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GraphMDL+: Interleaving the Generation and MDL-based Selection of Graph Patterns

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ABSTRACT
Graph pattern mining algorithms ease graph data analysis by extracting recurring structures. However, classic pattern mining approaches tend to extract too many patterns for human analysis. Recently, the GraphMDL algorithm has been proposed, which reduces the generated pattern set by using the Minimum Description Length (MDL) principle to select a small descriptive subset of patterns. The main drawback of this approach is that it needs to first generate all possible patterns and then sieve through their complete set. In this paper we propose GraphMDL+, an approach based on the same description length definitions as GraphMDL but which tightly interleaves pattern generation and pattern selection (instead of generating all frequent patterns beforehand), and outputs a descriptive set of patterns at any time. Experiments show that our approach takes less time to attain equivalent results to GraphMDL and can attain results that GraphMDL could not attain in feasible time. Our approach also allows for more freedom in the pattern and data shapes, since it is not tied to an external approach.

KEYWORDS
Pattern Mining, Graph Mining, Minimum Description Length

1 INTRODUCTION
Labeled graphs offer a powerful data representation in many fields. For example, in chemistry, molecules can be represented as graphs where vertices are atoms, and edges are bonds; in linguistics, sentences can be represented as graphs where words are atom tokens, and edges are dependency relationships; in the semantic web, knowledge is represented as graphs where vertices are entities and edges are semantic relationships. Extracting knowledge from graph datasets is desirable but difficult due to the complexity of analyzing graphs, and to the large size of datasets (either large single graphs, or large collections of small graphs). To support knowledge extraction from graphs, there has been a number of proposals for graph pattern mining, i.e. for extracting frequent structures in graph datasets [10, 14].

A well-known issue of pattern mining is the large number of patterns that are extracted. Several kinds of approaches have been proposed to tackle this problem (e.g., constraint based approaches [16] or condensed representation [15]). Among them, the methods based on the Minimum Description Length (MDL) principle demonstrated that it is possible to drastically reduce the number of patterns by selecting a small set of descriptive patterns among all the generated patterns [4, 5, 8, 12, 13]. The MDL principle [6] comes from information theory, and states that the model that describes the data the best is the one that compresses the data the best, i.e. which yields the shortest description length. Few MDL-based approaches have been proposed for graphs. SUBDUE [3] iteratively compresses a graph by replacing each occurrence of a pattern by a single vertex, which entails a loss of information. VoG [9] summarizes graphs as a composition of predefined families of patterns (e.g., paths, stars) which restricts the type of patterns that can be extracted. Another limitation is that VoG works on unlabeled graphs only. GraphMDL [1] is a recent approach that works on labeled graphs, and leverages the MDL principle to select graph patterns. Contrary to SUBDUE, it ensures that there is no loss of information thanks to the introduction of the notion of ports associated to graph patterns. Ports represent how adjacent occurrences of patterns are connected. GraphMDL is a two-phase method. First, a large collection of patterns is generated by a graph miner like gSpan [14] or Gaston [10]. Second, it iterates through all generated patterns in order to select a small subset of descriptive patterns. This two-phase method has several drawbacks. The combinatorial number of patterns in graphs entails a high computational cost for both the generation phase and the selection phase. In addition, to mitigate the computational cost, during the generation phase a minimum support has sometimes to be set at a higher value than desired, so that possibly useful patterns are overlooked.

In this paper we propose the GraphMDL+ approach to tackle those limitations. In MDL-based pattern mining, GraphMDL+ is to GraphMDL on graph patterns as Slim [11] is to Krimp [13] on itemsets. In other words, GraphMDL+ uses the same description length definitions as GraphMDL but tightly interleaves pattern generation and pattern selection (instead of generating all frequent patterns beforehand). As a positive consequence, it becomes an anytime approach.
that can output a descriptive set of patterns whenever the user desires so. Another benefit is to free from the limits of graph miners about the nature of graphs (e.g., directed vs undirected) and patterns (e.g., exactly one label on each vertex), and hence recover patterns that were excluded. For the sake of tractability, we propose a heuristic to rank the candidate patterns at each generation step. In addition, we present and assess a refinement of GraphMDL+ that exploits graph automorphisms, i.e., symmetries that exist in graph patterns, in order to reduce description length further. We conducted experiments on four different datasets to validate our approach, in particular we show that it takes less time and can attain results that GraphMDL could not attain in reasonable time.

