Seeded Graph Matching*

Donniell E. Fishkind, Sancar Adali, Carey E. Priebe†

May 2, 2014

Abstract

Graph inference is a burgeoning field in the applied and theoretical statistics communities, as well as throughout the wider world of science, engineering, business, etc. Given two graphs on the same number of vertices, the graph matching problem is to find a bijection between the two vertex sets which minimizes the number of adjacency disagreements between the two graphs. The seeded graph matching problem is the graph matching problem with an additional constraint that the bijection assigns some particular vertices of one vertex set to respective particular vertices of the other vertex set. Solving the (seeded) graph matching problem will enable methodologies for many graph inference tasks, but the problem is NP-hard. We modify the state-of-the-art approximate graph matching algorithm of Vogelstein et al. (2012) to make it a fast approximate seeded graph matching algorithm. We demonstrate the effectiveness of our algorithm – and the potential for dramatic performance improvement from incorporating just a few seeds – via simulation and real data experiments.

---

*This work is partially supported by National Security Science and Engineering Faculty Fellowship (NSSEFF) and Johns Hopkins University Human Language Technology Center of Excellence (JHU HLT COE).
†Department of Applied Mathematics and Statistics, Johns Hopkins University, Baltimore, MD 21218.
Corresponding author: cep@jhu.edu
1 Introduction

All graphs in this manuscript are simple; that is, the edges are undirected and there are no loops or multiple edges. In other words, the adjacency matrices for graphs are binary, symmetric, and hollow. This restriction to simple graphs is for convenience only; indeed, all of our work and analysis can be naturally extended to settings with more general graphs.

Suppose $G_1$ and $G_2$ are two graphs with respective vertex sets $V_1$ and $V_2$ such that $|V_1| = |V_2|$. For any bijective function $\phi : V_1 \rightarrow V_2$, the number of adjacency disagreements under $\phi$ is defined to be

$$d(\phi) := |\{(u, v) \in V_1 \times V_1 : u \sim_{G_1} v \text{ and } \phi(u) \not\sim_{G_2} \phi(v) \} \text{ or } \{u \not\sim_{G_1} v \text{ and } \phi(u) \sim_{G_2} \phi(v)\}|.$$  

The graph matching problem is to minimize $d(\phi)$ over all bijective functions $\phi : V_1 \rightarrow V_2$. This problem is NP-hard; in fact, even the simpler problem of deciding whether there exists a graph isomorphism between $G_1$ and $G_2$ is notoriously of unknown complexity (and, indeed, is suspected to belong to an intermediate complexity class which is strictly between P and NP-complete). Thus, in particular, there are no efficient algorithms known for graph matching, and it is suspected that none exist.

The development of graph matching heuristics is a venerable and active field. An excellent survey article by Conte, Foggia, Sansone, and Vento titled “Thirty years of graph matching in pattern recognition” [2] outlines successful application of approximate graph matching to two-dimensional and three-dimensional image analysis, document processing, biometric identification, image databases, video analysis, and biological and biomedical applications. The current state-of-the-art algorithms can provide effective and realtime approximate graph matching for graphs with hundreds or thousands of vertices [7].

In this manuscript, we utilize the approximate graph matching algorithm of Vogelstein et al. [7] which they call “FAQ” (an acronym for Fast Approximate Quadratic Assignment Problem Algorithm); its running time is cubic in the number of vertices and, in practice, the quality of the approximate solution and the speed of the algorithm are state-of-the-art. The relevant details of FAQ will be specified later, in Section 2.

