Reconstructing Sparse Illicit Supply Networks: A Case Study of Multiplex Drug Trafficking Networks

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Abstract

The network structure provides critical information for law enforcement agencies to develop effective strategies to interdict illicit supply networks. However, the complete structure of covert networks is often unavailable, thus it is crucially important to develop approaches to infer a more complete structure of covert networks. In this paper, we work on real-world multiplex drug trafficking networks extracted from an investigation report. A statistical approach built on the EM algorithm (DegEM) as well as other methods based on structural similarity are applied to reconstruct the multiplex drug trafficking network given different fractions of observed nodes and links. It is found that DegEM approach achieves the best predictive performance in terms of several accuracy metrics. Meanwhile, structural similarity-based methods perform poorly in reconstructing the drug trafficking networks due to the sparsity of links between nodes in the network. The inferred multiplex networks can be leveraged to (i) inform the decision-making on monitoring covert networks as well as allocating limited resources for collecting additional information to improve the reconstruction accuracy and (ii) develop more effective interdiction strategies.

Keywords: Multilayer networks, Partially observable networks, Network completion, Bayesian inference, Observation allocation

1. Introduction

Illicit supply networks, such as drug and human trafficking networks, compromise national security and prosperity as well as public health and safety [1]. Despite considerable advances in understanding and disrupting the operations of illicit supply networks (ISNs), a deep understanding of the structure and dynamical behaviors of ISNs is still lacking. Although topological information is crucial for understanding, monitoring, and controlling ISNs, this information is typically incomplete or missing [2, 3]. First, detailed information about the ISNs is often not available by definition because traffickers operate covertly and key witnesses

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who could fill information deficits are hard to identify [4]. Second, witnesses are often unwilling and unable to cooperate due to extreme trauma and drug dependencies, fear of retaliation by traffickers, and perceived risk of deportation (foreign national victims) [5, 6]. This study seeks to alleviate this problem by using a novel approach to reconstruct the topology of ISNs given partial observations of the topology.

Complex interactions among traffickers and their social ties cannot be conveniently represented by single-layer network models. Criminal actors, like their non-criminal counterparts, are embedded in different types of networks, i.e., friendships, kinship, legitimate business, and their interactions involve physical activity, as well as cyber communications and transactions. As such, a growing number of researchers are resorting to using multilayer network models to study illicit supply chains [7, 8, 9, 3, 10] since those models allow one to place people into different layers representing different characteristics of the ISNs. Going beyond mapping only the co-offending activity, multilayer models reveal more about the social processes that connect people, and this information can be used to infer missing information [11, 12, 13]. However, to the best of our knowledge, few studies have attempted to infer their multiplayer structure (topology).

Although reconstructing the topology from incomplete observations is a critical to understanding the structure and dynamics of covert multiplex networks and predicting future interactions between nodes in the networks [14], this task is exceedingly difficult primarily because (i) the number of missing nodes and links will be very large and (i) the illicit networks typically have much lower link density than non-covert social networks, reducing the many prediction methods developed for non-covert networks with a balanced ratio of position and negative labels.

The main findings of our study are:

1. Our method (DegEM) performs well for the reconstruction of the drug trafficking networks under study over several metrics for predictive accuracy.
2. None of the structural similarity-based methods, which are conventionally used for link prediction, perform well in reconstructing drug trafficking networks. This is because the networks are highly sparse, thus the structural similarity scores are lower for most pairs of nodes.

The rest of this paper is structured as follows. Section 2 presents the literature review. The methods are introduced in Section 3. Details about the multiplex drug trafficking networks are given in Section 4. The numerical experiments and the resultant results are reported in Section 5, followed by the concluding remarks and discussion of future work in Section 6.