2 PRELIMINARIES

In this section we first recall the MDL principle (Section 2.1). We then give graph definitions that are useful for this paper (Section 2.2). Finally, we present the concepts from GraphMDL [1] that are used in the following (Section 2.3).

2.1 The MDL Principle

The Minimum Description Length (MDL) principle [6] is a technique from information theory that allows to select the model, from a family of models, that best describes some data. In practice, MDL states that the model M that best describes some data D is the one that minimizes the description length, \( L(M, D) = L(M) + L(D|M) \), where \( L(M) \) is the description length of the model and \( L(D|M) \) the description length of the data encoded with the model. Since description lengths are often expressed in bits of information, MDL gives the way the graph model is used as a composition of pattern embeddings, where patterns are taken from the graph model. The way the graph model is used to compress the data graph is made explicit by a structure called the rewritten graph. We now walk through the creation of such a structure, which is shown in Fig. 4. Fig. 4a represents the graph model as a list of patterns. Those patterns are considered top to bottom\(^1\): for each one, its embeddings in the data (in this case the graph of Fig. 1) are computed. Not all embeddings are retained: for an embedding to be retained its edges must not overlap with edges of previously-chosen embeddings (be they of the same pattern or a different one). Fig. 4b shows the retained embeddings. Each of those embeddings generates what is called an embedding vertex in the rewritten graph. Each embedding vertex indicates that in the data there is an occurrence of the pattern corresponding to its label. Note that the embeddings overlap on some vertices: these are what GraphMDL calls port vertices. Port vertices are represented in the rewritten graph as well. Lastly, an embedding vertex is connected to a port vertex in the rewritten graph if that specific embedding uses that specific port: the label of the edge connecting them indicates which of the pattern’s ports is mapped to that vertex. Fig. 4c shows the rewritten graph which results from the embeddings of Fig. 4b. GraphMDL+ associates a description length to a

\[ L(G^P) + L(G^D) \]

Definition 2.2. Let \( G^P \) and \( G^D \) be graphs. An embedding (or occurrence) of \( G^P \) (the pattern) in \( G^D \) (the data) is an injective function \( \varepsilon \in V^P \to V^D \) such that: (1) \( \varepsilon^{-1}(v) \subseteq \varepsilon(v) \) for all \( v \in V^P \); (2) \( (\varepsilon(u), \varepsilon(v)) \in E^D \) for all \( (u, v) \in E^P \); and (3) \( \varepsilon^{-1}(\varepsilon(e)) = \varepsilon(e) \) for all \( e \in E^P \).

Fig. 2 shows the three embeddings (\( \varepsilon_1 \) in green, \( \varepsilon_2 \) in red, and \( \varepsilon_3 \) in blue) of a simple pattern (with 2 vertices and one edge) in the graph of Figure 1.

2.3 GraphMDL

GraphMDL takes two inputs: the graph dataset and a set of candidate patterns, and then outputs a subset of the candidate pattern set which yields the smallest possible description length. GraphMDL+ borrows five notions from GraphMDL: graph model, rewritten graph, ports, code table, and description length definitions. We recall those five notions in this section.

Graph model. The model, in the MDL sense, used to compress graph datasets in GraphMDL is a list of graph patterns, selected from the candidate patterns received as input. The simplest patterns handled by GraphMDL are called singletons. A vertex singleton pattern has one vertex with exactly one label, an edge singleton pattern has two vertices without label, connected by an edge (with a label). Fig. 3 shows an example of each type of singleton pattern. Singleton patterns can be seen as “building blocks” for other patterns: e.g. the pattern of Fig. 2 is the union of singleton vertex pattern \( Z \) and singleton edge pattern \( b \).

