Maximum Likelihood Estimation and Graph Matching in Errorfully Observed Networks

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Abstract

Given a pair of graphs with the same number of vertices, the inexact graph matching problem consists in finding a correspondence between the vertices of these graphs that minimizes the total number of induced edge disagreements. We study this problem from a statistical framework in which one of the graphs is an errorfully observed copy of the other. We introduce a corrupting channel model, and show that in this model framework, the solution to the graph matching problem is a maximum likelihood estimator. Necessary and sufficient conditions for consistency of this MLE are presented, as well as a relaxed notion of consistency in which a negligible fraction of the vertices need not be matched correctly. The results are used to study matchability in several families of random graphs, including edge independent models, random regular graphs and small-world networks. We also use these results to introduce measures of matching feasibility, and experimentally validate the results on simulated and real-world networks.

Keywords: Graph matchability, corrupting channel, consistency
1 Introduction

Graphs are a popular data structure used to represent relationships between objects or agents, with successful applications in many different fields, including finance, neuroscience, biology, and sociology, among others. Many applications deal with multiple graph observations that can come as different instances of the graph for the same or related set of vertices, and thus studying these data jointly usually requires knowledge of the correspondence between the vertices first. When this correspondence is unknown or observed with errors, graph matching can be used to first recover the true correspondence before performing subsequent inference. Simply stated, the graph matching problem consists in finding an alignment between the vertices of two different graphs that minimizes a measure of dissimilarity between them (usually specified to be the number of edge differences). This problem has found many useful applications in different areas including de-anonymizing social networks (Narayanan & Shmatikov 2009, Korula & Lattanzi 2014, Zhang & Tong 2016, Heimann et al. 2018), aligning biological networks (Yang & Sze 2007, Zaslavskiy et al. 2009, Vogelstein et al. 2014), and unsupervised word translation (Grave et al. 2018), among others; see the surveys Conte et al. (2004), Foggia et al. (2014), Yan et al. (2016) for a review (up to 2016) of the graph matching literature and applications.

1.1 The graph matching problem

Formally, given a pair of graphs $A = (E_1, V_1)$ and $B = (E_2, V_2)$, the graph matching problem (GMP) consists of finding a mapping $\pi : V_1 \rightarrow V_2$ which aligns the vertices between the two graphs to make the structure most similar; i.e., if $\Pi_n$ is the set of $n \times n$ permutation matrices, then the GMP is $\arg \min_{P \in \Pi_n} \| A - PBP^T \|_F$. Variants of this basic formulation have been proposed in the literature to accommodate more nuanced graph structure including, incorporating weighted and directed edges, $|V_1| \neq |V_2|$ (Fishkind et al. 2018), vertex and edge covariates (Lyzinski, Levin, Fishkind & Priebe 2016), and matching multiple graphs simultaneously (Yan et al. 2013).

A special case of the problem is exact graph matching, also known as the graph isomorphism problem (Babai 2015), where the goal is to determine if there exists an alignment between the vertices of the graphs yielding identical edge structure across networks. Even for this special case, it is currently not known whether the problem is solvable in polynomial time. However, an exact unique solution exists as long as there is no non-identity automorphisms (i.e., permutation matrix $P \neq I_n$ such that $A = PAP^T$). In practice, the applicability of exact graph matching is limited due to the fact that data often consists of noisy observations of a graph, and thus one can
only hope to recover an alignment that preserves a significant portion of the structure.

In the inexact version of the graph matching problem, a pair of graphs with the same number of vertices is observed, and the goal is to find an alignment of the vertices that best preserves the structure of the graphs. This is often accomplished by minimizing an appropriate dissimilarity measure over all the possible permutations (e.g., the Frobenius norm formulation considered above). To better understand the difficulty and feasibility of this problem, several random graph models have been proposed in the recent literature. These models often parametrically enforce a natural similarity between the graphs while still allowing for structural differences. They vary in complexity from correlated homogeneous Erdős-Rényi networks (Pedarsani & Grossglauser 2011, Yartseva & Grossglauser 2013, Lyzinski et al. 2014), to correlated stochastic blockmodel networks (Onaran et al. 2016, Lyzinski & Sussman 2018), to correlated general edge independent networks (Korula & Lattanzi 2014, Lyzinski, Fishkind, Fiori, Vogelstein, Priebe & Sapiro 2016), to independent graphon generated networks (Zhang 2018). Within these models, the dual problems of developing efficient GM algorithms and studying the theoretical feasibility of the GMP have been considered. However, beyond (conditionally) edge-independent networks, few theoretical guarantees exist for either algorithmic performance (see Korula & Lattanzi (2014) for an example of matching guarantees in a preferential attachment model).

1.2 Graph matchability and MLE

These random graph models have allowed for the exploration of the related notion of graph matchability: given a natural correspondence between the vertex sets of two networks, can the GMP uncover this correspondence (with high probability) (Lyzinski et al. 2014, Lyzinski, Fishkind, Fiori, Vogelstein, Priebe & Sapiro 2016, Lyzinski 2018, Onaran et al. 2016, Cullina & Kiyavash 2017)? In this paper, we cast the problem of graph matchability in the framework of maximum likelihood estimation, equating matchability with the consistency of the maximum likelihood estimate of an unknown correspondence. The results bear a similar flavor to those in Onaran et al. (2016) (and Cullina & Kiyavash (2016)), wherein a model for correlated stochastic blockmodels is proposed. In their framework, they showed that maximum a posteriori (MAP) estimation is the same as optimizing a weighted variant of the classical graph matching problem. Unlike previous work, our model (see Section 2) is designed to be distribution-free, allowing for corrupted or correlated observations of arbitrarily structured networks to be considered. We note that while we are not the first to frame GM as a MLE problem (see, for example, Luo & Hancock (2001), Lyzinski, Levin, Fishkind & Priebe (2016)), our model allows for a novel understanding of the
relationship between the two, seemingly disparate, ideologies.

While maximum likelihood estimation is a core concept in modern statistical inference (Stigler 2007), estimation of an unknown correspondence between two networks presents the challenge of MLE in the presence of a growing parameter dimension. Our model is parameterized by the shuffling permutation, which is the parameter of interest, and corrupting probabilities for each edge that are nuisance parameters. Indeed, viewing the correspondence between vertices as a parameter to be estimated, this parameter naturally is situated in $\mathbb{R}^{n-1}$ where $n$ is the number of vertices in the observed network, while the number of nuisance parameters can grow as $O(n^2)$. Asymptotics (as $n \to \infty$, yielding $\binom{n}{2}$ sample size) resist the classical theoretical framework when the number of (nuisance) parameters grows with the sample size (see, for example, Bickel & Doksum (2015)), and the MLE can be inconsistent in this setting (Neyman & Scott 1948, Lancaster 2000). Recently, statistical network inference (see, for example, Bickel & Chen (2009), Bickel et al. (2013)) has presented further examples of consistent MLE in networks when the parameter dimension is growing, notably for the inference task of community detection in stochastic blockmodel random graphs. By equating consistent MLE with graph matchability, we provide another class of examples in the network literature for which consistency of the MLE is achieved as the graph size (and parameter dimension) increases.

The paper is organized as follows. In Section 2 we introduce the corrupting channel model and show that maximum likelihood estimation of the latent vertex correspondence is a solution to the graph matching problem (and vice versa). Next, in Section 3 we derive necessary and sufficient conditions (depend on the structure of the given graph and the channel noise) for consistency of the MLE. In Section 4 we introduce a notion of quasi-consistency in which we allow a fraction of the vertices to be incorrectly matched, and present sufficient conditions to achieve this property. Results of consistency and quasi-consistency of the MLE in a variety of random graph models are presented, including some new results for small-world and random regular graphs. In Section 5 we introduce a practical approach to studying matchability, and validate our theoretical results with numerical experiments on simulated networks from popular random graph models and real-world data from different domains. We conclude with a discussion and remarks in Section 6.

