Coding of Graphs with Application to Graph Anomaly Detection

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Abstract—This paper has dual aims. First is to develop practical universal coding methods for unlabeled graphs. Second is to use these for graph anomaly detection. The paper develops two coding methods for unlabeled graphs: one based on the degree distribution, the second based on the triangle distribution. It is shown that these are efficient for different types of random graphs, and on real-world graphs. These coding methods is then used for detecting anomalous graphs, based on structure alone. It is shown that anomalous graphs can be detected with high probability.

I. INTRODUCTION

A popular research problem in data mining is graph anomaly detection, which has applications in areas ranging from finance to power grid operation to detecting social trends [1], [2], [3]. In this paper we explore using description length for graph anomaly detection; that is, we encode the graph using a lossless source coder, and use the resulting codelength as the decision criteria. While minimum description length (MDL) has been used in the connection with graph anomaly detection, the application has only been for model selection in time-series analysis. As far as we know, this paper is the first to consider using description length directly for anomaly detection.

Reference [4] was the first paper to develop practical source coding algorithms for graphs. To use source coding for description length analysis, the codelength has to reflect the information in the graph, and the only information [4] reflects really is the edge probability \( p \) (see discussion later). This paper therefore develops new practical (universal) source coding algorithms based on more informative statistics. This focus is different than other recent papers in graph coding [5], [6], [7], [8] that are aimed more at entropy analysis.

A. Graphs

The structure of a graph is defined by the set of vertices (also called nodes) \( \mathcal{V} \), and the set of edges, \( \mathcal{E} \). Usually, the ordering of the vertices are irrelevant, and in that case we call the graph unlabeled; we will only consider unweighted, unlabeled, undirected graphs in this paper. A graph, \( G(\mathcal{V}, \mathcal{E}) \), is often represented by the adjacency matrix, \( A = [A_{ij}] \), a \( |\mathcal{V}| \times |\mathcal{V}| \) matrix where \( A_{ij} = 1 \) if \( (i, j) \in \mathcal{E} \). The degree of a vertex is the number of edges emanating from the vertex. The degree distribution is the collection of the degrees of all the nodes in the graph and is an often used statistics to differentiate between different classes of random graphs such as Erdös-Rényi Barábasi-Albert or Watts-Strogatz graphs [9]. There is a one-to-one correspondence between binary, symmetric matrices and unlabeled, undirected graphs, and coding of graphs is therefore equivalent to coding binary, symmetric matrices.

B. Description Length

The description length of the data is the number of bits required to describe the data exactly: the data is turned into a stream of bits, and from this the data should be able to be recovered exactly by a decoder. We are only concerned with the length of the encoding, i.e., the number of bits output be encoder.

The central idea here is that the description length has some relationship with the "meaning" of data. For example, Rissanen considered "useful information" in [10]. More concretely, description length can be used for data analysis. A traditional application, in particular in terms of minimum description length (MDL) [11], has been for model selection in data analysis. The methodology we will develop for graph coding can also be used for model selection for more general data sets. However, we are more interested in description length as a general data processing tool beyond simple model selection. One example is atypicality which is described in Section III.

A central principle of description length is the constraint that a decoder should be able to reconstruct the original data from an (infinite) stream of bits. One manifestation is of course the Kraft inequality [12], but the principle is more general. Since most source coding algorithms are sequential, decodability then means that the decoder can only use past decoded information to decode future data. For graphs, this is much more complicated to satisfy than for sequences. Decodability now becomes an algorithmic constraint rather than a probabilistic one, moving description length theory closer to Kolmogorov complexity [13], [12].

II. CODING

We will base graph coding on the adjacency matrix – due to symmetry, only the lower triangular part has to be coded. However, usually the numbering of nodes is irrelevant. The resulting graph modulo automorphisms is called the structure [4]. Using this in encoding can lead to smaller codelength. Importantly, for data analysis, clearly the structure is more relevant, and description length therefore should be based on the structure.