Rewritten graph and ports. The intuition behind GraphMDL is that a data graph can be encoded and compressed as a composition of pattern embeddings, where patterns are taken from the graph model. The way the graph model is used to compress the data graph is made explicit by a structure called the rewritten graph. We now walk through the creation of such a structure, which is shown in Fig. 4. Fig. 4a represents the graph model as a list of patterns. Those patterns are considered top to bottom\(^1\): for each one, its embeddings in the data (in this case the graph of Fig. 1) are computed. Not all embeddings are retained: for an embedding to be retained its edges must not overlap with edges of previously-chosen embeddings (be they of the same pattern or a different one). Fig. 4b shows the retained embeddings. Each of those embeddings generates what is called an embedding vertex in the rewritten graph. Each embedding vertex indicates that in the data there is an occurrence of the pattern corresponding to its label. Note that the embeddings overlap on some vertices: these are what GraphMDL calls port vertices. Port vertices are represented in the rewritten graph as well. Lastly, an embedding vertex is connected to a port vertex in the rewritten graph if that specific embedding uses that specific port: the label of the edge connecting them indicates which of the pattern’s ports is mapped to that vertex. Fig. 4c shows the rewritten graph which results from the embeddings of Fig. 4b. GraphMDL+ associates a description length to a

\[ L(G^P) + L(G^D) \]

\(^1\)The order of patterns is determined by a heuristic, as detailed in [1]
rewritten graph. This numerical value corresponds to the $L(D|M)$ term of the MDL formula and is used to evaluate the “complexity” of the rewritten graph.

**Description length definitions.** The definition of $L(M,D)$ is decomposed into the definitions of $L(M)$, the description length of a code table, and of $L(D|M)$, the description length of a rewritten graph. Each definition boils down to a sum of code lengths. Those code lengths are determined according to different distributions depending on the symbols to encode. Vertex and edge labels are encoded according to their distribution in the data graph, patterns and ports are encoded according to their usage in the rewritten graph, and standard encodings are used for various integers (e.g., number of vertices). The detailed definitions of those description lengths are available in [1].

### 3 GRAPHMDL+:: INTERLEAVING GENERATION AND SELECTION

In this section we present our approach, GraphMDL+. The key contribution of GraphMDL+ is to define a way to interleave pattern generation and pattern selection. Instead of using an external independent pattern generation algorithm, patterns are generated during the selection process. The idea is to generate candidate patterns that may be a good addition to the code table, and yield a better description length.

In this section, first we present the approach informally (Section 3.1). We then introduce the definition of candidates (Section 3.2) and how their compression capability is estimated in order to rank them (Section 3.3). Finally, the complete algorithm of GraphMDL+ is given (Section 3.4) with its extension that handles graph automorphisms (Section 3.5).

#### 3.1 A Sketch of GraphMDL+

We base the candidate generation around GraphMDL’s notion of rewritten graph: given a code table, the rewritten graph represents how the algorithm uses the patterns in the code table to encode the data. Our intuition is to take the rewritten graph and observe which patterns appear frequently together: two patterns appear together if some of their embeddings share at least one port vertex of the rewritten graph. If two patterns appear frequently together, we merge them to create a larger pattern covering their common occurrences. The shared ports may then become internal vertices of the larger pattern, and hence not ports anymore.