### 2 Uniformly corrupting channel; MLE=GM

Let $p \in [0, 1]$, $P \in \Pi_n = \{n \times n$ permutation matrices$\}$, and $A \in \mathcal{G}_n = \{n$ vertex labeled graphs$\}$. We model passing $A$ through an edge and vertex-label corrupting channel as follows.
Definition 1. Define the graph-valued random variable $B_{p,P}$ (i.e., the channel-corrupted $A$) parameterized by $(p,P)$ via $B_{p,P} := P(X \circ (1-A) + (1-X) \circ A)P^T$, where $X \in \mathbb{R}^{n \times n}$ is a symmetric, hollow matrix with i.i.d. Bernoulli($p$) entries in its upper triangular part, and “$\circ$” is the Hadamard matrix product. For ease of notation, we shall write $B_{p,P} = B \sim C(A,p,P)$ for $B$ distributed as the channel corrupted $A$.

This model is similar to the noisily observed network models of Pedarsani & Grossglauser (2011), Yartseva & Grossglauser (2013), Korula & Lattanzi (2014), Chang et al. (2018). Note that here we make no assumptions on the distribution of the underlying graph $A$; indeed, below we often view $A$ as deterministic and not random.

Stated simply, $B_{p,P}$ is formed by first uniformly corrupting (i.e., bit-flipping) edges in $A$ independently with probability $p$ and then shuffling the labels via $P$. Given observed $(A,B)$, the likelihood of $(p,P)$ in this model is given by

$$L(p,P) = \prod_{i<j}(1-p) I\{A_{i,j} = (P^TBP)_{i,j}\}p I\{A_{i,j} \neq (P^TBP)_{i,j}\},$$

so that the log-likelihood is given by

$$\ell(p,P) = \sum_{i<j} I\{A_{i,j} = (P^TBP)_{i,j}\} \log(1-p) + I\{A_{i,j} \neq (P^TBP)_{i,j}\} \log p$$

With $p$ fixed, this is proportional to

$$\ell(p,P) \propto \text{tr}(AP^TBP) \log(1-p) - \text{tr}(AP^TBP) \log p$$

$$= \text{tr}(AP^TBP)(\log(1-p) - \log p),$$

and, observing that $\text{tr}(AP^TBP) = \|AP - BP\|_F^2 - \|A\|_F^2 - \|B\|_F^2$, the (possibly non-unique) MLE of $P$ is then given by

$$\hat{P} = \begin{cases} 
\text{any } P \in \arg \min_{P \in \Pi_n} \|AP - BP\|_F & \text{for } p < 1/2 \\
\text{any } P \in \arg \min_{P \in \Pi_n} \|AP - \tilde{B}P\|_F & \text{for } p > 1/2 \\
\text{any } P \in \Pi_n & \text{for } p = 1/2,
\end{cases}$$

where $\tilde{B}$ is the complement of the graph $B$ (i.e., $\tilde{B}_{ij} = 1 - B_{ij}$). In the $p < 1/2$ setting, the problem of maximum likelihood estimation is the problem of graph matching, as the classical graph matching problem (GMP) formulation is to find $P$ in $\arg \min_{P \in \Pi_n} \|AP - BP\|_F$. When $p > 1/2$, MLE is graph matching one graph with the complement of the other.
When \( p < 1/2 \), a natural first question is what properties \( A \) (and \( p \)) must possess in order for the MLE for \( P \) to be consistent, and hence the vertex-label corruption introduced into \( B \) can be undone via graph matching. We note here that the parameter dimension of \( P \) is growing in \( n \) and classical MLE consistency results do not directly apply (see, for example, Bickel \& Doksum (2015)). Nonetheless, in Section 3 our main result, Theorem 4, will establish consistency of the MLE under fairly modest assumptions on \( A \) and \( p \).

### 2.1 Heterogeneous corrupting channel; MLE=GM

The uniform corrupting channel model defined above assumes that all edges of \( A \) are corrupted with the same probability. However, in some cases it is more reasonable to consider a model in which each pair of vertices might be corrupted with different probabilities. For example, we can consider the setting in which edges and non-edges in \( A \) are corrupted by the channel independently with different probabilities, or in which certain vertices or edges are more likely to be corrupted. Thus, we also consider an heterogeneous corrupting channel defined as follows.

**Definition 2.** Let \( \Psi^{(m)} \in [0,1]^{n \times n}, m = 1, 2 \) be two matrices that correspond to the corrupting probabilities for edges and non-edges, and \( P \in \Pi_n \). For a given adjacency matrix \( A \in \{0,1\}^{n \times n} \), we define \( B_{\Psi^{(1)},\Psi^{(2)},P} \) as

\[
B_{\Psi^{(1)},\Psi^{(2)},P} = P(X \odot (1 - A) + (1 - Y) \circ A)P^T,
\]

where \( X \) and \( Y \) are symmetric hollow matrices such that \( X_{ij} \sim \text{Bernoulli}(\Psi^{(1)}_{ij}) \) and \( Y_{ij} \sim \text{Bernoulli}(\Psi^{(2)}_{ij}) \) and \( \{X_{i,j}, Y_{i,j}\}_{i<j} \) are independent. Dropping subscripts to ease notation when possible, we denote it via \( B \sim C(A, \Psi^{(1)}, \Psi^{(2)}, P) \) for \( B \) distributed as the heterogeneous corrupting channel \( A \).

The flexibility of having different corrupting probabilities for each edge allows us to incorporate other popular graph models within this framework. In particular, by conditioning on \( A \sim \text{Bernoulli}(\Lambda) \), the heterogeneous corrupting channel model can be used to describe a pair of correlated Bernoulli graphs. This correlated Bernoulli graph model (Lyzinski, Fishkind, Fiori, Vogelstein, Priebe \& Sapiro 2016) is another popular model used to study the inexact graph matching problem. In more detail, given a pair of hollow symmetric matrices \( R, \Lambda \in [0,1]^{n \times n} \), the pair of graphs \( A, B \) is said to be distributed as \( R \)-correlated random Bernoulli(\( \Lambda \)) graphs if marginally \( A, B \sim \text{Bernoulli}(\Lambda) \) (i.e., for \( 1 \leq i < j \leq n \), \( A_{ij} \) are independently distributed
as Bern(Λ_{ij}) random variables; similarly for B) and \{A_{ij}, B_{jk}\}_{1 \leq i < j \leq n, 1 \leq \ell < k \leq n} are mutually independent except that for each 1 \leq i < j \leq n, \text{corr}(A_{ij}, B_{ij}) = R_{ij}. Note that in the correlated Bernoulli graphs model, \(\mathbb{P}(B_{ij} = 1|A_{ij}) = A_{ij}R_{ij} + (1 - R_{ij})\Lambda_{ij}\), so the distribution of B conditioned on A can be written using an heterogeneous channel with Ψ_{ij}^{(1)} = (1 - R_{ij})(1 - A_{ij}) and Ψ_{ij}^{(2)} = (1 - R_{ij})A_{ij}.

It is also possible to show that the MLE on the heterogeneous corrupting channel is equivalent to the minimizer of the graph matching objective. First, note that the likelihood is given by

\[
\ell(\Psi^{(1)}, \Psi^{(2)}, P) = \sum_{i < j} \left\{ (P^TBP)_{ij} \log \left( (1 - \Psi^{(1)}_{ij})A_{ij} + \Psi^{(2)}_{ij}(1 - A_{ij}) \right) \right. \\
+ \left. (1 - (P^TBP)_{ij}) \log \left( \Psi^{(1)}_{ij}A_{ij} + (1 - \Psi^{(2)}_{ij})(1 - A_{ij}) \right) \right\}.
\]

In general, the MLE for P in this model is not unique since the corrupting probabilities can arbitrarily alter the graph. Thus, we impose a further assumption, which is equivalent to requiring the edges of the two graphs A and B to be positively correlated. Let \(\tilde{p} = \max_{i,j,k} \Psi_{ij}^{(k)}\) be the largest corrupting probability for an edge. Under the assumption that \(\tilde{p} \leq \frac{1}{2}\), we can calculate the profile MLE for Ψ_{ij}^{(k)}, k = 1, 2, as

\[
\hat{\Psi}_{ij}^{(k)}(P)_{ij} = \begin{cases} 
0 & \text{if } A_{ij} = (P^TBP)_{ij} = 1 (k = 1), \\
\frac{1}{2} & \text{if } A_{ij} = 1 (k = 1), (P^TBP)_{ij} = 1 (k = 2), \\
\text{any } c \in [0,1/2] & \text{otherwise},
\end{cases}
\]

Thus, the profile likelihood for P can be expressed as

\[
\ell \left( \hat{\Psi}^{(1)}(P), \hat{\Psi}^{(2)}(P), P \right) = \sum_{i < j} 21(A_{ij} \neq (P^T\tilde{B}P)_{ij}) \log(1/2) = -\log(2)\|A - (P^T\tilde{B}P)\|_F^2,
\]

yielding that the MLE for estimating P is the solution to the GMP (and vice versa).