Now consider that we are also given subsets $W_1 \subset V_1$, $W_2 \subset V_2$ such that $|W_1| = |W_2|$ and we are given a fixed bijection $\psi : W_1 \rightarrow W_2$. The seeded graph matching problem is defined to be the problem of minimizing $d(\phi)$ over all bijections $\phi : V_1 \rightarrow V_2$ that are extensions of $\psi$ — that is, $\phi$ must agree with $\psi$ on $W_1$ (i.e., for all $u \in W_1$, $\phi(u) = \psi(u)$). The elements of $W_1$ are called seeds and the bijection $\psi$ is a seeding. In Section 2 we modify the approximate graph matching FAQ algorithm for use in approximate seeded graph matching.
When we say that “$G_1$ on vertex set $V_1$, and $G_2$ on vertex set $V_2$ are random graphs drawn from the same distribution, with correspondence function $\Psi$”, (for the bijective function $\Psi : V_1 \rightarrow V_2$), we mean that there are specified probabilities for each of the $2^{(|V_1|)}$ possible graphs on the vertex set $V_1$ and, from this probability distribution, the two graphs $G_1$ and $G_2$ are realized (perhaps independently, or perhaps with dependence) and then – just in $G_2$ – each vertex $u \in V_1$ is relabeled as $\Psi(u) \in V_2$, so that $G_1$ remains on vertex set $V_1$ but $G_2$ now has vertex set $V_2$. The approximate graph matching solution $\phi : V_1 \rightarrow V_2$ may be viewed as an approximation for the underlying correspondence function $\Psi : V_1 \rightarrow V_2$, if $\Psi$ is partially or completely unknown.

We will see in Section 3 that minimizing $\phi$ may be a poor approximation for $\Psi$, perhaps agreeing with $\Psi$ at only a few vertices, not much better than chance. However, we will also see that utilizing seeds $W_1 \subset V_1$ – and the seeding function $\psi$ consisting of the restriction of $\Psi$ to $W_1$ – can yield an approximate seeded graph match solution which agrees with $\Psi$ on a much more substantial fraction of the nonseeded vertices from $V_1$.

While the literature on graph matching is vast, with [2] and [7] providing a comprehensive survey (2004) and a recent literature review (2012), respectively, there is precious little prior art for seeded graph matching: in [4] a very small seeded graph matching problem (12 vertices) is addressed, while [8] and [5] incorporate constraints that enforce correspondences to be only between vertices of the same “type”.

The structure of this paper is as follows: in Section 2 we adapt the FAQ algorithm of [7] into an algorithm for approximate seeded graph matching; in Section 3 we demonstrate the effectiveness of our algorithm – and the potential for dramatic performance improvement from incorporating just a few seeds – via simulation and three real data experiments; we conclude in Section 4 with a discussion of implications and future work.

2 Modified-FAQ for approximate seeded graph matching

We are interested in solving the seeded graph matching problem but, as discussed earlier, this problem is NP-hard and so we have no expectation that there even exists an efficient algorithm. Thus we seek an approximate solution that can be efficiently computed.

In Section 2.1 we express the seeded graph matching problem as an optimization problem with integer constraints, and then we relax the integer constraints by replacing them with nonnegativity constraints. In Section 2.2 we modify the FAQ algorithm of [7] into an algorithm that approximately solves the relaxed seeded graph matching problem. Of course, when solving a relaxation, the solution may not in general be integer valued, and as such it would not be appropriate even as an approximate solution to the original (unrelaxed) problem. Therefore, in Section 2.3 we project
the solution of the relaxed optimization problem to the nearest element of the feasible region of the unrelaxed problem, and we then declare that to be the approximate solution to the original (unrelaxed) problem.

2.1 The relaxation

Recall that $G_1$ is a graph on vertex set $V_1$ and $G_2$ is a graph on vertex set $V_2$ such that $|V_1| = |V_2| = n + m$, the set of seeds $W_1$ is a subset of $V_1$ and $W_2$ is a subset of $V_2$ such that $|W_1| = |W_2| = m$, and the bijection $\psi : W_1 \rightarrow W_2$ is the seeding. Without loss of generality, we will take $V_1$ and $V_2$ to each be the set of integers $\{1, 2, \ldots, m + n\}$, we will take $W_1$ and $W_2$ to each be the set of integers $\{1, 2, \ldots, m\}$, we will take $\psi$ to be the identity function, for some fixed nonnegative integer $m$ and positive integer $n$. (When $m = 0$ we have the (unseeded) graph matching problem.)