Every time two patterns are merged, the resulting pattern is added to the code table and this new code table is again used to encode the data: if the description length of the new
At the same time, they induce a higher description length. The intuition behind vertices, candidates, and therefore can be generated by successive merges through patterns (describing a single edge or a single vertex label). A candidate represents the vertices of each pattern that are to be merged. This would allow to describe both patterns, merging their vertices $v_A$ and $v_B$, to the same data vertex $v_D$. The intuition behind GraphMDL+ is to say that it may be interesting to merge $P_A$ and $P_B$, merging their vertices $v_A$ and $v_B$. This would allow to describe with a single pattern all those parts of the data where there is an embedding of $P_A$ and an embedding of $P_B$ mapping their respective vertices $v_A$ and $v_B$ on the same data vertex. The structure describing this possible merge of two patterns is called a candidate:

**Definition 3.1.** A candidate $C = < P_A, P_B, \Pi >$ is composed of two patterns, $P_A$ and $P_B$, and a non-empty set of port tuples $\Pi = \{ (\pi_{A,1}, \pi_{B,1}), (\pi_{A,2}, \pi_{B,2}), \ldots \}$ that represents the vertices of each pattern that are to be merged together to form the new pattern.

**Definition 3.2.** A candidate $< P_A, P_B, \{(\pi_{A,1}, \pi_{B,1}), \ldots\} >$ is symmetric if and only if it is equal to $< P_B, P_A, \{(\pi_{B,1}, \pi_{A,1}), \ldots\} >$.

Fig. 5 shows what it means to merge two patterns $P_A$ and $P_B$ following a candidate, by showing the resulting merged pattern for three different candidates. The last one is symmetric.

Note that any pattern can be decomposed into singleton patterns (describing a single edge or a single vertex label) and therefore can be generated by successive merges through candidates.

### 3.3 Candidate Ranking

On a given rewritten graph, many candidates can be generated. A choice has to be made about which one to consider first for insertion into the list of selected patterns (a.k.a. the code table). A naive approach may be to try them all separately and rank them based on how much the description length lowers when they are inserted in the code table, in order to choose the one that improves the description length the most. However such an approach would be computationally expensive because it implies recomputing the MDL encoding of the data for each candidate, which is an expensive operation. In this section we present the heuristic that GraphMDL+ uses to rank candidates without needing to compute the exact description length gain that they give. This heuristic is evaluated experimentally in Section 4.2.

Our intuition is to select the candidate that is expected to be used the most in the MDL encoding of the data. Remember that the more frequently something appears in the data, the more interesting it tends to be according to MDL. We estimate the usage of a candidate $C = < P_A, P_B, \Pi >$ by looking at the number of embeddings of $P_A$ and $P_B$ that participate to the candidate in the rewritten graph. For example, if there are 3 embeddings of each pattern, we can reasonably expect the candidate to be used at least 3 times. However, if there are only 2 embeddings of $P_A$ versus 3 of $P_B$, it means that two embeddings of $P_B$ share the same embedding of $P_A$. In that case, we take the smaller of the two counts, because embeddings are not allowed to overlap.

We call this measure the usage estimate of the candidate. It is similar to the minimum image based support proposed in [2]. To break equalities, we compute for each candidate its number of exclusive ports: the rewritten graph port vertices around which only the two patterns of the candidate are present. Those ports will disappear since they are completely covered by the candidate, and since ports increase the description length of the rewritten graph, we favor candidates that eliminate more of them. To further break equalities, we compute the description length of the pattern resulting from the candidate: we consider first the candidate with the smallest description length, because from an MDL point of view it is the “simplest”.

**Special cases of usage estimation.** There are some special cases in which the general formula for estimating the usage of a candidate needs to be adapted. If one of the two patterns does not have edges (i.e. it only has one vertex), its number of embeddings is not a limiting factor to the number of embeddings of the candidate. This is because GraphMDL+ only forbids edge overlaps, and does not forbid multiple patterns to describe the same vertex labels. In that case, the usage estimate of the candidate is the number of embeddings of the other pattern. If both patterns do not have edges, the

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2The exact number depends on the position that the generated pattern will have in the code table. The higher the pattern is in the code table, the more its embeddings have a chance of being retained (See Section 2.3). In order to know the exact number of retained embeddings, the full rewritten graph would have to be recomputed.
usage estimate of the candidate is the number of embeddings—that participate to the candidate—of any of the two (both patterns will have the same number).