2. Literature Review

Network reconstruction methods can be divided into three categories: similarity-based approach, probabilistic (statistical) approach, and algorithmic (machine learning) approach. Structural similarity-based methods assume that nodes tend to be connected to other nodes with a higher level of similarity computed by a certain distance function [15]. These approaches give a similarity value for missing or unobserved links between every pair of nodes, then links with high similarity scores will be predicted to be present. For example,
in Abdolhosseini-Qomi et al. [16], the eigenvectors of the layer adjacency matrix are used to measure the layer topological similarity and then the topological similarity (element of the layer similarity matrix) of the unconnected nodes is used to predict the presence of a link between them. Berlusconi et al. [17] and Calderoni et al. [18] apply multiple similarity metrics, such as Common Neighbor, Resource Allocation, to identify missing links in a criminal network. They demonstrated that these similarity metrics can identify possible missing links in criminal networks with noise or incomplete information. However, the performance of similarity-based methods depends on the specific networks [19], therefore prior knowledge about the networks under study is usually required to improve the predictive performance [16]. For sparse networks, this approach may be limited due to the small number of links in the networks.

Statistical approaches for link prediction assume that the network has a known structure and a parametric or nonparametric model is built to fit the structure, such as the stochastic block model and its variants, as well as Dirichlet network distribution model [20, 21, 22]. Then the model parameters are estimated using statistical methods, such as maximum likelihood estimation. The model parameters are then used to compute the formation probability of each unobserved link, such as stochastic block model, hierarchical structure model. In particular, Kim and Leskovec [23] develop a scalable Kronecker Expectation-Maximization (KronEM) approach to reconstruct a single-layer network with a known number of missing nodes by alternating between inferring the unobserved part of the network (E-step) and estimating the optimal model parameters (M-step) until convergence. The network structure is assumed to be described by the Kronecker graphs model. Note that this approach does not require attributes about nodes or edges. Wu et al. [11] use a Bayesian approach to reconstruct two-layered multiplex network structure from the available aggregate topology of all layers (the aggregation of all the layers into a single layer) and partial observations of nodes in each layer. The inference is conducted using the Expectation-Maximization algorithm. However, the statistical approaches can be computationally challenging for large networks, especially when a large number of samples are required for the inference [23].

The previous two approaches are based on computing a score for each unobserved link by defining a similarity or a probability function. However, link prediction can also benefit from other algorithmic (machine learning) approaches, including supervised learning and optimization techniques. In particular, Zhang and Chen [24] develop GNN models to predict missing links. However, the method is mainly developed for single-layer networks. Gao et al. [25] develop a network embedding method called interactive learning across relations that exploits the existing multiple types of relational data in to predict inductive links (new or unobserved relation) between existing nodes instead of inter- or intra-layer links in a known layer.

In this study, we adopt the statistical approach in [11] because the sparsity of links in illicit supply networks, i.e., the negatives (no links between nodes) significantly outnumber the positives, leads to challenges in inference and thus significantly affects the predictive performance of classical learning-based method [26]. For covert networks, a more challenging and more common problem than link prediction is a fraction of nodes in each layer are also missing. The approach in [11] is promising because it can infer the unobserved nodes besides predicting the links. Since this approach is developed for two-layered networks, we extend it and apply to a multiplex drug trafficking networks with more than two layers.
3. Methodology

3.1. Problem Description

Multiplex networks are typically used to represent a set of interactions or relations between the same of entities or individuals (Fig. 1). Mathematically, a multiplex network can be described $\mathcal{M} = \{G_\alpha, \alpha = 1, 2, \ldots, m\}$ where $m$ is the number of layers. Each $G_\alpha$ consists of the set of nodes $\mathcal{V}_\alpha$ and set of edges $\mathcal{E}_\alpha$ of relation type $R_\alpha$, i.e., $G_\alpha = (\mathcal{V}_\alpha, \mathcal{E}_\alpha, R_\alpha)$. For an incomplete multiplex networks, only some part of a network, are observed, i.e., a fraction $c$ of nodes and the associated links of the complete network. If we denote the unobserved subgraph in layer $\alpha$ by $Z_\alpha$ and the observed subgraph by $H_\alpha$, then $G_\alpha = H_\alpha \cup Z_\alpha$. The objective of the multiplex network reconstruction problem is to estimate the complete, $\mathcal{M}$, the set of the typologies of all layers, given the set of observed part of all layers, $\mathcal{M}_{\text{obs}} = \{H_\alpha, \alpha = 1, \ldots, m\}$.