In the heterogeneous channel model, Ψ^{(1)} and Ψ^{(2)} are nuisance parameters when estimating the permutation parameter P. In the rest of the paper we focus on studying the uniformly corrupting channel model presented in Definition 1. Nevertheless, we note that all of our results presented in the following sections hold more generally as a function of the largest corrupting probability \(\tilde{p}\). Note that in the heterogeneous model, the number of nuisance parameters is \(n(n - 1)\), which scales with the sample size. In this setting, one should be careful when using the MLE since this estimator can be inconsistent even if the parameter of interest has a fixed dimension, as shown in the famous Neyman-Scott paradox [Neyman & Scott 1948]. Fortunately, this is not the case here and the MLE can consistently estimate \(\tilde{P}\) (see Remark 5).
3 Consistency of the MLE

Let $n_0 > 0$, and consider a sequence of graphs $(A_n)_{n=n_0}^\infty$ (with the order of $A_n$ being $n$). For the parameter sequence $((p_n, P_n))_{n=n_0}^\infty$, consider the sequence of channel-corrupted $A_n$’s defined via

$$(B_n = P_n(X_n \circ (1 - A_n) + (1 - X_n) \circ A_n)P_n^T)_{n=n_0}^\infty,$$

where each $X_n$ is a symmetric, hollow matrix with i.i.d. Bernoulli($p_n$) entries in its upper triangular part, and the $X_n$’s are mutually independent across index $n$. In this setting, we define consistency of the MLE as follows.

**Definition 3.** With $(B_n \sim C(A_n, p_n, P_n))_{n=n_0}^\infty$ defined as above, for $n \geq n_0$ define

$$\hat{P}_n = \arg\min_{P \in \Pi_n} \|A_n P - B_n P\|_F.$$

We say that a sequence of maximum likelihood estimators $(\hat{P}_n := \hat{P}_n(A_n, B_n))_{n=n_0}^\infty$ of $(P_n)_{n=n_0}^\infty$, where $\hat{P}_n \in \hat{P}_n$ for all $n \geq n_0$, is a (weakly strongly) consistent estimator if

$$\|\hat{P}_n - P_n\|_F \xrightarrow{\text{a.s.}} 0 \text{ as } n \to \infty, \text{ for all sequences } (P_n)_{n=n_0}^\infty.$$

It is clear that consistency of the MLE hinges on the properties of $(A_n)_{n=n_0}^\infty$. Indeed, if infinitely many $A_n$ have a non-trivial automorphism group, then the MLE has no hope of consistency in the strong or weak sense. If, on the other hand, the $A_n$’s are sufficiently asymmetric (see Theorem 4 for a precise definition of this) then the MLE will be strongly consistent under mild model assumptions. To wit we have the following (proof provided in Appendix A.1):

**Theorem 4.** Let $n_0 > 0$, and consider a sequence of graphs $(A_n)_{n=n_0}^\infty$. Define the sequence $(B_n \sim C(A_n, p_n, P_n))_{n=n_0}^\infty$ of channel-corrupted $A_n$’s with parameter sequence $((p_n, P_n))_{n=n_0}^\infty$ with $p_n < 1/2$. For each $n \in \mathbb{Z} \geq n_0$ and each $k \in [n]$, $k \geq 2$, let $\Pi_{n,k}$ be the set of permutation matrices in $\Pi_n$ permuting precisely $k$ labels.

i. If there exists an $n_1 \geq n_0$ such that for all $n \geq n_1$ and all $k \in [n]$,

$$\min_{Q \in \Pi_{n,k}} \|A_n Q - Q A_n\|^2_F > \frac{6k \log(n)}{\log \left( \frac{1}{4p_n(1-p_n)} \right)},$$

then any maximum likelihood estimator sequence $(\hat{P}_n)_{n=n_0}^\infty$ is strongly consistent.
ii. If for infinitely many $n > n_0$ there exists a set of disjoint permutations $S_{n,k_n} \subset \Pi_{n,k_n}$ with $|S_{n,k_n}| = \Theta(n)$, a $\delta > 0$ such that $(\frac{1}{2} - p_n)n^\delta = o(1)$, and

$$\max_{Q_n \in S_{n,k_n}} \|A_nQ_n - Q_nA_n\|_F^2 = o\left(\frac{\log(n)}{(\frac{1}{2} - p_n)^2}\right),$$

then any maximum likelihood estimator sequence $(\hat{P}_n)_{n=n_0}^\infty$ is not weakly consistent.

iii. If for infinitely many $n \geq n_0$, there exists $Q_n \in \Pi_n \setminus \{I_n\}$ such that $\|A_nQ_n - Q_nA_n\|_F^2 = \Theta(1)$, then any maximum likelihood estimator sequence $(\hat{P}_n)_{n=n_0}^\infty$ is not weakly consistent for any $(p_n)$ bounded away from 0.

Note that for a given sequence of graphs $(A_n)_{n=1}^\infty$, Equation (1) implies that any sequence of corrupting probabilities $(p_n)$ that satisfies for all $k \in [n], p_n \leq \frac{1}{2} - \frac{1}{2}\exp\left(-\frac{6k\log n}{\min_{Q_n \in \Pi_{n,k}} \|A_nQ_n - Q_nA_n\|_F^2}\right),$ (3)

will ensure that the MLE is strongly consistent. The right hand side of Equation (3) thus quantifies how much noise can be supported by the graph, and hence provides a measure of matching feasibility. In addition, note that $\log\left(\frac{1}{4p_n(1-p_n)}\right) \asymp (\frac{1}{2} - p_n)^2$ when $1/2 - p_n = o(1)$, so the growth rates in Eq. (1) and in Eq. (2) coincide.

Remark 5. An equivalent result to Theorem 4 for the heterogeneous corrupting channel model also holds. Define a sequence of corrupting matrices $(\Psi_n^{(1)}, \Psi_n^{(2)})_{n=n_0}^\infty$ with each $\Psi_n^{(m)}$ a $n \times n$ hollow symmetric matrix with entries on $[0, 1/2)$, and consider $	ilde{p}_n = \max_{i>j, m} (\Psi_n^{(m)})_{i,j}$ and $\tilde{\rho}_n = \min_{i>j, m} (\Psi_n^{(m)})_{i,j}$. Then the MLE in the heterogeneous corrupting channel model is strongly consistent if the conditions in part i. in Theorem 4 hold, with $\tilde{p}_n$ substituted for $p_n$ in Eq. (1). Conversely, the MLE is not weakly consistent when part ii. of the previous theorem holds, with $\tilde{\rho}_n$ substituting for $p_n$ in Eq. 2. The proof is a straightforward extension to the proof of Theorem 4 and hence we omit it.

While the correlation structure between $A$ and $B$ in the above Theorem is different than the $\rho$-correlated Bernoulli model of Lyzinski et al. (2014), Lyzinski (2018), Lyzinski, Fishkind, Fiori, Vogelstein, Priebe & Sapiro (2016), this theorem, in a sense, partially unifies many of the edge-independent matchability results appearing in previous work (Lyzinski et al. 2014, Lyzinski, Fishkind, Fiori, Vogelstein, Priebe & Sapiro 2016, Lyzinski 2018, Onaran et al. 2016, Cullina & Kiyavash 2017). To wit,
we have the following corollary, whose proof follows immediately from Theorem 4 and results in Lyzinski, Fishkind, Fiori, Vogelstein, Priebe & Sapiro (2016) (see Appendix A.2 for proof details).