If a candidate is symmetric (see Def. 3.2), it means that embeddings of $P_A$ can count as embeddings of $P_B$ and conversely. In that case, we aggregate the embeddings of both patterns and take as usage estimate half their number (rounded down). We need to take half the number of embeddings, because the candidate merges the patterns two by two.

We summarise the computation of the usage estimate as follows:

- if the candidate is symmetric, combine embeddings of the two patterns. Usage estimate is half the size of the resulting set;
- otherwise, if one of the patterns does not have edges, usage estimate is the number of embeddings of the other pattern;
- otherwise, usage estimate is the number of embedding of the pattern that has less embeddings.

Fig. 6 shows a rewritten graph and the candidates that can be generated from it, along with their usage estimate and number of exclusive ports. For example, the first line of the table shows the general case, in which pattern $P_1$ and pattern $P_2$ are connected through the vertex 2 of $P_1$ and the vertex 1 of $P_2$. There are three embeddings of each pattern that take part in this candidate (they are around the topmost port vertex). Therefore, the usage estimate of the candidate is 3.

The candidate on the second line is symmetric: it describes an embedding of $P_1$ connected to another embedding of $P_1$, through the vertex 1 of both. Two embeddings of $P_1$ take part in this candidate (embeddings $c$ and $d$). Each of them could be both an embedding of the first pattern of the candidate and the second. Therefore we aggregate the two embeddings and take half their number as usage estimate. Also, these embeddings are the only embeddings around the leftmost port vertex, so this candidate has an exclusive port. Finally, the fourth line describes the last case: an embedding of $P_1$ connected to an embedding of $P_3$, which is a pattern that has no edges. In this case, only the number of embeddings of $P_1$ that participate to the candidate (i.e. embedding $d$) is considered for the usage estimate.

### 3.4 The GraphMDL+ Algorithm

The GraphMDL+ algorithm is presented in Alg. 1. The code table is initialised with the code table containing all singleton patterns (line 1). At each iteration, from the current code table, GraphMDL+ generates the associated rewritten graph (line 5). Then (lines 6-7), the rewritten graph is parsed, and for each pair of embeddings that share at least a port, a candidate is generated. The most interesting candidate w.r.t. usage estimate (see Section 3.3) is added to the code table (line 9). If this new code table lowers the MDL description length, a new iteration is done with the new code table (line 11). Otherwise, the candidate is removed from the code table and the next candidate is tested. When all candidates from the current rewritten graph have been tested without any of them yielding a better description length, the program exits returning the best code table found (line 14).

An interesting aspect of the GraphMDL+ algorithm is that it can be interrupted whenever the user desires so, since it can just return the best code table found so far. This makes GraphMDL+ an anytime algorithm, and effectively a parameter-less one as well, since the only input it needs is the data graph.

### 3.5 Handling Automorphisms

A peculiar characteristic of graphs w.r.t. other types of data (e.g. itemsets, sequences) is that different graphs can be related by isomorphisms and automorphisms [7].

**Definition 3.3.** Let $G = (V, E, l_V, l_E)$ and $G' = (V', E', l_{V'}', l_{E'})$ be two graphs. $G$ and $G'$ are said to be isomorphic, if there exists a bijection $\gamma \in V \mapsto V'$, called an isomorphism, such that:

1. $(u, v) \in E \iff (\gamma(u), \gamma(v)) \in E'$;
2. $l_E(v) = l_{E'}(\gamma(v))$ for all $v \in V$; and
3. $l_E(e) = l_{E'}(\gamma(e))$ for all $e \in E$.

An isomorphism between a graph and itself is called an automorphism.