Let $A, B \in \mathbb{R}^{(m+n) \times (m+n)}$ be the adjacency matrices for $G_1$ and $G_2$, respectively; this means that for all $i, j \in \{1, 2, \ldots, m + n\}$ it holds that $a_{ij} = 1$ or $0$ according as $i \sim_{G_1} j$ or not, and $b_{ij} = 1$ or $0$ according as $i \sim_{G_2} j$ or not. It will soon be useful to let $A$ and $B$ be partitioned as

$$A = \begin{bmatrix} A_{11} & A_{12} \\ A_{21} & A_{22} \end{bmatrix}, \quad B = \begin{bmatrix} B_{11} & B_{12} \\ B_{21} & B_{22} \end{bmatrix}$$

where $A_{11}, B_{11} \in \mathbb{R}^{m \times m}, A_{12}, B_{12} \in \mathbb{R}^{m \times n}, A_{21}, B_{21} \in \mathbb{R}^{n \times m},$ and $A_{22}, B_{22} \in \mathbb{R}^{n \times n}$.

It is clear that the seeded graph matching problem is minimize $\|A - (I_{m \times m} \oplus P)B(I_{m \times m} \oplus P)^T\|_1$ over all $n \times n$ permutation matrices $P$, where $I_{m \times m}$ is the $m$-by-$m$ identity matrix, $\oplus$ is the direct sum of matrices, and $\|\cdot\|_1$ is the $\ell_1$ vector norm on matrices; say the optimal $P$ is $\hat{P}$. Then the corresponding bijection $\phi_{\hat{P}} : \{1, 2, \ldots, m + n\} \rightarrow \{1, 2, \ldots, m + n\}$ defined as, for all $i \in \{1, 2, \ldots, m\}$, $\phi_{\hat{P}}(i) = i$ and, for all $i, j \in \{1, 2, \ldots, n\}$, $\phi_{\hat{P}}(i + m) = j + m$ precisely when $\hat{p}_{ij} = 1$, is the bijection which solves the seeded graph matching problem.

Of course, this optimization problem is equivalent to minimizing $\|A(I_{m \times m} \oplus P) - (I_{m \times m} \oplus P)B\|_1$ or $\|A - (I_{m \times m} \oplus P)B(I_{m \times m} \oplus P)^T\|_2$ or $\|A(I_{m \times m} \oplus P) - (I_{m \times m} \oplus P)B\|_2$, over all permutation matrices $P$, where $\|\cdot\|_2$ is the $\ell_2$ vector norm on matrices. Expanding $\|A - (I_{m \times m} \oplus P)B(I_{m \times m} \oplus P)^T\|_2^2 = \|A\|_2^2 + \|B\|_2^2 - 2 \cdot \text{trace}(A^T(I_{m \times m} \oplus P)B(I_{m \times m} \oplus P^T))$, we see that this optimization problem is equivalent to maximizing $\text{trace}(A^T(I_{m \times m} \oplus P)B(I_{m \times m} \oplus P^T)$ over permutation matrices $P$.

As mentioned previously, graph matching in NP-hard, so we do not expect to ever find an efficient algorithm for seeded graph matching. In looking for an approximate solution for seeded graph matching, it makes sense to work with a relaxation; specifically, we concern ourselves with

\[\text{Note that although } A \text{ and } B \text{ are symmetric matrices, we nonetheless keep transposes in place wherever they are present to enable further generalization; our analysis will not change if we instead were in a broader setting where } A \text{ and } B \text{ are generic (nonsymmetric, nonhollow, and/or nonintegral) matrices in } \mathbb{R}^{(m+n) \times (m+n)}.\]
first solving maximize trace $A^T (I_{m \times m} \oplus P) B (I_{m \times m} \oplus P^T)$ over all doubly stochastic matrices $P$, which means that $P \in \mathbb{R}^n$ such that $P \mathbf{1}_n = \mathbf{1}_n$, $P^T \mathbf{1}_n = \mathbf{1}_n$, and $P \geq 0_{n \times n}$ coordinatewise, where $0_{n \times n}$ is the $n$-by-$n$ matrix of zeros and $\mathbf{1}_n$ is the $n$-vector of all ones. Indeed, this is a relaxation of seeded graph matching in the sense that if we were to add integrality constraints – that $P$ is integer-valued – then we would precisely return to the constraint that $P$ is a permutation matrix, hence we would have returned to the seeded graph matching problem.