Corollary 6. Let \( n_0 > 0 \), and consider an independent sequence of graphs \( (A_n)_{n=n_0}^{\infty} \) where for each \( n \), \( A_n \sim \text{Bernoulli}(\Lambda_n) \) with \( \alpha_n \leq \Lambda_n \leq 1 - \alpha_n \) entry-wise. Define the sequence \( (B_n \sim C(A_n, p_n, P_n))_{n=n_0}^{\infty} \) of channel-corrupted \( A_n \)'s with parameter sequence \( \left( p_n, P_n \right)_{n=n_0}^{\infty} \) and \( p_n < \frac{1}{2} \). If \( \alpha_n \left( \frac{1}{2} - p_n \right) = \omega \left( \sqrt{\frac{\log n}{n}} \right) \), then any maximum likelihood estimator sequence \( \left( \hat{P}_n \right)_{n=n_0}^{\infty} \) is strongly consistent.

The Erdős-Renyi model (ER) (Erdős & Rényi 1963) \( G(n, \alpha) \), \( \alpha \in (0, 1) \) is a particular example of a Bernoulli graph \( \text{Bernoulli}(\Lambda) \) in which all entries of \( \Lambda \) are equal to \( \alpha \), and hence the result of the previous corollary directly applies. By considering concentration bounds on the number of edges in Erdős-Rényi \( G(n, \alpha) \) random graphs (i.e., the number of edges is in \( n\alpha \pm \sqrt{n\log n} \) with high probability) and the growth rate of \( \alpha_n \) in Corollary 6, we arrive at the following corollary for Erdős-Renyi graphs \( G(n, m) \) (i.e., uniformly distributed on the set of graphs with exactly \( m \in \mathbb{N} \) edges):

Corollary 7. Let \( n_0 > 0 \), and consider an independent sequence of graphs \( (A_n)_{n=n_0}^{\infty} \) where for each \( n \), \( A_n \sim G(n, m_n) \). Define the sequence \( (B_n \sim C(A_n, p_n, P_n))_{n=n_0}^{\infty} \) of channel-corrupted \( A_n \)'s with \( p_n < \frac{1}{2} \). If

\[
 m_n \left( \frac{1}{2} - p_n \right) = \omega \left( \sqrt{n \log n} \right),
\]

then any maximum likelihood estimator sequence \( \left( \hat{P}_n \right)_{n=n_0}^{\infty} \) is strongly consistent.

Small-world graph models aim to reproduce the property that in many real networks the clustering coefficient is relatively small and paths between any pair of vertices have a short length, usually of order \( \log n \) (Watts & Strogatz 1998). The Newman-Watts (NW) model (Newman & Watts 1999)—a more easily analyzed variant of the original Watts-Strogatz model—is one such model that adheres to these properties with high probability. The NW model \( \text{NW}(n, d, \beta) \) starts with a \( d \)-ring lattice \( A \) in which each vertex is connected with all neighbors that are at a distance no larger than \( d \); that is, \( A_{ij} = 1 \) whenever \( 0 < |i - j| \mod (n - 1 - d) < d \). To generate a small-world behavior, random edges are added independently with probability \( \beta \) between vertices that are not connected in the \( d \)-ring lattice, so \( A_{ij} \sim \text{Bernoulli}(\beta) \) for \( |i - j| \mod (n - 1 - d) \geq d \).

In the Newman-Watts model, the average path length when \( \beta = 0 \) is \( O(n/d_n) \), and as \( \beta \) increases and more edges are added to the graph, there is a phase transition
in which the small-world property appears. The next corollary establishes a similar phenomenon in the matching feasibility context: when \( \beta \) is small, the MLE is not weakly consistent for matching a NW graph \( A \) with a random copy generated from the corrupting channel model, but once there are enough random edges included, the MLE becomes strongly consistent and hence graph matching is feasible. See Appendix A.3 for the proof details.

Corollary 8. Let \( n_0 > 0 \) and \( (A_n)_{n=n_0}^{\infty} \) an independent sequence of graphs such that \( A_n \sim NW(n,d_n,\beta_n) \), and define \( (B_n)_{n=n_0}^{\infty} \) as a sequence of channel corrupted graphs with \( B_n \sim C(A_n,p_n,P_n) \) and \( p_n < 1/2 \).

a) For any sequence \( (d_n)_{n=n_0}^{\infty} \), if \( (1/2 - p_n)^2 = o\left(\sqrt{\log n/n}\right) \) and

\[
\beta_n = o\left(\frac{\log n}{(1/2 - p_n)^2 n}\right),
\]

then all MLE sequences \( (\hat{P}_n)_{n=n_0}^{\infty} \) are not weakly consistent.

b) If \( d_n = o(\beta_n^2 n) \), \( \beta_n \leq 1/2 \) and

\[
\beta_n = \omega\left(\sqrt{\frac{\log n}{(1/2 - p_n)^2 n}}\right),
\]

then any MLE sequence \( (\hat{P}_n)_{n=n_0}^{\infty} \) is strongly consistent.

Using results on the diameter of Erdős-Rényi graphs (Chung & Lu 2001), it can be verified that if \( \beta_n \) satisfies equation (4) for a fixed value of \( p_n < 1/2 \) and \( \beta_n = \omega(1/n) \), then \( \text{diam}(A_n) = O\left(\frac{\log(n)}{\log(n\beta_n)}\right) \). Thus, there is a regime for \( \beta_n \) in which NW graphs are small-world but the MLE is not consistent. However, since \( \omega(1) = \log(n\beta_n) = o(\log \log n) \) in this regime, the diameter of the graph is close to \( O(\log n) \) and hence it is not far from the phase transition of small-world graphs. If part b) of Corollary 7 holds, then \( \text{diam}(A_n) = O(1) \), so the average path length in NW graphs with a strongly consistent MLE is much smaller than in small-world graphs.

Corollary 8 also suggests a way of making any given graph \( A \), with a sufficiently large number of vertices \( n \), matchable with a graph corrupted with probability \( p \). By setting \( \beta = \frac{\sqrt{\log(n)}}{((1/2 - p)^2 n)} \) as in equation (5) and generating a graph \( A' \sim C(A,\beta,I) \), the solution of the graph matching problem between \( A' \) and \( B \) will correctly align all of the vertices with high probability. This result can have applications in settings such as network anonymization (Narayanan & Shmatikov 2009) and differential privacy (Dwork & Roth 2014), among others.
4 Relaxed consistency

In many label recovery settings in the network literature, consistency is defined as recovering the correct labels of all but a small, vanishing fraction of the vertices; for examples in the community detection literature, see [Rohe et al. (2011), Sussman et al. (2014), Fishkind et al. (2013), Qin & Rohe (2013)], in the graph matching literature, see [Zhang (2018)]. In real data settings, networks are often complex, heterogeneous objects, and defining consistency as perfect recovery of the alignment/labels is an often unrealistic standard to apply in practice. This is especially the case in the presence of network sparsity, as often recovering the alignment/labels of low degree vertices is practically and theoretically impossible.

In our errorful channel setting it is entirely reasonable to expect low-degree vertices in $A$ to have their labels irrevocably permuted by the channel permutation $P$. We demonstrate this in the following illustrative example.

**Example 9.** Consider $A_n$ constructed as follows. Let $G_n \sim \text{G}(n-2,q)$ be an ER graph for fixed $q$. $A_n$ is then formed by attaching two leaves (labeled $n-1$ and $n$) to $G_n$ at two uniformly randomly chosen elements of $G_n$. Form $B_n$ via the channel parameters $(p_n, P_n)$ with $p_n = p$ fixed and $P_n$ the transposition of $n-1$ and $n$. It is immediate that with probability at least $p^2$ (i.e., if the two edges connecting the leaves to $G_n$ are corrupted), the MLE will not equal $P_n$.

In the previous example, we see that the MLE will often be unable to recover periphery vertex labels. However, in Example 9 it is not difficult to see that for $p$ fixed, the MLE will recover all but potentially the two peripheral vertex labels. It will be practically useful to extend the definition of consistency to account for these situations where the MLE can recover almost all of the vertex labels. This motivates our next definition.

