500 as an example. After some calculation we can get

$$T(S) = 33.69, T(C) = 181.49$$

 $E_{\sigma^*} = n - T(S) - T(C) = 784.82$

 5 which means in a graph given by G(1000, 1/500), more than 3/4 nodes can be (expected to be) de-anonymized. We will validate the result in the experiment section. The following theorem is used to prove the correctness of the method, which shows that, there is almost no symmetric node pairs in the giant component of Erdős-Rènyi graphs.

Theorem C.2. For the Erdős-Rènyi model, $p = \Omega(\frac{1}{n})$ and $p \leq \frac{1}{2}$, there are o(1) nodes that are symmetric in the giant component.

PROOF. Suppose there are n nodes in the giant component and the edge existence probability is p, where $p = \Omega(\frac{1}{n})$ and $p \leq \frac{1}{2}$. The distribution of the node degree satisfies Poisson distribution. We aim to figure out the probability of two nodes N_a , N_b being symmetric given that both of their degrees are larger than one. Before the derivation, we first denote the nodes that are both N_a and N_b 's neighbors to

 $^{^5}$ In calculation, we do some modification to our formula in order to prevent extra orbits to be contracted. The detail will be described in the experiment part.

be 1-hop shared neighbors, and denote the nodes that are only N_a 's or N_b 's neighbors to be 1-hop free neighbors. If N_a and N_b are symmetric, these 1-hop free neighbors can be divided into several pairs, and each of them contains one N_a 's neighbor and one N_b 's, which are also symmetric. Similarly, we denote those nodes that connect two symmetric (k-1)-hop free neighbors as k-hop shared neighbors and nodes that only connect to one of them as k-hop free neighbors. Suppose the numbers of N_a 's and N_b 's k-hop free neighbors are n_{ak} and n_{bk} , and the numbers of N_a 's and N_b 's k-hop share neighbors are n'_{ak} and n'_{bk} .

If N_a, N_b are symmetric, $n_{ak} = n_{bk} = n_k$ and $n'_{ak} =$ $n'_{bk} = n'_{k}$. Moreover, since their k-hop free neighbors can be divided into symmetric pairs, the number of N_a 's k-hop free neighbors whose degrees are even is equal to that of N_b 's. The probability of a node with even degree is:

$$P_{even} = \sum_{j=1}^{\lfloor \frac{n-1}{2} \rfloor} \frac{\lambda^{2j}}{(2j)!} e^{-\lambda}, \tag{6}$$

where $\lambda = (n-1)p$. Since $n \to \infty$, we can derive that

$$\frac{P_{even}}{P_{odd}} = \frac{\sum_{j=1}^{\lfloor \frac{n-1}{2} \rfloor} \frac{\lambda^{2j}}{(2j)!} e^{-\lambda}}{\sum_{j=1}^{\lfloor \frac{n-2}{2} \rfloor} \frac{\lambda^{2j+1}}{(2j+1)!} e^{-\lambda}} \to \frac{e^{\lambda} + e^{-\lambda}}{e^{\lambda} - e^{-\lambda}} \to 1$$
 (7)

Therefore, $P_{even} \to \frac{1}{2}$ and $P_{odd} \to \frac{1}{2}$. Let A_1 be the event that the number of N_a 's k-hop free neighbors whose degrees are even is equal to that of N_b 's. Based on Stirling's formula, we can get that:

$$P_{A_{1}} = \sum_{i=0}^{n-1} \left[P_{even}^{i} P_{odd}^{n_{k}-i} \binom{n_{k}}{i} \right]^{2}$$

$$\rightarrow \sum_{i=0}^{n-1} 2^{-2n_{k}} \binom{n_{k}}{i}^{2}$$

$$= 2^{-2n_{k}} \binom{2n_{k}}{n_{k}}$$

$$= \frac{(2n_{k})!}{2^{2n_{k}} (n_{k}!)^{2}}$$

$$\rightarrow \frac{\sqrt{4\pi n_{k}} (\frac{2n_{k}}{e})^{2n_{k}}}{2\pi n_{k} 2^{2n_{k}} (\frac{n_{k}}{e})^{2n_{k}}}$$

$$= \frac{1}{\sqrt{\pi n_{k}}}$$
(8)

Furthermore, when A_1 is satisfied, without loss of generality, we suppose the number of k-hop free neighbors with even degree is larger than or equal to $\frac{n_k}{2}$. Let A_2 be the event that the number of N_a 's k-hop free neighbors whose degrees satisfy d = 4i, where $i \ge 0$, is equal to that of N_b 's. With the same derivation, we can get that $P_{A_2} \geq \sqrt{\frac{2}{\pi n_k}}$. With the same analysis, we can also derive that $P_{A_3} \geq \sqrt{\frac{4}{\pi n_k}}$, $P_{A_4} \ge \sqrt{\frac{8}{\pi n_k}}$ and $P_{A_5} \ge \sqrt{\frac{16}{\pi n_k}}$, where A_3, A_4 and A_5 are events that the number of N_a 's k-hop free neighbors whose

degrees satisfy d=8i, d=16i and d=32i, where $i \geq 0$, is equal to that of N_b 's respectively.