2.2 Modified-FAQ

The modified-FAQ algorithm is a modification of the state-of-the-art graph matching algorithm of [7], which they call FAQ, so that it can be used for approximate seeded graph matching. Modified-FAQ approximately solves the relaxed seeded graph matching problem – maximize trace $A^T (I_{m \times m} \oplus P) B (I_{m \times m} \oplus P^T)$ subject to $P$ being a doubly stochastic matrix – by using the Frank-Wolfe Method, which is an iterative procedure that involves successively solving linearizations. It turns out that the linearizations can be cast as linear assignment problems that are solved with the Hungarian Algorithm.

We first briefly review the Frank-Wolfe Method before proceeding to apply it. The general kind of optimization problem for which the Frank-Wolfe Method is used is

\[(\text{FWP}) \quad \text{Minimize } f(x) \text{ such that } x \in S, \quad (1)\]

where $S$ is a polyhedral set (i.e., is described by linear constraints) in a Euclidean space of some dimension, and the function $f : S \to \mathbb{R}$ is continuously differentiable. A starting point $x^{(1)} \in S$ is chosen in some fashion, perhaps arbitrarily. For $i = 1, 2, 3, \ldots$, the following is done. The function $\tilde{f}^{(i)} : S \to \mathbb{R}$ is defined to be the first order (i.e., linear) approximation to $f$ at $x^{(i)}$ – that is, $\tilde{f}^{(i)}(x) := f(x^{(i)}) + \nabla f(x^{(i)})^T (x - x^{(i)})$; then solve the linear program: minimize $\tilde{f}^{(i)}(x)$ such that $x \in S$ (this can be done efficiently since it is a linear objective function with linear constraints, and note that, by ignoring additive constants, the objective function of this subproblem can be abbreviated: minimize $\nabla f(x^{(i)})^T x$ such that $x \in S$), say the solution is $\tilde{x}^{(i)} \in S$. Now, the point $x^{(i+1)} \in S$ is defined as the solution to: minimize $f(x)$ such that $x$ is on the line segment from $x^{(i)}$ to $\tilde{x}^{(i)}$ in $S$. (This is a just a one dimensional optimization problem; in the case where $f$ is quadratic this can be exactly solved analytically.) Go to the next $i$, and terminate this iterative procedure when the sequence of iterates $x^{(1)}$, $x^{(2)}$, $x^{(3)}$, \ldots stops changing much or develops a gradient close enough to zero. This concludes our review of the Frank-Wolfe Method.

We now describe how modified-FAQ employs the Frank-Wolfe Method to solve the relaxed
the derivative of
and
loss of generality, since it will not affect the maximization) we have
\[ Q \text{ will in fact find the optimal } \]

\[ \text{Thus the next Frank-Wolfe algorithm iterate will either be } \tilde{\alpha} \]

\[ \text{or } \tilde{\alpha} \]

\[ \text{which has gradient} \]

\[ \nabla(P) := A_{21}B_{21}^T + A_{12}B_{12} + A_{22}PB_{22} + A_{22}PB_{22}. \]

We start the Frank-Wolfe Algorithm at the doubly stochastic matrix \( \tilde{P} = \frac{1}{n} \mathbb{1}_n \mathbb{1}_n^T \). (This is only for simplicity, and any other choice of doubly stochastic \( \tilde{P} \) might be as effective). In the next paragraph we describe a single step in the Frank-Wolfe algorithm. Such steps are repeated iteratively until the iterates empirically converge.