The adjacency matrix is a binary matrix, and coding this is therefore similar to the problem considered by Steinruecken.
in Table I, which can be used for encoding. Steinruecken considered coding of unordered iid sequences, which we will think of as a matrix. We can state the approach more abstractly as follows: we first sort the rows according to some criterion (e.g., lexicographically). The coding is done on the sorted matrix, and only the sorted matrix is reproduced (exactly) at the receiver. The trick is to sort in such a way that coding of the sorted matrix is more efficient than coding the original matrix. The procedure in Table I is to first sort the sequences lexicographically (with 1 coming before 0). We say that the sequences are grouped: the first group is all sequences, the next two groups are sequences that start with 1/0, which is then subgrouped into sequences starting with 11/10/01/00, see Table I. An efficient code is as follows: we first transmit the number of ones in the first column (the first group). The next column is divided into two groups: those rows that have 1 in the first column, and those that have 0. We transmit the number of ones in each group. When the sequences are iid, the number of ones is binomially distributed, which can be used for encoding. We continue this way (with empty groups not encoded).

This approach can also be applied to adjacency matrices, with the modification that when we permute the rows during sorting, we have to do the same permutation of columns to preserve symmetry. This turns out to be equivalent to the algorithm in Table I, but describing it this way reveals that the approach in Table I is strongly aimed at Erdős-Rényi graphs. From a data analysis point of view, this is problematic. The only parameter the algorithm in Table I is sensitive to is the average node degree \( \bar{k} \) (equivalently \( p \)). Consider anomalous graph detection in terms of atypicality (this is described in more detail in Section III-A): We compare the code length of encoding the graph with a given learned coder and a universal coder. Since the only parameter in Table I is sensitive to \( p \), this corresponds to a hypothesis test of \( p = p_0 \) versus \( p \neq p_0 \). This is not irrelevant, but it is far from what we do with sequences, where we can test a given FSM against the whole class of alternative FSM. Thus, to be effective for data analysis, we need much more effective coders. In the following we will describe two such coders.

### A. Coding Using Degree Distribution

Assume we know the degree distribution \( P(k) \), either from a model, from learning, or from the given graph. How can we take this into account in coding? Consider coding of a given column of the sorted adjacency matrix, as outlined above. Important here is what the decoder already knows, from previous columns: it knows the number of ones above the diagonal, it knows the number of groups \( g \), and it knows the size \( s_i \) of each group; let \( s = \sum_{i=1}^{g} s_i \). We first encode the (total) degree of the node. Call the number of ones above the diagonal \( \tilde{k} \). We can use the coding distribution

\[
P(k|k \geq \tilde{k}) = \frac{P(k)}{\sum_{j=\tilde{k}}^{\infty} P(j)}
\]

The decoder now has encoded the number of new ones (or edges) to encode. The encoder needs to encode which configuration of the \( k - \tilde{k} \) is seen; that is, how many ones \( k_i \) are in each group, subject to the total count being \( k - \tilde{k} \). We assume that every sequence with \( k - \tilde{k} \) ones is equally likely, so calculating the probability of seeing a specific configuration is just a counting problem. In total there are \( \binom{s}{k - \tilde{k}} \) sequences with \( k - \tilde{k} \), and there are \( \binom{s_i}{k_i} \) ways to arrange the \( k_i \) ones in each group. The coding probability of a specific configuration therefore is

\[
\log P = \sum_{i=1}^{g} \left( \frac{s_i}{k_i} \right) + \log \left( \frac{s}{k - \tilde{k}} \right)
\]

A central assumption here is that at time of decoding a given column, the decoder knows the number of ones \( \tilde{k} \) above the diagonal so that it can calculate (1). This is satisfied if the rows and columns are first sorted lexicographically, which can be seen as follows. Suppose \( i \) columns have been coded/decoded. The decoder knows the first \( i \) columns and rows in the (sorted) adjacency matrix; this is clearly possible to reconstruct from the number of ones in each group until column \( i \) and the fact of the sorting. The next row is chosen by the encoder among those among the remaining \( n - i \) columns that has highest sort order based on the first \( i \) columns. No matter which column is chosen, the decoder knows the first \( i \) bits, and therefore the number of ones above the diagonal.