**Definition 10.** With notation as above, for $n > n_0$ define

$$\hat{P}_n = \arg\min_{P \in \Pi_n} \|A_n P - B_n P\|_F.$$ 

For a sequence $(\alpha_n)_{n=n_0}^{\infty}$, we say that a sequence of maximum likelihood estimators $(\hat{P}_n := \hat{P}_n(A_n, B_n))_{n=n_0}^{\infty}$ of $(P_n)_{n=n_0}^{\infty}$, where $\hat{P}_n \in \hat{P}_n$ for all $n \geq n_0$, is a (weakly) $\alpha_n$-consistent estimator of $(P_n)_{n=n_0}^{\infty}$ if

$$\max_{Q \in \hat{P}_n} \frac{\|Q - P_n\|_F}{\alpha_n} \xrightarrow{P \in a.s.} 0$$

as $n \to \infty$ for all sequences $(P_n)_{n=n_0}^{\infty}$.
This relaxed definition allows us to consider situations in which the MLE will correctly align all but a vanishing fraction of the vertices in $(A_n, B_n)$; indeed, if $\alpha_n = o(n)$, then the fraction of misaligned vertices is $o(1)$. In the remainder of this section, we will establish $\alpha_n$ consistency for a variety of models.

**Example 9 continued.** Consider $A_n$ as constructed in Example 9. If we consider $p_n \equiv p < 1/2$ fixed, then it is immediate that the MLE will be strongly $\alpha_n$-consistent for any $\alpha_n = \omega(1)$. Indeed, with high probability the only two vertices potentially misaligned by the MLE for $n$ sufficiently large are the two leaves attached to $G_n$.

The $\alpha_n$-consistency analogue of part i. of Theorem 4 can be formulated as follows. The proof is omitted, as it follows the proof of Theorem 4 mutatis mutandis.

**Theorem 11.** Let $n_0 > 0$, and consider a sequence of graphs $(A_n)_{n=n_0}^\infty$. As above, define $(B_n)_{n=n_0}^\infty$ to be the sequence of channel-corrupted $A_n$’s with parameter sequence $((p_n, P_n))_{n=n_0}^\infty$ and $p_n < 1/2$. If we have that there exists an $n_1$ such that for all $n \geq n_1$ and all $k \geq k_n$, 

$$
\min_{Q \in \Pi_{n,k}} \| A_n Q - Q A_n \|_F^2 \geq \frac{6k_n \log(n)}{\log \left( \frac{1}{4p_n(1-p_n)} \right)},
$$

then any maximum likelihood estimator sequence $(\hat{P}_n)_{n=n_0}^\infty$ is strongly $k_n$-consistent.

Note that part ii. of Theorem 4 is capturing the setting when the MLE with high probability will not align a small ($\Theta(1)$ in the Theorem) number of vertices. As such, it is not immediate what the $\alpha_n$-consistency analogue of this result would be.

Our next result partially extends Corollaries 6 and 7 to the case of random regular graphs. Let $A \sim G_{n,d}$ be shorthand for $A$ is uniformly distributed on the set of $d$-regular, $n$-vertex graphs. Solving the exact version of the graph matching problem (that is, for $p = 0$ in the corrupting channel model) is usually possible, as these graphs almost surely do not have a non-trivial automorphism (Kim et al. 2002). The next corollary thus partially extends this result to the inexact graph matching setting (proof provided in Appendix A.4).

**Corollary 12.** Let $\epsilon \in (0, 1/3)$ be fixed, and consider $d_n = \omega(n^{2/3+\epsilon})$. If $A \sim G_{n,d_n}$ and $1/2 - p_n \geq \sqrt{13d_n^{-1}\log n}$, then any maximum likelihood estimator sequence $(\hat{P}_n)_{n=n_0}^\infty$ is strongly $\alpha_n$-consistent for $\alpha_n = \omega(n^{2/3})$.

The previous result raises the question of whether there will always be a fraction of misaligned node in a random regular graph. Although we do not have a definite
answer, it is possible to construct non-trivial examples of sequences of $d$-regular graphs for which the MLE is not strongly consistent according to Definition 3. In fact, consider $A_n$ as the $d_n$-ring lattice with $n$ vertices and any sequence of $(d_n)$. Then, according to part a) of Corollary 8 the MLE is not strongly for any $(P_n)_{n=n_0}$. Numerical simulations on the $d_n$-ring lattice (see Section 5.1) suggest that for the $d_n$-ring lattice in particular, a large fraction of the vertices can be correctly aligned if $d_n$ is large enough.

5 Experiments

In light of the theoretical results presented in the previous sections, we perform experiments to study the matchability of channel corrupted graphs. Using simulated and real data, we study whether the vertices of a given graph are matchable to the vertices of a random graph generated after passing the original graph through a corrupting channel.

As observed in the previous sections, the feasibility of graph matching in the errorful channel model depends on the number of edge disagreements between the original graph and a shuffled version of it. Given a graph $A$ with $n$ vertices, we measure matching feasibility in two ways. First, motivated by the bounds in Theorems 4 and 11, we count the number of edge disagreements introduced in $A$ by a uniform shuffling of $k$ vertices. We estimate the average value of $\|A - PAP^T\|_F^2$ where $P \sim \text{Unif}(\Pi_{n,k})$, by generating a sample of $m = 1000$ random permutations $P_1, \ldots, P_m$, uniformly distributed on $\Pi_{n,k}$ and calculating

$$\hat{X}_k(A) = \frac{1}{m} \sum_{i=1}^{m} \frac{1}{2} \|AP_i - P_iA\|_F^2.$$ (7)

In practice, we have found that larger values of $\hat{X}_k(A)$ indicate that graph matching (at least recovering all but $k$ labels) is more feasible. We use a normalized version of this quantity $\frac{1}{k \log n} \hat{X}_k(A)$ to compare this number between different permutation sizes and number of vertices, where the normalizing constant is motivated by Theorem 4.

We also use equation (3) to obtain a bound on the probability $p_k^*(A)$ of the corrupting channel model that ensures that the MLE is a consistent estimator; indeed, $\min_{k} p_k^*(A)$ gives a measure of how much noise can a graph $A$ safely tolerate while keeping the feasibility of perfect graph de-anonymization in the limit. Moreover, $\min_{k \geq k_0} p_k^*(A)$ gives a (limiting) measure of how much noise can a graph $A$ safely tolerate while keeping the feasibility of de-anonymizing all but $k_0$ of the vertices. The value of $p_k^*$ depends on $X_{k,\min}(A) = \min_{P \in \Pi_{n,k}} \|AP - PA\|_F^2$, the smallest number of
edge disagreements over all permutations of $k$ vertices. Computing the exact value of $p_k^*$ is unfeasible for large values of $k$, but using a sample of random permutations we can obtain a theoretical upper bound for $p_k^*(A)$ by

$$
\hat{p}_k^*(A) = \frac{1}{2} - \frac{1}{2} \exp \left( - \frac{6k \log n}{\hat{X}_{k,\min}(A)} \right),
$$

where $\hat{X}_{k,\min}(A) = \min_{i=1,\ldots,m} \|AP_i - P_iA\|_F^2$.

These two statistics, $\hat{X}_K(A)$ and $\hat{p}_k^*(A)$, are calculated for different values of $k$, and they are used to measure matching feasibility in a variety of graphs generated from popular statistical models and real networks from different domains. The results are also validated in real networks by studying the accuracy of a matching algorithm for a given graph $A$ and a corrupted version of it.

5.1 Simulations

In the first example, we generate graphs from two popular graph models and compare the effect of the parameters that control the structure of the network. First, we simulate Erdős-Renyi graphs $G(n, \alpha)$ with $n = 500$ vertices and rate $\alpha$, changing the value of $\alpha \in \{0.1, 0.2, 0.3, 0.4, 0.5\}$ to compare the effect of the average degree. We also generate graphs using the Watts-Strogatz small-world model $WS(n, d, \beta)$, which are very similar to the Newman-Watts model (see Corollary 8); these graphs are intended to produce graphs with the small-world property. The WS model is initialized with a regular $d$-ring lattice like the NW model, and each edge is randomly rewired with probability $\beta$. As $\beta$ increases, the distribution of the WS model becomes more similar to an ER graph.

For each graph, we compute the estimated probability bounds $\hat{p}_k^*(A)$ and the normalized average disagreements $\frac{1}{k \log n} \hat{X}(A)$ according to equations (7) and (8). We generate 35 random graphs according to each model and compute the average quantities. These results are summarized on Figure 1a. We can see that in the ER model channel probability bounds and the average number of disagreements increase with $\alpha$, which suggests that matching in the corrupting channel model becomes more feasible as the average degree of the graph increases, and verifies the results in Corollary 6. Graphs with a WS distribution increase their matchability measures as the rewiring probability increases in accordance to Corollary 8, and this suggests that graphs that have a more uniformly random structure are easier to match. Matching all the vertices correctly in the WS model is difficult when $\beta$ is small since the near degree regularity ensures that vertices are very similar to their neighbors, and hence switching a few
of the vertices with their neighbors causes a small number of disagreements. This results agrees with Corollary 8 for the related Newman-Watts small-world model. Nevertheless, Figure 1c also shows that even for small $\beta$ it might be still feasible to match a large portion of the vertices correctly.