Given any particular doubly stochastic matrix \( \tilde{P} \in \mathbb{R}^{n \times n} \) the Frank-Wolfe-step linearization involves maximizing \( \text{trace} Q^T \nabla(\tilde{P}) \) over all of the doubly stochastic matrices \( Q \in \mathbb{R}^{n \times n} \). This is precisely the linear assignment problem (since it is not hard to show that the optimal doubly stochastic \( Q \) can in fact be selected to be a permutation matrix) and so the Hungarian Algorithm will in fact find the optimal \( Q \), call it \( \tilde{Q} \), in \( O(n^3) \) time. The next task in the Frank-Wolfe algorithm step will be maximizing the objective function over the line segment from \( \tilde{P} \) to \( \tilde{Q} \); i.e., maximizing \( g(\alpha) := f(\alpha \tilde{P} + (1 - \alpha) \tilde{Q}) \) over \( \alpha \in [0, 1] \). Denote \( c := \text{trace} A_{22}^T \tilde{P} B_{22} \tilde{P}^T \) and \( d := \text{trace} (A_{22}^T \tilde{P} B_{22} \tilde{Q} + A_{22}^T \tilde{Q} B_{22} \tilde{P}^T) \) and \( e := \text{trace} (A_{22}^T \tilde{Q} B_{22} \tilde{Q}^T) \) and \( u := \text{trace} (\tilde{P}^T A_{12} B_{12} + \tilde{P}^T A_{12} B_{12}) \) and \( v := \text{trace} (\tilde{Q}^T A_{21} B_{21}^T + \tilde{Q}^T A_{12} B_{12}). \) Then (ignoring the additive constant \( \text{trace} A_{11}^T B_{11} \) without loss of generality, since it will not affect the maximization) we have \( g(\alpha) = c\alpha^2 + d\alpha(1 - \alpha) + e(1 - \alpha)^2 + u\alpha + v(1 - \alpha) \) which simplifies to \( g(\alpha) = (c - d + e)\alpha^2 + (d - 2e + u - v)\alpha + (e + v) \). Setting the derivative of \( g \) to zero yields potential critical point \( \tilde{\alpha} := \frac{(d - 2e + u - v)}{2(c - d + e)} \) (if indeed \( 0 \leq \tilde{\alpha} \leq 1 \)); thus the next Frank-Wolfe algorithm iterate will either be \( \tilde{P} \) (in which case algorithm would halt) or \( \tilde{Q} \) or \( \tilde{\alpha} \tilde{P} + (1 - \tilde{\alpha}) \tilde{Q} \), and the objective functions can be compared to decide which of these three matrices will be the \( \tilde{P} \) of the next Frank-Wolfe step.

At the termination of the Frank-Wolfe Algorithm, we have an approximate solution, say the doubly stochastic matrix \( \tilde{P} \), to the problem maximize \( \text{trace} A^T (I_{m \times m} \oplus P) B (I_{m \times m} \oplus P^T) \) subject to \( P \) being a doubly stochastic matrix.
2.3 Projecting the approximate solution of the relaxed problem

After the termination of the Frank-Wolfe Algorithm with $\tilde{P}$, what if $\tilde{P}$ is not a permutation matrix? How do we get out of $\tilde{P}$ a meaningful approximate solution to the seeded graph matching problem? The answer is that we will do one more step; we will find the permutation matrix $\tilde{Q}$ which solves the optimization problem $\min \|Q - \tilde{P}\|_1$ subject to $Q$ being a permutation matrix, and finally $\phi_{\tilde{Q}}$ is our approximate seeded graphmatch solution. To solve this latter optimization problem, observe that for any permutation matrix $Q$

$$\|Q - \tilde{P}\|_1 = \sum_{i,j \in \{1,2,\ldots,n\} : q_{ij} \neq 1} \tilde{p}_{ij} + \sum_{i,j \in \{1,2,\ldots,n\} : q_{ij} = 1} (1 - \tilde{p}_{ij})$$

$$= \sum_{i,j \in \{1,2,\ldots,n\}} \tilde{p}_{ij} + \sum_{i,j \in \{1,2,\ldots,n\} : q_{ij} = 1} (1 - 2\tilde{p}_{ij})$$

$$= n + n - 2 \cdot \sum_{i,j \in \{1,2,\ldots,n\} : q_{ij} = 1} \tilde{p}_{ij}$$

$$= 2n - 2 \text{ trace} Q^T \tilde{P}.$$ 

Thus, minimizing $\|Q - \tilde{P}\|_1$ subject to $Q$ being a permutation matrix is equivalent to maximizing $\text{trace} Q^T \tilde{P}$ subject to $Q$ being a permutation matrix; this latter optimization formulation is precisely a formulation of the well-known linear assignment problem, and it is efficiently solvable in $O(n^3)$ time with the Hungarian Algorithm. In this manner we can efficiently obtain $\phi_{\tilde{Q}}$, which is our approximate seeded graph matching solution.