It is not necessary to explicitly sort the adjacency matrix. Instead one can use the same partitioning algorithm from Table I. While not very explicit in the paper, they actually sort the adjacency matrix in the way they choose the next node to encode. It is seen most clearly from Table I. Fig. 3.

### B. Coding of Triangles

Edges are the most fundamental building block of graphs. A more complex building block is triangles, i.e., a cycle graph with three nodes, which is also a 3-clique. Statistics about triangles are often used to characterize graphs [9]. One statistic is the following. Consider three connected nodes \( i \leftrightarrow j \leftrightarrow k \); we let \( p_\triangle \) be the probability that there is also an edge \( i \leftrightarrow k \). We can use this for coding as follows. Let the current node to be coded be node \( i \), and suppose we want to code whether or not there is an edge to node \( k \). We now look for a common neighbor \( j \) of nodes \( (i,k) \) among nodes already coded. If such a node exists, we encode the edge \( i \leftrightarrow k \) using \( p_\triangle \); otherwise, we use \( p \). This can be used together with the structure encoding of Table I. Notice that all groups have exactly the same

|   |   |   |   |
|---|---|---|---|
| 1 | 1 | 1 | ... |
| 1 | 1 | 1 | ... |
| 1 | 1 | 0 | ... |
| 0 | 1 | 1 | ... |
| 0 | 0 | 1 | ... |
| 0 | 0 | 0 | ... |

Table I: Notice that all groups have exactly the same

\[
\begin{align*}
\mathbf{1} & \quad \mathbf{1} & \quad \mathbf{1} & \quad \ldots \\
\mathbf{1} & \quad \mathbf{1} & \quad \mathbf{1} & \quad \ldots \\
\mathbf{1} & \quad \mathbf{1} & \quad \mathbf{0} & \quad \ldots \\
\mathbf{0} & \quad \mathbf{1} & \quad \mathbf{1} & \quad \ldots \\
\mathbf{0} & \quad \mathbf{0} & \quad \mathbf{1} & \quad \ldots \\
\mathbf{0} & \quad \mathbf{0} & \quad \mathbf{0} & \quad \ldots \\
\end{align*}
\]
connections to prior encoded nodes. Thus all the nodes $k \in G$ in a group either has a common previously encoded neighbor with node $i$, or none have. Therefore, they can all be encoded with either $p_\Delta$ or $p$. That is, the number of ones in the group can be encoded with a binomial distribution with probability either $p_\Delta$ or $p$.

C. Calculation and Encoding of Statistics

We consider encoding in two scenarios: learned coding, where we are given a set of training graphs and have to learn the statistics; this statistics is known both by encoder and decoder. Second, universal coding, where the encoder encodes a single graph and also has to communicate to the decoder what is the statistic.

For learned coding, the edge probability $p$ can be estimated straightforwardly as an average. The degree distribution is estimated through a histogram. To estimate $p_\Delta$ is more tricky. We select randomly three connected nodes $i \leftrightarrow j \leftrightarrow k$ and calculate $p_\Delta$ as an average. However, the value of $p_\Delta$ depends on how the nodes are selected. When $p_\Delta$ is used for coding, the triple of nodes is chosen in a specific way. The best estimate is therefore found by performing the coding on the training graphs. Notice that in that case the edges are divided into those coded with the triangle probability $p_\Delta$ and those coded with $p$. However, those edges not (coded) in a triangle could be special. Instead of using the general $p$, we could estimate that $p$ directly; we call this $\hat{p}_\Delta$. In general $p \neq \hat{p}_\Delta$, but in many cases they are very close.