In the second experiment, we compare the same statistics across different popular random graph models. In particular, we use again the ER model $G(n, m)$ but now with $m$ fixed edges and the WS model. We additionally include the preferential attachment $\text{PA}(n, \gamma, d)$ model proposed by (Albert & Barabási 2002). This model creates a graph by a random process in which a new vertex with $d$ edges is added to the graph on each step $t$. For each new vertex the probability that it connects to an existing vertex $i$ is proportional to $d_{it}^\gamma$, where $d_{it}$ is the degree of vertex $i$ at time $t$, and $\gamma \geq 0$ is a constant that controls the preferential effect. Larger values of $\gamma$ increase the preference of new vertices to connect with high degree vertices.

As observed in the previous experiment, the edge density of the graph plays an important role for matching feasibility. Thus, to make fair comparisons between the different models we adjust the model parameters to generate graphs with the same average degree $d$, by fixing $d = 5$ (1% density) and $d = 50$ (10% density). For the WS model, we generate graphs from a WS($n, d, 0.05$) and WS($n, d, 0.75$), and for the PA model, we change the exponent $\gamma$ to generate $\text{PA}(n, 1, d)$ and $\text{PA}(n, 2, d)$. In all cases, we use the default implementation of igraph (Csardi & Nepusz 2006) to simulate the graphs. The results of these experiments are shown in Figure 1c. We observe that in general the graphs that have a more random structure (the ER model and the WS model with a large rewiring probability) are the ones in which the measures of matching feasibility are larger. Matching in the PA model is complicated due to the low degree of many vertices, and thus the theoretical probability bound for perfect matchability is low.

### 5.2 Real-world networks

We also analyze graph matching in the corrupting channel model for real-world networks from different domains. The networks that we use are the Zachary’s karate club friendship network (Zachary 1977), the graph of synapses between neurons of the C. elegans roundworm (Watts & Strogatz 1998), the graph of hyperlinks between political blogs from the 2004 US election (Adamic & Adar 2005), a protein-protein interaction network in yeast (Von Mering et al. 2002), and a citation network between arXiv papers in the condensed matter section (Newman 2001). Some graph statistics to summarize the data are included in Table I. These include the number of nodes $n$, the average node degree $d = \frac{1}{n} \sum_{ij} A_{ij}$, the density of the graph $d/(n - 1)$, the
Figure 1: Measures of matching feasibility for different random graph models as a function of the fraction of shuffled vertices $k/n$. The top left figure compares Erdős-Rényi graphs $G(n, \alpha)$ with different edge probability $\alpha$. The top right figure shows the Watts-Strogatz model $WS(n, d, \beta)$ with different rewiring probabilities $\beta$. The bottom figure compares these two models and the preferential attachment model with exponent $\gamma$ ($PA(\gamma, d)$) for a fixed degree $d$. In each figure, the top panel shows an upper bound on the corrupting probability $p$ supported by the channel, and the bottom panel shows the normalized mean edge disagreements after shuffling $k$ random vertices of the graph. Graph matching is more feasible in denser and less structured graphs.
clustering coefficient $C$ which counts the number of triangles in the graph divided over the maximum number of triangles possible, the skewness $\gamma_1$ and the relative standard deviation (RSD) of the degree distribution. In general, as observed in the simulations, we should expect that as the graphs become denser and with a more random structure (lower clustering coefficient and homogeneous degrees), matching becomes more feasible.

| Network            | $n$  | $d$  | Density | $C$  | $\gamma_1$ | RSD |
|--------------------|------|------|---------|------|-------------|-----|
| Karate             | 34   | 4.588| 0.14    | 0.25 | 2.00        | 0.84|
| C. elegans         | 297  | 15.79| 0.05    | 0.181| 3.50        | 0.88|
| Pol. blogs         | 1,222| 27.35| 0.02    | 0.226| 3.06        | 1.4 |
| Prot. interaction  | 2,617| 9.06 | 0.003   | 0.47 | 3.96        | 1.65|
| arXiv              | 16,726| 6.69| 0.0004  | 0.36 | 4.07        | 0.96|

Table 1: Summary statistics of the network data: number of vertices ($n$), average vertex degree ($d$), density of the graph, clustering coefficient ($C$), skewness ($\gamma_1$) and relative standard deviation (RSD) of degree distribution.

Figure 2 shows the bounds in the channel probability $\hat{p}_k(A)$ (top panel) and the normalized average number of edge disagreements $\hat{X}_k(A)$ (bottom panel) for the selected networks. When the fraction of shuffled vertices is small, all networks have a zero tolerance for noise in the corrupting channel model, which can be due to the periphery nodes and the existence of (near) graph automorphisms between some of the vertices. Thus, exactly solving the graph matching problem in general is not feasible if $p > 0$. However, as the fraction of shuffled vertices gets larger the value of $\hat{p}_k(A)$ increases for some of the networks, which suggests that partial matching is still possible. The political blogs and the C. elegans networks have the highest values for the measured quantities, $\hat{X}_k(A)$ and $\hat{p}_k(A)$, which can be explained by their large average degree and small clustering coefficient. On the other hand, the protein-protein interaction and arXiv citation networks have the lowest values, possibly because of their low density. The probability bounds in the karate network might be very conservative since the results of Theorem 4 are asymptotic, and $n$ is small for this network.

In practice, computing the MLE of the unshuffling permutation is computationally unfeasible. Thus, to validate the results above, we use the following strategy. Given a graph $A$ we generate a random graph $B$ using a uniformly corrupting channel $(p,I)$. Then we perform graph matching using the Fast Approximate Quadratic programming algorithm of Vogelstein et al. (2014), Lyzinski, Fishkind, Fiori, Vogelstein, Priebe & Sapiro (2016), which uses the Frank-Wolfe methodology (Franke & Wolfe 2016) to solve an indefinite relaxation of the graph matching objective function before projecting the relaxed solution to the feasible space of permutations. Frank-Wolfe is a constrained gradient descent procedure, and the algorithm terminates in an estimated
permutation $\hat{P}^{FAQ}$ that is a local minimum of the relaxed GM objective function. We use the true parameter $I$ as the initialization value of the FAQ algorithm in order to check whether $I$ (the unshuffling permutation) is a local minimum of the matching objective function. While this is not finding a globally optimal solution to the graph matching problem, this provides a useful surrogate for the difficulty/feasibility of the deanonymization task.

For each network $A$, we generate 30 independent random graphs $B$ from the uniformly corrupting channel with the same value of $p$, and measure the average matching accuracy of the solution $\hat{P}^{FAQ}$. This process is repeated for different values of $p \in \{10^{-3}, 10^{-2.5}, \ldots, 10^{-0.5}\}$. The accuracy of the solution is measured in two ways: First, we calculate the total matching accuracy as the percentage of vertices that are correctly matched; i.e., we compute $\frac{1}{n} \sum_{i=1}^{n} 1(\hat{P}^{FAQ}_{ii} = 1)$. As mentioned in Section 4, matching periphery vertices is usually hard in practice, thus, we also investigate whether it is possible to correctly match the core vertices by measuring the accuracy of matching a fraction $c$ of the vertices with the highest degree is given by $\frac{1}{\lceil cn \rceil} \sum_{i=1}^{\lceil cn \rceil} 1(\hat{P}^{FAQ}_{j_i j_i} = 1)$, with $c \in (0, 1]$.