2.4 Modified-FAQ is fast and accurate

By limiting the number of Frank-Wolfe steps to a constant, the running time of modified-FAQ is cubic in the number of vertices, since that is the complexity of the Hungarian Algorithm. Since there is no appreciable difference in running time between modified-FAQ and FAQ, we have state-of-the-art running time, in practice, as reported for FAQ in [7]. In addition, FAQ finds the optimal solution for several of the benchmarks considered in [7].

3 Demonstrations

We demonstrate the effectiveness of our fast approximate seeded graph matching algorithm via a simple but illustrative simulation study and three real data experiments. The potential for dramatic performance improvement from incorporating just a few seeds is undeniable.

\[\text{http://www.cis.jhu.edu/~parky/SGM}\]
In all four examples, we increase the number of seeds \( m \) from zero to some substantial fraction of the (fixed) total number of vertices in the graphs, \( c \), and attempt to match the remaining \( n \) vertices \((n + m = c)\). (For the Wikipedia graphs in Section 3.2 \( c = 1382 \); for the Enron email graphs in Section 3.3 \( c = 184 \); for the C. elegans nervous system graphs in Section 3.4 \( c = 279 \). For the simulation in Section 3.1 we consider \( c = 300 \).) We report performance as the fraction of unseeded vertices correctly matched – where \( \phi^{(m)} \) agrees with correspondence function \( \Psi \). That is, the match ratio is given by

\[
\delta^{(m)} := \frac{|\{v \in V_1^{(m)} \setminus W_1^{(m)} : \phi^{(m)}(v) = \Psi(v)\}|}{n}.
\]

The expected number of vertices for which a randomly chosen bijection \( V_1 \rightarrow V_2 \) agrees with \( \Psi \) is 1. For a given value of \( m \), we need to match only the remaining \( n = c - m \) vertices; thus chance performance \( 1/n = 1/(c - m) \) increases as \( m \) increases. In all cases, we observe that \( \delta^{(m)} \) increases much faster than chance.

### 3.1 Simulation

Here we present a simple but illustrative simulation study, where the graphs are (dependent) Erdos-Renyi. We must specify a joint probability model for the pair \((G_1, G_2)\). We use \( G_1 \sim ER(c = n + m, p) \); \( G_2 \) is obtained by flipping bits in \( G_1 \) according to the “perturbation parameter” \( \rho \in [0, 1] \): given that edge \( uv \in E_1 \), we let \( uv \in E_2 \sim Bernoulli(1 - \rho) \); given that edge \( uv \notin E_1 \), we let \( uv \in E_2 \sim Bernoulli(\rho) \). Thus \( \rho = 0 \) means \( G_2 \) is identical to \( G_1 \) and we can hope for best case performance of \( n \) correct matches recovered, while \( \rho = 1/2 \) means \( G_2 \) is independent of \( G_1 \) and we expect chance performance of 1 correct match recovered. We consider \( c = 300 \) and \( p = 1/2 \).

![Simulation](image.png)

Figure 1: Matching simulated graphs, plotting match ratio \( \delta^{(m)} \) against the number of seeds \( m \) for various degrees of dependency between graphs. The perturbation parameter \( \rho \) increases from 0 to 0.5 (from dark blue to red) in increments of 0.05, with performance decreasing monotonically as \( \rho \) increases. The right plot is a zoom-in, showing details for small \( m \). NB: \( \rho = 0 \) gives perfect matching, even for \( m = 0 \).
The graphs $G_1$ and $G_2$ are matched using modified-FAQ. Figure 1 plots the mean and standard error of the match ratio $\delta(m)$ against the number of seeds $m$, based on 400 randomly chosen seed sets $W_1^{(m)}$ for each $m$, for perturbation parameter $\rho$ increasing from 0 to 0.5 in increments of 0.05. (Chance is plotted in black, but is indistinguishable from $\rho = 0.5$ (red).) Notice that $\delta(m)$ increases quickly as $m$ increases and decreases as $\rho$ increases, as expected.

We note that perfect performance when $\rho = 0$ – the darkest blue line in Figure 1 shows that the match ratio $\delta(m) = 1$ even for $m = 0$ – indicates that modified-FAQ finds the isomorphism when it exists.