3.2. Expectation-Maximization

The Expectation-Maximization (EM) is an iterative method for estimation problems in which the value of model parameters and latent variables depend on each other. For the network reconstruction problem, to find the most probable topology of the missing subgraph, it is required to first estimate the network model parameters, which establish a connection between the observed subgraph $G$ and the unobserved $Z$. This framework can be formulated...
as follows. The objective is to estimate the missing part of multiplex networks given the observed part, which is given by

$$\mathcal{M} \sim P(\mathcal{M} | \mathcal{M}_{\text{obs}}, \Theta)$$  \hspace{1cm} (1)

The estimation is conducted by alternating between the E-step and the M-step until convergence. In the E-step, the expected likelihood function given the model parameters at iteration $t$ and the observations is computed as

$$Q(\Theta | \Theta^{(t)}) = \mathbb{E}_{\mathcal{M} | \mathcal{M}_{\text{obs}}, \Theta^{(t)}} \left[ P(\mathcal{M}^{(t)} | \mathcal{M}_{\text{obs}}, \Theta) \right]$$  \hspace{1cm} (2)

In the M-step, the optimal value of model parameters is update by

$$\Theta^{(t+1)} = \arg \max_{\Theta} Q(\Theta | \Theta^{(t)})$$  \hspace{1cm} (3)

In EM framework using degree sequence (DegEM) [11], the objective is to use maximum likelihood estimation to obtain the probability distribution of the complete topology

$$Q(M) = P(M | \mathcal{A}^{O}, \mathcal{M}_{\text{obs}}, d)$$  \hspace{1cm} (4)

where $\mathcal{M}_{\text{obs}}$ is the observed part of the multiplex networks, $d$ is the degree sequence, and $\mathcal{A}^{O}$ is the aggregate topology of multiplex networks. Notice that $d$ can be considered as the model parameter while the missing part of the network, or equivalently the complete topology, can be considered as the latent variables. The configuration model is employed to estimate the probability of a link between any two nodes using the degree sequence $d$ of nodes in a network. To make the problem less challenging, it is assumed that the aggregate topology, denoted by $\mathcal{A}^{O}$ is available besides the observed part of multiplex networks.

![Figure 1: Schematic of a multiplex network with three layers and five nodes. In a multiplex network, the nodes are shared across layers and links in each layer represent the one type of relation between nodes. An interlayer link connects the same nodes in different layers.](image)
the E-step becomes

\[
W(\mathbf{d} | \mathbf{d}^{(t)}) = \mathbb{E}_{M | A^O, M_{\text{obs}}, \mathbf{d}^{(t)}} \left[ \ln P( M | A^O, M_{\text{obs}}, \mathbf{d}^{(t)}) \right]
\]

or equivalently the expectation of the likelihood over the hidden variable ($\mathbf{d}^{(t)}$ is used at this step), which can be considered a function of $\mathbf{d}$. The M-step is

\[
d^{(t+1)} = \arg \max_{\mathbf{d}} W(\mathbf{d} | \mathbf{d}^{(t)})
\]

It is shown that the M-step method can be simplified as

\[
d^{(t+1)}(i) = \sum_{j=1}^{[\mathcal{V}]} M_{i,j}^{(t)}, \forall \ i \in \mathcal{N}
\]

Note that the DegEM is originally developed to infer the multiplex networks with two layers, but in this paper, we will apply this method to the four-layer drug-trafficking networks. One modification we make is: when a link exists between two nodes in the aggregate topology, the four link probabilities between these two nodes in the four layers are scaled up by dividing the probabilities by the maximum among them, such that at least one link between these two nodes will be predicted.

3.3. Structural Similarity-Based Methods

We also use several local structure similarity-based methods to reconstruct the network, including Preferential Attachment (PA), Jaccard coefficient (JC), Adamic Adar coefficient Index (AA) [27], and Resource Allocation Index (RA). These metrics have been shown to achieve good predictive accuracy on several social networks [27]. PA measure the extent of two nodes forming new links based on how many existing neighbors they have, which is computed as

\[
PA(i, j) = |N(i)||N(j)|
\]

JC measures the proportion of shared neighbors between all neighbors of two nodes, which is computed by

\[
JC(i, j) = \frac{|N(i) \cap N(j)|}{|N(i) \cup N(j)|}
\]

where $N(i)$ is the set of neighbors of node $i$.