The overall matching accuracy and the matching accuracy of the vertices with highest degrees are shown in Figures 3a and 3b. When looking to all the vertices aggregated in Figure 3a, the accuracy in the arXiv and protein interaction networks decreases fast as $p$ increases, which agrees with the predicted matching feasibility of
Figure 3: Matching accuracy calculated as the fraction of vertices that are correctly matched. The left plot shows the accuracy of matching correctly all the vertices as a function of the channel probability. In the right plot, vertices are ranked from highest to lowest degree, and the accuracy is calculated considering only the vertices with a normalized degree rank smaller than $c \in (0, 1]$. The plots show the resulting accuracy as a function of the fraction $c$ of vertices considered, and for different values of the corrupting channel probability $p$. 
The Karate and C. elegans networks have the highest matching accuracy for most of the values of $p$. This suggests that the bound obtained in Theorem 4 might be conservative for networks with a small number of vertices. However, when looking only to the vertices with the highest degree (Figure 3b), the matching accuracy is higher in the political blogs networks, in which almost 25% of the vertices with the highest degree can be matched accurately even for large values of $p$; this is as expected by the results on Figure 2 in which this network is the more resistant to noise for large values of $k$. Figure 3b also shows the difficulty of matching vertices in the protein-protein interaction and arXiv citation networks, in which even the vertices with the highest degrees are usually incorrectly matched. This is especially true for the protein-protein interaction network, which has a core-periphery structure in which high-degree nodes are highly connected between each other. As observed in Table 1, this graph is characterized by a large clustering coefficient and a heavy tailed degree distribution.

6 Discussion

The inexact graph matching problem aims to find the alignment that minimizes the number of edge disagreements between a pair of graphs. In this paper, we have shown that this intuitive notion of matching coincides with a maximum likelihood estimator in errorfully observed graphs, which is formally defined using the corrupting channel model. This model is able to accommodate different correlation structures between the edges of a pair of graphs, and many other popular models for the paired and correlated networks can be are encompassed by this framework. Within this model, we derive necessary and sufficient conditions to determine whether the MLE is consistent, and introduce a relaxed notion of consistency in which all but a small fraction of the vertices are correctly matched.

Since the distribution of the corrupting channel model conditions on a given graph $A$, the consistency results we presented here only depend on the structure of $A$ and the channel noise. This property allowed us to derive conditions that can be used to check whether the MLE is consistent for a given family of graphs, and hence whether it is feasible to solve the GMP. We used these results to study matching feasibility in some popular random graph models, unifying some previous matchability results within our framework and introducing some new ones as well. Our results were tested in simulated and real networks, and we introduced a statistic that can be used in practice to estimate matching feasibility. In addition, we believe that our results can be used to study the feasibility of solving the GMP in other graph models of interest.
This paper studies the information limits of the graph matching problem in the corrupting channel model, and currently there is no known efficient algorithm for finding the solution to the graph matching problem in this model framework. Hence, finding a polynomial-time algorithm to solve the GMP in this model and studying the corresponding computational limits are important open questions for future work. These questions have been partially addressed in a number of settings (see for example [Lyzinski et al. (2014), Shirani et al. (2017), Zhang (2018a, b)]), but existing methods usually require seeds to initialize the method, or impose restrictive constraints in the type of graphs or edge correlations that can be handled. Our framework offers a new insight which can be potentially useful in this direction.

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A Proof of main results

A.1 Proof of Theorem 4

Proof. We will first prove part iii. of the theorem. To this end, for a graph $A \in \mathcal{G}_n$, define $B$ to be the channel corrupted $A$ with parameters $(p, I)$. For $Q \in \Pi_n$, define

$$X_Q(A) = X_Q := \frac{1}{2}\|AQ - QA\|_F^2,$$

$$\hat{X}_Q(A) = \hat{X}_Q := \frac{1}{2}(\|AQ - QB\|_F^2 - \|A - B\|_F^2).$$

Let $Q \in \Pi_{n,k}$ have associated permutation $\sigma$. Letting

$$\Delta_1 := \left\{ \{i, j\} \in \begin{pmatrix} V \\ 2 \end{pmatrix} \text{ s.t. } A_{i,j} \neq A_{\sigma(i),\sigma(j)}, A_{i,j} = B_{\sigma(i),\sigma(j)} \right\}$$

$$\Delta_2 := \left\{ \{i, j\} \in \begin{pmatrix} V \\ 2 \end{pmatrix} \text{ s.t. } A_{i,j} = A_{\sigma(i),\sigma(j)}, A_{i,j} \neq B_{\sigma(i),\sigma(j)} \right\}$$

We have that

$$\frac{1}{2}\|AQ - QB\|_F^2 = X_Q + \Delta_2 - \Delta_1,$$

$$\frac{1}{2}\|A - B\|_F^2 = \Delta_2 + \Delta_1.$$
And hence $\hat{X}_Q = X_Q - 2\Delta_1$. Noting that $\Delta_1 \sim \text{Binom}(X_Q, p_n)$, we have
\[
\mathbb{P}(\hat{X}_Q \leq 0) = \mathbb{P}(\Delta_1 \geq X_Q/2) \leq \exp \left\{ -X_Q H(1/2, p_n) \right\}
\exp \left\{ \frac{1}{2} X_Q \log(4p_n(1 - p_n)) \right\},
\]
where $H(1/2, p)$ is the relative binomial entropy [Arratia & Gordon 1989, Theorem 1]. As there are at most $n^k$ such $Q$, we have that for $n$ sufficiently large
\[
\mathbb{P}(\exists Q \neq I \text{ s.t. } \hat{X}_Q \leq 0) \leq \sum_k \exp \left\{ k \log n - \frac{1}{2} X_Q \log \left( \frac{1}{4p_n(1 - p_n)} \right) \right\}.
\leq \sum_k \exp \{ -2k \log n \} \leq \exp \{ -4 \log n + \log n \} = n^{-3}.
\]
Therefore, by the Borel-Cantelli lemma, the sequence $(\hat{P}_n)_{n=0}^\infty$ is strongly consistent.

To prove part ii., note that if $p < 1/2$ then
\[
p_Q : = \mathbb{P}(\hat{X}_Q \leq 0) = \mathbb{P}(\Delta_1 \geq X_Q/2) = \Theta \left( e^{-X_Q H(1/2, p_n)} \left( 1/2 - p_n \right) \sqrt{X_Q} \right)^{-1}
\leq \Theta \left( e^{1/2 X_Q \log(4p_n(1 - p_n))} \left( 1/2 - p_n \right) \sqrt{X_Q} \right)^{-1}
\]
where the second equality follows from the large deviations bound on the binomial distribution [Arratia & Gordon 1989, Theorem 2]. Consider $\Theta(n)$ disjoint $Q_n \in \Pi_{k_n,n}$ (let $S_{n,k_n}$ be the set of these $Q_n$), and let $Z_n = \sum_{Q_n \in S_{n,k_n}} \mathbb{1}\{ \hat{X}_Q \leq 0 \}$. We have that
\[
\text{Var}(Z_n) \leq \mathbb{E}(Z_n) + \sum_{Q_n \in S_{n,k_n}} \sum_{Q_n' \neq Q_n} p_{Q_n} \frac{1}{\sqrt{X_{Q_n'}}},
\]
where the covariance bound is a result of the disjointedness of the $Q_n$ and the large deviations bound in Eq. (9). The second moment method can be applied to show
\[
\mathbb{P}(\exists Q_n \in \Pi_{n,k_n} \text{ s.t. } \hat{X}_{Q_n} \leq 0) = \mathbb{P}(Z_n > 0) \geq 1 - \frac{\text{Var}(Z_n)}{\mathbb{E}(Z_n)^2}
\geq 1 - \frac{\mathbb{E}(Z_n)}{(\mathbb{E}(Z_n))^2} \frac{\sum_{Q_n \in S_{n,k_n}} \sum_{Q_n' \neq Q_n} p_{Q_n} \frac{1}{\sqrt{X_{Q_n'}}}}{\sum_{Q_n} \sum_{Q_n'} p_{Q_n} p_{Q_n'}}
\]
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Now for each $Q_n \in S_{n,k}$, the growth rate in Eq. (2) implies

$$\frac{1}{\sqrt{X_{Q_n}}} = \Theta \left( (1/2 - p_n) e^{X_{Q_n}(1/2 - p_n)^2} \right) = o((1/2 - p_n)n^{\delta/2}) = o(n^{-\delta/2})$$

We then have that

$$\frac{\sum_{Q_n \in S_{n,k}} \sum_{Q'_n \neq Q_n} p_{Q_n} 1/\sqrt{X_{Q'_n}}}{\sum_{Q_n} \sum_{Q'_n} p_{Q_n} p_{Q'_n}} = o(1)$$

Next note that by Eq. (2)

$$\mathbb{E}(Z_n) = \Theta \left( \frac{n}{(1/2 - p_n)\sqrt{X_Q}} e^{-X_Q(1/2 - p_n)^2} \right) = \omega \left( \frac{n}{\sqrt{n \log n}} \right) = \omega(1),$$

so that

$$\mathbb{P}(\exists Q_n \in \Pi_{n,k} \text{ s.t. } \hat{X}_{Q_n} \leq 0) = \mathbb{P}(Z_n > 0) \geq 1 - o(1),$$

as desired.