3.2 Wikipedia

Wikipedia is an online editable encyclopedia with 22 million articles (more than 4 million articles in English) in 285 languages. A collection of $c = 1382$ English articles were collected by crawling the (directed) 2-neighborhood of the document “Algebraic Geometry” using inter-language links from one English article to another. This first graph will be made a simple undirected graph by symmetrizing its adjacency matrix. In Wikipedia, intra-language links between articles of the same topic in different languages are available; thus, 1-1 correspondence information between the vertices of this English Wikipedia subgraph and some vertices of the French Wikipedia graph is available. Corresponding articles in French were collected and their inter-language links yield a second graph (not necessarily connected) which is also symmetrized. Following the notation in previous sections, the English Wikipedia subgraph is denoted $G_1$ and the French Wikipedia subgraph induced by the correspondents of the English Wikipedia articles is denoted $G_2$.

Figure 2: Matching French & English Wikipedia graphs, plotting match ratio $\delta(m)$ against the number of seeds $m$.

\footnote{This data set was collected by Dr. David J. Marchette.}
The English and French Wikipedia subgraphs $G_1$ and $G_2$ are matched using modified-FAQ. Figure 2 plots, in red, the mean and standard error of the match ratio $\delta^{(m)}$ against the number of seeds $m$, based on 100 randomly chosen seed sets $W_1^{(m)}$ for each $m$. (Chance is plotted in black.) We see dramatic performance improvement from incorporating just a few seeds: with no seeds $\delta^{(0)} \approx 1/100$ (chance is 1/1382), while with just $m = 50$ seeds $\delta^{(50)} > 1/2$ (chance is 1/1332).

The blue curve in Figure 2 shows the match ratio $\delta^{(m)}$ for the unseeded problem on $c-m$ vertices. While the problem becomes smaller as $m$ increases, performance does not improve appreciably in terms of match ratio.

### 3.3 Enron

The Enron email corpus consists of messages amongst $c = 184$ employees of the Enron Corporation. Publicly available emails are used to compute a time series of graphs $\{G_t : t = 1, \ldots, T\}$ on the actors, where each graph represents one week of emails. The inference task is to identify “chatter” anomalies – small groups of actors whose activity amongst themselves increases significantly for some week $t$. Previous work identified such an anomaly at week $t = 132$ (see [3]).

![Figure 3: Matching Enron email graphs, plotting match ratio $\delta^{(m)}$ against the number of seeds $m$.](image)

The Enron email graphs for consecutive weeks $t = 130, 131, 132$ are matched, one pair at a time, using modified-FAQ. Figure 3 plots, for each pair, the mean and standard error of the match ratio $\delta^{(m)}$ against the number of seeds $m$, based on 100 randomly chosen seed sets $W_1^{(m)}$ for each $m$. (Chance is plotted in black.) The results are consistent with the finding reported in [3]: the match ratio $\delta^{(m)}$ is much higher between graphs for weeks $t = 130, 131$, where there was no significant change, compared to matching across the change (between $t = 131, 132$ and between $t = 130, 132$). The anomalous event at week $t = 132$ makes the graphs more different and the
graph matching more difficult. Indeed, investigation shows that the difference in performance is largely attributable to the vertices participating in the anomaly, as reported in [3].

3.4 C. elegans

C. elegans is a roundworm that has been extensively studied; its particular usefulness comes from its simple nervous system, consisting of \( c = 279 \) neurons whose connections have been mapped [6]. There are two types of connections between neurons: chemical (chemical synapses) and electrical (junction potentials). The adjacency matrices for both graphs are sparse. Both \( G_1 \) and \( G_2 \) are weighted graphs; for sake of uniformity with our other examples, the adjacency matrices are binarized and symmetrized.

![Graph Matching Diagram](image)

Figure 4: Matching Chemical and Electrical connectivity graphs of C. elegans nervous system, plotting match ratio \( \delta(m) \) against the number of seeds \( m \).