For universal coding, there are two possible approaches, best outlined in [12, Section 13.2]: the encoder can estimate the parameters of the coding distribution and inform the decoder. Or, the coding distribution can be sequentially calculated. For encoding $p$ for iid coding the two approaches are essentially equivalent. The number of bits required to encode the number of ones is about $\log \frac{n(n-1)}{2} \approx 2 \log n$ bits. For the degree distribution, we calculate the degree histogram for the whole graph, and use this for coding. The degree of a node is between 0 and $n$. We can therefore think of the degree histogram as putting each of the $n$ unlabeled nodes into one of $n$ buckets, and encoding this can be done by encoding the counts in the buckets. The number of possible configurations is a standard problem in combinatorics: $\binom{2n-1}{n}$, which can be transmitted with

$$\log \binom{2n-1}{n} = nH\left( \frac{n}{2n-1} \right) + \frac{1}{2} \log \frac{2n-1}{n^2} + c \approx n - \frac{1}{2} \log n$$

bits ($|c| \leq 2$). Of course, there is a relationship between the degrees of nodes in the graph, and if we took this into consideration, it might be possible to encode the degree histogram slightly more efficiently.

For triangle coding, we use sequential estimation of $p_\Delta$ and $\hat{p}_\Delta$, specifically the KT estimator [15], [16], which is

$$\hat{p} = \frac{n_1 + \frac{1}{2} n_0}{n_1 + n_0 + \frac{1}{2}},$$

where $n_1, n_0$ is the number of ones and zeros seen previously. The probabilities $p_\Delta$ and $\hat{p}_\Delta$ are not updated after each bit, but rather after each group is encoded.

D. Numerical Results

Some results can be seen in Fig. 1-3. In all cases, learning was done on 50 graphs prior to coding. For Erdős-Rényi graphs, the iid structure code is most efficient, but all structure codes give about the same codelength. For Barabási-Albert graphs, coding using the degree distribution is most efficient, and for Newman Watts Strogatz graphs [17], using the triangle probability is most efficient. This shows that there is no single efficient code for all graph structures.

We also did some experiments on real-world graphs, both obtained from [18]. For those graphs there is no training, so the universal coding is needed. For both graphs, using degree distribution is most efficient. However, transmitting the degree histogram is expensive, and considering that, the triangle coding is most efficient. In light of this one could consider better ways to represent the degree distribution (e.g., a parametric representation), but we have not explored that.
III. ANOMALY DETECTION

For detecting anomalous graphs, we will use atypicality developed in [19], which is described by

Definition 1. A sequence is atypical if it can be described (coded) with fewer bits in itself rather than using the (optimum) code for typical sequences.

The papers [19], [20] show that atypicality has many desirable theoretical properties and that it works experimentally for sequences. Specifically for anomaly detection, the paper [20] shows that atypicality is (asymptotically) optimum for finite state machine (FSM) We will say that two FSM are distinct if they have no identical classes. Then

Theorem 2 ([20]). Suppose that the typical model is an FSM. Let the atypicality detector be given an anomalous sequence generated by an FSM distinct from the typical FSM. Then as the length of the sequence \( l \to \infty \), the probability of detecting the anomaly converges to 1, while the probability of false alarm converges to 0.

As far as we know, nothing similar has been proven for any other anomaly detection methods.

A. Anomalous Graph Detection

In anomalous graph detection, we are given a set of training graphs \( G_1, \ldots, G_T \), and the problem is then to determine if a given graph \( G \) is anomalous based on the training. We will apply atypicality to this problem. The methodology follows directly from Definition 1. We learn coding of typical graphs, Section II-C and compare this with applying a universal source coder to \( G \). In this paper, we consider unweighted, undirected graphs.

For Erdös-Rényi graphs, atypicality reduces to a hypothesis test of \( \hat{p} = p \) versus \( \hat{p} \neq p \), which is of the form \( |\hat{p} - p| \geq \tau \) for some threshold. There is no reason to use coding, and even coding structure as in [4] does not help: in a test of \( \hat{p} = p \) versus \( \hat{p} \neq p \), the structural decomposition would be the same, only the coding of the resulting bitstreams would be different.

For more complicated classes of random graphs such Barabási-Albert or Watts Strogatz [17], more information can be obtained using the coding algorithms developed in Section II The general procedure is as follows

1) On the set of training graphs, we run all the coding algorithms. For each we learn the values of the parameters (e.g., the histogram) for the algorithm. We choose the coder that gives the shortest code length. The typical coder is now that algorithm with the learned parameters. Both coder and decoder know the values of the parameters, so this does not need to be encoded.