Finally, to prove part iii., note that by equation (9) we have that for each $Q_n$, $p_{Q_n} = \Theta(1)$. Therefore, there exists infinitely many values of $n$ such that

$$\mathbb{P}(\exists Q_n \in \Pi_n \text{ s.t. } \hat{X}_{Q_n} \leq 0) \geq p_{Q_n} = \Theta(1),$$

and so the MLE is not weakly consistent.

A.2 Proof of Corollary 6

**Proof.** By Lemma 4 in Lyzinski, Fishkind, Fiori, Vogelstein, Priebe & Sapiro (2016), we have that for $n$ sufficiently large and all $Q \in \Pi_{n,k}$,

$$\mathbb{P} \left( \|A_n Q - QA_n\|_F^2 \leq \frac{\alpha_n kn}{3} \right) \leq 2 \exp \left( -\alpha_n^2 kn/128 \right). \quad (10)$$

Note that for sufficiently large $n$, the condition of the corollary implies that

$$\frac{6k \log n}{-\log(4p_n(1 - p_n))} \leq \frac{6k \log n}{(1/2 - p_n)^2} \leq \frac{\alpha_n kn}{3}.$$
The same condition also implies that \( \alpha_n = \omega\left(\sqrt{\log n/n}\right) \), and combining these facts with equation (10), we have that

\[
\mathbb{P}\left( \min_{Q \in \Pi_{n,k}} \| A_n Q - Q A_n \|_2^2 \leq \frac{-6k \log n}{\log(4p_n(1-p_n))} \forall k \in [n] \right) \leq \sum_{k=2}^{n} \sum_{Q \in \Pi_{n,k}} \exp\left(-\frac{\alpha_n^2 k n}{128}\right)
\leq \sum_{k=2}^{n} \exp\left(k \log n - 4k \log n\right) \leq \frac{1}{n^2}
\]

for \( n \) sufficiently large. By the Borell-Cantelli lemma, the result follows. \( \square \)

### A.3 Proof of Corollary 8

**Proof.** To prove part a), define \( P^{(i)} \) as the permutation that only switches vertices \( i \) and \( i+1 \), i.e., \( P^{(i)}_{i,i+1} = P^{(i)}_{i+1,i} = 1 \) and \( P^{(i)}_{j,j} = 1 \) for \( j = [n] \setminus \{i, i+1\} \), and let \( S_n = \{ P^{(i)} : i \mod 2 = 1 \} \) be a set of disjoint permutations of this type. Without loss of generality, take \( P = P^{(1)} \). Then

\[
\frac{1}{4} \| A P - P A \|_F^2 = \sum_{j=3}^{n} (A_{j2} - A_{j1})^2
\]

\[
= (1 - A_{d_n+2,1})^2 + (A_{n-d_n+1,2} - 1)^2 + \sum_{j=d_n+3}^{n-d_n} (A_{j2} - A_{j1})^2,
\]

which is a sum of \( n - 2d_n \) Bernoulli random variables. If \( n - 2d_n = O(1) \), then part iii. of Theorem 4 completes the proof. Hence, consider \( n - 2d_n = \omega(1) \). Define

\[
f(\beta_n) := \frac{1}{4} \mathbb{E}\| A P - P A \|_F^2 + \sqrt{2n \log n} = \alpha\left(\frac{\log n}{(1/2 - p_n)^2}\right),
\]

where the last equality follows from the conditions. By Hoeffding’s inequality,

\[
\mathbb{P}\left( \frac{1}{4} \| A P - P A \|_F^2 \geq f(\beta_n) \right) \leq \exp\left(-4 \log n\right).
\]

Hence,

\[
\mathbb{P}\left( \max_{P \in S_n} \frac{1}{4} \| A P - P A \|_F^2 \geq f(\beta_n) \right) \leq \frac{n}{2} \exp\left(-4 \log n\right) = \frac{1}{2n^3}.
\]
By the Borell-Cantelli lemma, \( \max_{P \in S} \frac{1}{2} \|AP - PA\|_F^2 < f(\beta_n) = o\left(\frac{\log n}{(1/2 - p_n)^2}\right) \) for all \( n > n_0 \), and using Theorem 4 part ii., the result follows.

For part b), define a \( n \times n \) graph \( B \) such that \( B_{ij} = A_{ij} \) whenever \( |i - j| \mod (n - 1 - d_n) \geq d_n \), and \( B_{ij} = B_{ji} \sim \text{Ber}(\beta_n) \) otherwise. Then \( B \sim G(n, \beta_n) \). Consider a permutation \( Q \in \Pi_{n,k} \), and observe that

\[
\|AQ - QA\|_F^2 = \|BQ - QB + (A - B)Q - Q(A - B)\|_F^2 \\
\geq \|BQ - QB\|_F^2 - 2kd_n = \|BQ - QB\|_F^2 - o\left(k \frac{\log n}{(1/2 - p_n)^2}\right). \tag{11}
\]

Since \( B \) is an ER graph, following the proof of Corollary 7 mutatis mutandis, it can be shown that

\[
\min_{Q \in \Pi_{n,k}} \|BQ - QB\|_F^2 \geq -6k \log n \frac{\log(4p_n(1 - p_n))}{\log(4p_n(1 - p_n))} + o\left(k \frac{\log n}{(1/2 - p_n)^2}\right),
\]

and combining with Equation (11) and Theorem 4 part i., the result follows. \( \square \)

### A.4 Proof of Corollary 12

**Proof.** Let \( H \sim G(n, d/n) \) be an ER graph with rate \( d/n \). Define the events

\[
\mathcal{A}_{n,d} = \{ \text{Eq. 6 holds for } A \text{ for all } k = \omega(n^{2/3}) \} \\
\mathcal{A}_{n,d/n} = \{ \text{Eq. 6 holds for } H \text{ for all } k = \omega(n^{2/3}) \} \\
\mathcal{R}_{n,d/n} = \{ H \text{ is } d\text{-regular} \}
\]

We then have that

\[
\mathbb{P}(\mathcal{A}_{n,d/n}^c) \geq \mathbb{P}(\mathcal{A}_{n,d/n}^c | \mathcal{R}_{n,d/n}) \mathbb{P}(\mathcal{R}_{n,d/n}) = \mathbb{P}(\mathcal{A}_{n,d}^c) \mathbb{P}(\mathcal{R}_{n,d/n}).
\]

By Lyzinski et al. (2014) Eq. (9), for \( Q \in \Pi_{n,k} \) with \( k = \omega(n^{2/3}) \) we have that there exists a constant \( c \) such that for \( n \) sufficiently large

\[
\mathbb{P}(\mathcal{A}_{n,d/n}^c) \leq \mathbb{P}\left( \|H_n Q - QH_n\|_F^2 < \frac{6k \log n}{\log(4p_n(1 - p_n))} \right) \\
= \mathbb{P}\left( \|H_n Q - QH_n\|_F^2 < \frac{6 \log n}{kd_n(1 - d_n/n)} \right) \leq \exp\left(-cnk \frac{d_n}{n} \left(1 - \frac{d_n}{n}\right) \right) \leq \exp(-ckd_n),
\]

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Hence, by Lemma 4.1 in Kim et al. (2002),

$$
\mathbb{P}(A_{n,d}^c) \leq \mathbb{P}(R_{n,d/n})^{-1}\mathbb{P}(A_{n,d/n}^c) \leq \exp\left\{n\sigma_n^{1/2+\epsilon/2} - \omega(n^{2/3}d_n)\right\}
\leq \exp\left\{\left(n - \omega(n^{2/3}d_n^{1/2-\epsilon/2})\right)d_n^{1/2+\epsilon/2}\right\}
\leq n - \omega(n) = -\omega(n)
$$

With this bound, the result follows by using the Borel-Cantelli lemma. □

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