The objective of this experiment is to match the chemical graph \( G_1 \) to the electrical graph \( G_2 \), using modified-FAQ. Figure 4 plots, in red, the mean and standard error of the match ratio \( \delta(m) \) against the number of seeds \( m \), based on 100 randomly chosen seed sets \( W_1^{(m)} \) for each \( m \). (Chance is plotted in black.) Although performance improves when incorporating seeds, the match ratio for this experiment is significantly lower than for either Wikipedia or Enron. For instance, with \( m = 200 \) seeds, the remaining \( n = 79 \) vertices are matched with \( \delta^{(200)} \approx 0.15 \) (chance is 1/79). This suggests that the similarity between the two types of brain graphs, while significant, is tenuous.
4 Discussion

Many graph inference tasks are more easily accomplished if the graphs under consideration are labeled – if we know the correspondence between vertices in graphs $G_1$ and $G_2$. We have demonstrated, via a simple but illustrative simulation and three real data experiments, the potential for dramatic performance improvement in identifying this correspondence from incorporating just a few seeds.

In practice, identifying seeds $W_1, W_2$, and their bijection $\psi$ may be costly. Thus, understanding the cost-benefit trade-off between inference without correspondence and inference performed subsequent to seeded graph matching is essential. This paper provides the foundation for that analysis.

(Note that once the value of a few seeds is accepted, it seems clear that there will be a demand for an active learning methodology to identify the most cost-effective vertices to use as seeds.)

As noted above, our methodology applies immediately in the broader setting where adjacency matrices are generic (nonsymmetric, nonhollow, and/or nonintegral); that is, to weighted, directed, loopy graphs. Figure 5 provides results for matching the C. elegans graphs of Section 3.4, but in the case where the adjacency matrices have not been binarized and symmetrized. Comparing results for the original graphs vs. their simplified versions, we see that the addition of edge weights actually degrades performance significantly, suggesting that the edge weights in this case are not consistent across the two modalities.

![Figure 5: Matching the original weighted directed loopy Chemical and Electrical connectivity graphs of C. elegans nervous system (blue), compared to the case where the adjacency matrices have been binarized and symmetrized (red).](image_url)

Obvious extensions to this work include: (a) the case where $|V_1| \neq |V_2|$ – say, $V_1 \subset V_2$; (b) the case where the correspondence may be many-to-many; and (c) the case where the seeds are...
“soft” rather than “hard” – that is, we know that it is likely (but not certain) that the bijection \( \psi \) between seed sets \( W_1 \) and \( W_2 \) holds. Each of these extensions can be addressed within the framework presented here.

In conclusion, we contend that the methodology presented herein forms the foundation for improving performance in myriad graph inference applications for which there exists a partially unknown correspondence between the vertices of various graphs.

References

[1] H.A. Almohamad and S.O. Duffuaa, A linear programming approach for the weighted graph matching problem, *IEEE Transactions on Pattern Analysis and Machine Intelligence* **15** (1993) pp 522–525.

[2] D. Conte, P. Foggia, C. Sansone, and M. Vento, Thirty years of graph matching in pattern recognition, *International Journal of Pattern Recognition and Artificial Intelligence* **18** (2004) pp 265–298.

[3] C.E. Priebe, J.M. Conroy, D.J. Marchette, and Y. Park, Scan Statistics on Enron Graphs, *Computational and Mathematical Organization Theory* **11** (2005) pp 229–247.

[4] Y. Feng, R.L. Goldstone, and V. Menkov, A graph matching algorithm and its application to conceptual system translation, *International Journal on Artificial Intelligence Tools* **14** (2005) pp 77–99.

[5] C. Fraikin and P. Van Dooren, Graph matching with type constraints on nodes and edges, in *Web Information Retrieval and Linear Algebra Algorithms* (A. Frommer, M.W. Mahoney, and D.B. Szyld, eds) (2007).

[6] L.R. Varshney, B.L. Chen, E. Paniagua, D.H. Hall, and D.B. Chklovskii, Structural Properties of the Caenorhabditis elegans Neuronal Network, *PLoS Computational Biology* **7** (2011).

[7] J.T. Vogelstein, J.M. Conroy, L.J. Podrazik, S.G. Kratzer, E.T. Harley, D.E. Fishkind, R.J. Vogelstein, and C.E. Priebe, Brain graph matching via fast approximate quadratic programming, *submitted for publication* (2012) available at <arxiv.org/pdf/1112.5507>.

[8] M. Zaslavskiy, F. Bach, and J.-P. Vert, Global alignment of protein-protein interaction networks by graph matching methods, *Bioinformatics* **25** (2009) pp 259–267.