AA measures the number of shared links between two nodes in the same layer, which is formally given by

\[
AA(i, j) = \sum_{h \in N(i) \cap N(j)} \frac{1}{\ln d(h)}
\]

where $d(h)$ is the degree of node $h$. 

RA is similar to AA but penalizes shared neighbors with a higher degree. It is computed as

\[
RA(i, j) = \sum_{h \in N(i) \cap N(j)} \frac{1}{d(h)}
\]  

(11)

To use the attributes of nodes in prediction, we use Eskin to measure the similarity between attributes since the attributes are categorical variables. If we denote the number of attributes as \( K \) and the number of categories that attribute \( p \) has as \( n_k \), then the Eskin score between the attributes of two nodes, \( x \) and \( y \), is computed as [28]

\[
\text{Eskin} = \sum_{k=1}^{K} \frac{1}{K} s_k(x, y)
\]  

(12)

where

\[
s_k(x, y) = \begin{cases} 
1 & \text{if } x_k = y_k \\
\frac{n_k^2}{n_k^2 + 2} & \text{otherwise}
\end{cases}
\]  

(13)

When each local structural and attribute similarity-based method is used for predicting the missing links, a score for each pair of possible unobserved links is calculated, then the pairs of nodes with the top highest scores will be predicted to be connected.

Since the observed links are sparse, self-supervised learning can be naturally leveraged here [29, 30]. Here we use one of the most popular graph self-supervised learning techniques, random-walk (global structural similarity) based method to obtain the similarity of the nodes (actors) in the embedded space [31]. Nodes appear more on the same random walks will be closer to each other in the embedded space.

4. Multiplex Drug Trafficking Networks

4.1. Data Source

The data about the drug trafficking networks in this study was obtained from the 2007 ‘E’ Division Provincial Threat Assessment (PTA) report generated by Criminal Intelligence Service Canada and the Royal Canadian Mounted Police (RCMP) [32]. This report includes an inventory of the social relations of individuals from groups that engaged in criminal activities within the Pacific Region from 2004 to 2006. This information about all members of the drug trafficking group include: their demographic characteristics, description of drug trafficking activity, role in drug trafficking, and their relations among each other, including co-offenders (individuals who commit crimes together), legitimate business partners (including friends), their kinship, and involvement in a formal crime organization (including enemies) (Fig. 2). In total, there are 2197 individuals (nodes) and 2891 connections (links) of different relations among them in this multiplex networks. The attributes of the actors include: date of birth, gender, age when they were first analyzed (AFA) by law enforcement, whether or they are involved in drug activity, drug type, role in drug trafficking, crime group membership (GM), crime group type (GMT), and the code for crime group (GMC) (Fig. 3). Some key network statistics of each of the four layers are presented in Table 1. We can see from the table that each layer has a low link density (\( \rho \)), low average degree (\( < d > \)), small average size of
connected component ($<|CC|>$). Although the size of the greatest connected component is not small, particularly the one in the co-offender network, the coefficient of variance (CoV, i.e., ratio of standard deviation and mean) of the size of connected component is small, indicating that members in drug trafficking groups are generally isolated.

Figure 2: Sociograms of the drug trafficking networks. A. Co-offender. B. Kinship. C. Legitimate. D. Formal organization groups.

Figure 3: Example of the attributes of actors (nodes)
Table 1: Statistics of each layer in the drug trafficking network

| Layer                | |N| | |E| |ρ |< d > (×10⁻³) |< |CC| > |GCC| |CoV of |CC| |
|---------------------|-----------------|---------------|---------------|-------|---------------|---------------|---------------|
| Co-offender         | 1645            | 1808          | 1.32          | 2.19  | 19.01         | 1024          | 5.71          |
| Legitimate          | 1022            | 1041          | 2.00          | 2.04  | 10.99         | 462           | 4.43          |
| Formal Crim. Org.   | 560             | 597           | 3.81          | 2.13  | 14.36         | 150           | 2.24          |
| Kinship             | 399             | 308           | 3.88          | 1.54  | 3.22          | 25            | 0.99          |