2) On the set of test graphs, we run first the typical coder and obtain the typical code length \( L_T \), then we run all the coding algorithms from Section II to each code length we have to add the overhead of encoding the parameters (e.g., histogram). The atypical code length, \( L_A \), is now the minimum of these code lengths, plus a few bits to tell which coder was the shortest. The atypicality measure is the difference between the atypical code length and the typical code length, \( L_A - L_T \). If \( L_A - L_T < 0 \), or is smaller than some threshold, then following Definition 1 the graph is declared atypical (anomalous).

We tested this procedure by generating various random graphs with \( n = 100 \) nodes.

The typical graphs were generated by using Barabási-Albert graphs model (\( m = 10 \)). We trained on 100 randomly generated graphs. We then generated 500 test graphs each of:

1) Barabási-Albert graphs (\( m = 10 \)) (i.e., typical graphs)

2) Barabási-Albert graphs (\( m = 9 \))

3) Erdös-Rényi graphs (\( p = 0.182 \)), chosen so that the graph has the same average degree as the typical graph.

4) Mixture graph: combination of Barabási-Albert graphs (\( m = 10 \)) and Erdös-Rényi graphs with \( p = 0.5 \); these are essentially Barabási-Albert graphs with extra edges added (\( p \)) to make more triangles.

We then estimated the probability density function (pdf) of the atypicality measure: \( L_A - L_T \). The results are in Fig. 4

We can see that Erdös-Rényi and Barabási-Albert (\( m = 9 \)) test graphs can be easily distinguished from the typical graphs, Barabási-Albert (\( m = 10 \)). Identifying mixture graph from Barabási-Albert (\( m = 10 \)) is more difficult. However, due to the law of large numbers, anomaly detection improves as graph size increases. Figure 5 shows the estimated pdf of atypicality

The threshold has a coding interpretation: it is the number of bits required to tell the decoder an atypical coder is used [19].

![Protein graph](image)

![Power graph](image)

| Procedure | Protein graph | Power graph |
|-----------|---------------|-------------|
| Codelength | Labeled iid | 20513 | 81077 |
|           | iid structure | 8796 | 32013 |
|           | Degree distribution | 7290 | 27651 |
|           | Degree distribution with overhead | 8743 | 32586 |
| Triangle  | 8369 | 26507 |

### Table II

Real-world graphs. The protein graph is the largest connected component of a network of protein interactions in the yeast *Saccharomyces cerevisiae*. The power graph represents the US Western Power Grid.
measures between mixture graph and Barabási-Albert ($m = 10$) for graphs with $n = 400$ nodes; if we choose the threshold to be 305, we get $P_{\text{false alarm}} = P_{\text{miss}} = 2.4\%$.

\begin{figure}[h]
\centering
\includegraphics[width=0.5\textwidth]{fig4.png}
\caption{Pdf of atypicality measure for different types of graphs ($n = 100$). The typical graphs are BA(10), which are used for training.}
\end{figure}

\begin{figure}[h]
\centering
\includegraphics[width=0.5\textwidth]{fig5.png}
\caption{Pdf of atypicality measure for different types of graphs ($n = 400$). The typical graphs are BA(10), which are used for training.}
\end{figure}

IV. CONCLUSIONS AND FUTURE WORK

In this paper we have developed a number of new universal graph coding algorithms. The minimum codelength is found by coding with each algorithm, and then finding the minimum (or weighting as in [21]). However, this still far from the state of the art for sequences, where there a single algorithms such as CTW [16] and Lempel-Ziv [12] that can code sequences with variable complexity. One possibility is to generalize the triangle coding to consider structures of variable complexity, and weight these in an approach similar to CTW.

We have shown that the coding algorithms can be used for graph anomaly detection based on structure alone. We will consider a number of extensions. First, in most graph-based anomaly detection problems, the anomaly is in the data on the graph. Our idea is to combine graph structure coding with coding of the data to get a single measure that takes into account both data and structure. Second, we need to be able to consider graphs of variable size; the complication here is that statistics might very well depend on size. Finally, we will consider detecting anomalous subgraphs.

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