Suppose N_a, N_b have k-hop free neighbors, where $k \leq l$, then we can bound the probability that N_a , N_b are symmetric

$$P_{(N_a,N_b)\in sym} \leq P_{deg(N_a)=deg(N_b)} \prod_{k=1}^{l} \prod_{j=1}^{5} P_{A_j}$$

$$= P_{deg(N_a)=deg(N_b)} \prod_{k=1}^{l} \frac{32}{(\pi n_k)^{\frac{5}{2}}},$$
(9)

where $P_{deg(N_a)=deg(N_b)} = \sum_{i=2}^{n-1} \left(\frac{\lambda^i}{i!}e^{-\lambda}\right)^2$. If there exists k_0 satisfies that $n_{k_0} = \Theta(n)$, then we have:

$$P_{(N_a,N_b)\in sym} \le \frac{32}{(\pi n_{k_0})^{\frac{5}{2}}} = o(\frac{1}{n^2}).$$
 (10)

Then we have $\binom{n}{2}P_{(N_a,N_b)\in sym}=o(1)$. Otherwise, for any constant $\epsilon>0$ and two nodes N_1,N_2 in the network, let B be the event: $deg(N_1) = deg(N_2) \ge$ $(\frac{1}{2} + \epsilon)n$. Since $p \leq \frac{1}{2}$, then $\lambda = (n-1)p < \frac{n}{2}$ and we have:

$$P_{B} = \sum_{i=(\frac{1}{2}+\epsilon)n}^{n-1} \left(\frac{\lambda^{i}}{i!}e^{-\lambda}\right)^{2} \leq \max_{i\geq(\frac{1}{2}+\epsilon)n} \left(\frac{\lambda^{i}}{i!}e^{-\lambda}\right) \sum_{i=(\frac{1}{2}+\epsilon)n}^{n-1} \frac{\lambda^{i}}{i!}e^{-\lambda}$$
$$< \left(\frac{\lambda}{\frac{1+\epsilon}{2}n}\right)^{\frac{\epsilon}{2}n} e^{-\lambda} < \left(\frac{1}{1+\epsilon}\right)^{\frac{\epsilon}{2}n}.$$
(11)

Then we have $\binom{n}{2}P_B=o(1)$, which means there are almost no node pairs that have the same degree larger than $(\frac{1}{2} + \epsilon)n$. Therefore, for N_a , N_b or two nodes in k-hop free heighbors, suppose the degrees of them are both d, where $2 < d < (\frac{1}{2} +$ ϵ)n. The probability of the number of nodes that connect only one of them is n_f satisfies $P_f \leq \sum_{d=2}^{(\frac{1}{2}+\epsilon)n} P_{deg=d}\binom{d}{d-n_f} p^{d-n_f}$, when $n_f = o(d)$, we can derive that $P_f = O(\frac{1}{n^2})$. Therefore, $n_f = \Theta(d)$ with probability 1 and the total number of free neighbors is $\sum_{k=1}^{l} n_k = n - 1 - \sum_{k=1}^{l} n_k' = \Theta(n)$. Then we can derive that

$$P_{(N_a,N_b)\in sym} < \prod_{k=1}^{l} \frac{32}{(\pi n_k)^{\frac{5}{2}}}$$

$$\leq \frac{32}{\pi^{\frac{5}{2}} (\sum_{k=1}^{l} n_k - l)^{\frac{5}{2}}} \prod_{k=1}^{l-1} \frac{1}{\sqrt{\pi}}$$

$$= \frac{32}{\pi^{\frac{5}{2}} \left(\pi^{\frac{l-1}{5}} (\sum_{k=1}^{l} n_k - l)\right)^{\frac{5}{2}}}$$

$$< \frac{32}{\pi^{\frac{5}{2}} \left(\sum_{k=1}^{l} n_k\right)^{\frac{5}{2}}}$$

$$= o(\frac{1}{\pi^2})$$
(12)

Therefore, $\binom{n}{2} P_{(N_a, N_b) \in sym} = o(1)$.

Above all, there are almost no symmetric node pairs with degree larger than 1 in the network.

C.2 Partially Sampled Case

The partially sampled case is relatively difficult to analyze. First, the assumption we made in Section 4.3.1 that each G has the same prior probability does not hold, which brings difficult to find the probability distribution of the true mapping σ_0 . Therefore, we bound the de-anonymizability of the problem using the de-anonymizability of G_1 and G_2 according to the result in 4.3.3.

The underlying network G is generated by model G(n,p), and G_1 , G_2 are independent samplings of G, the sampling rate of which is s_1,s_2 , respectively. In fact, G_1 and G_2 can be seen generated by $G(n,ps_1)$ and $G(n,ps_2)$ respectively. We can calculate the orbit number of G_1 and G_2 , and take the smaller one as an upper bound of de-anonymizability of the problem.