5. Experiments

5.1. Experiment Setup

The random walk similarity-based model is implemented with stellargraph [33]. It predicts missing links through learning node representations inductively with attri2vec, which performs a linear or non-linear mapping on node similarity obtained with random walks [34]. 10 random simulations at each fraction of missing nodes are run to obtain the average predictive performance (we find that 10 repetitions can already obtain a stable mean value). Missing attributes are imputed using decision tree [35]. For the DegEM method, the tolerance is set to $1 \times 10^{-2}$, i.e., the solution is considered converged the difference between the predicted probabilities at two consecutive iterations for all unobserved links is lower than the tolerance.

Because the covert networks are sparse, the associate datasets are typically imbalanced toward negatives (no links between nodes), we first use the area under the precision-recall curve (AUC-PR) as a metric for the performance of binary classifiers instead of the area under the receiver operating characteristic curve (AUC-ROC) [36, 37]. Additionally, we employ the Matthews Correlation Coefficient (MCC) and G-mean to measure the prediction (classification) performance [38, 39]. MCC can be computed as

$$\text{MCC} = \frac{TP \cdot TN - FP \cdot FN}{\sqrt{(TP + FP) \cdot (TP + FN) \cdot (TN + FP) \cdot (TN + FN)}}$$

(14)

where TP represents true positives, FP represents false positives, and FN represents false negatives. G-mean is given by

$$\text{G-mean} = \sqrt{\frac{TP}{TP + FN} \cdot \frac{TN}{TN + FP}} = \sqrt{\text{Recall} \cdot \text{Specificity}}$$

(15)

We also include the null model (binary random classifier) as a baseline model. Note that the value of MCC for the null model is always 0 because $TP \cdot TN - FP \cdot FN = 0.5P \cdot 0.5N - 0.5N \cdot 0.5P = 0$. The value of G-mean for the null model is always 0.5, which is obtained as $\sqrt{\frac{0.5P}{0.5P+0.5P} \cdot \frac{0.5N}{0.5N+0.5N}} = 0.5$.

5.2. Results

The predictive performance measured by the AUC-PR is presented in Fig. 4. We can see that DegEM achieves the best performance, followed by the random model, and then the random walk based method. The local structural similarity-based method all fail badly. Notice that the typical baseline model that results in flat line with precision equal to percentage
of positives is not included in the precision-recall curve because the percentage of positives is exceedingly low for this dataset. It is obvious that using the MCC, the conclusion about the predictive performance of all models considered is similar. In terms of G-mean, DegEM also outperforms all other models. Note that the random model achieves a G-mean value of 0.5 (discussed earlier) over different fractions of observed components.

Figure 4: AUC-PR under different fractions of observed components

Figure 5: MCC under different fractions of observed components

Note that for the predictive performance over all the metrics considered, the predictive performance does not necessarily increase as more nodes and the links between them are
observed. This is because in calculating the values of the performance metrics, we only use the unobserved links in the multiplex, including the links between nodes in the observed subgraph and nodes in the unobserved subgraph, $E^{o,u}$, and the links between the nodes within the unobserved subgraph, $E^{u,u}$.

6. Conclusions

In this study, we apply the DegEM and other structural similarity-based method to reconstruct a sparse multiplex drug trafficking networks given different fractions of observed part of the complete networks. We find that the DegEM achieves the best predictive performance in terms of AUC-PR, G-mean, and MCC over different level of available observed parts of the true networks. Meanwhile, structural similarity-based methods perform poorly in reconstructing multiplex drug trafficking networks due to the sparsity of links between nodes.

Although the DegEM method outperforms the baseline models on this drug trafficking networks, it assumes that the aggregate topology is available, which is almost impossible to obtain for covert networks. As such, future work will relax this assumption and develop a more general method. Another promising direction is to leverage graph neural networks to reconstruct the sparse multiplex networks. Although GNN has been widely applied to predict missing links [40, 24, 41], its application in reconstructing sparse networks is limited.

Data and Code Availability Statement

Data sharing is not applicable to this paper since no new data were created. The code for the numerical experiments will be shared publicly upon publication of this paper.
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