An automorphism can be seen as an alternative numbering of the vertices of a graph, and exhibits symmetries in the graph structure. For example, in the graph of Fig. 7 the vertices 1 and 4 are completely equivalent: exchanging them does not change the structure of the graph. The same happens for vertices 3 and 5. All the possible configurations issued by exchanging those pairs of vertices (listed in the table) are called the automorphisms of the graph. We integrate in GraphMDL+ the bliss algorithm [7] for the computation of all automorphisms of a labeled graph. It is important for a graph mining algorithm to handle automorphisms as otherwise it may consider several graphs or vertices as different whereas they are—in fact—equivalent. For example, let $P_A$ be a pattern that has two vertices, $v_1$ and $v_2$, that are equivalent under automorphism. If GraphMDL+ did not detect this automorphism, it would consider

<table>
<thead>
<tr>
<th>Algorithm 1 The GraphMDL+ algorithm</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Require:</strong> A data graph $D$</td>
</tr>
<tr>
<td>1: $CT \leftarrow$ singleton-only code table</td>
</tr>
<tr>
<td>2: <strong>return</strong> GraphMDL+Iteration($D$, $CT$)</td>
</tr>
<tr>
<td>3:</td>
</tr>
<tr>
<td>4: <strong>function</strong> GraphMDL+Iteration($D$, $CT$)</td>
</tr>
<tr>
<td>5: $G' \leftarrow$ rewritten graph from $D$ and $CT$</td>
</tr>
<tr>
<td>6: $C \leftarrow$ candidates generated from $G'$ * See Sec. 3.2</td>
</tr>
<tr>
<td>7: Sort $C$ by usage estimate * See Sec. 3.3</td>
</tr>
<tr>
<td>8: for all $C \in C$ do</td>
</tr>
<tr>
<td>9: $CT' \leftarrow CT \cup C$</td>
</tr>
<tr>
<td>10: if $L(CT', D) &lt; L(CT, D)$ then</td>
</tr>
<tr>
<td>11: <strong>return</strong> GraphMDL+Iteration($D$, $CT'$)</td>
</tr>
<tr>
<td>12: end if</td>
</tr>
<tr>
<td>13: end for</td>
</tr>
<tr>
<td>14: <strong>return</strong> $CT$</td>
</tr>
<tr>
<td>15: end function</td>
</tr>
</tbody>
</table>
that candidate \(< P_A, P_B, \{(v_1, v_3)\} >\) is different from candidate \(< P_A, P_B, \{(v_2, v_3)\} >\), whereas they are—in fact—the same. This would lead to underestimating the usage of that candidate.

Another instance where handling automorphisms is important is in the description length computation. A pattern with many ports has a higher description length than with few ports. If two vertices are equivalent under automorphism, the same. This would lead to underestimating the usage of that candidate.

4 EXPERIMENTAL EVALUATION

In this section we present a quantitative evaluation of GraphMDL and GraphMDL+ we ran some experiments, allowing each experiment 4 hours maximum runtime. For GraphMDL, we chose a gSpan support as low as possible that would yield a set of candidate patterns which could be treated within the given time limit. The gSpan runtime is not included in the GraphMDL runtime. One first observation that we made while running these experiments is that it is difficult to control the runtime of GraphMDL; a small change in gSpan support can drastically change the number of candidates generated and therefore the GraphMDL runtime. On the

**Table 1: Characteristics of the datasets in experiments.**

<table>
<thead>
<tr>
<th>Dataset</th>
<th>Graph count</th>
<th>Vertices</th>
<th>Edges</th>
<th>Vertex labels</th>
<th>Edge labels</th>
</tr>
</thead>
<tbody>
<tr>
<td>AIDS-CA</td>
<td>123</td>
<td>17k</td>
<td>18k</td>
<td>21</td>
<td>3</td>
</tr>
<tr>
<td>AIDS-CM</td>
<td>1082</td>
<td>34k</td>
<td>37k</td>
<td>26</td>
<td>3</td>
</tr>
<tr>
<td>Mutag</td>
<td>125</td>
<td>2k</td>
<td>3k</td>
<td>7</td>
<td>4</td>
</tr>
<tr>
<td>PTC-FM</td>
<td>143</td>
<td>2k</td>
<td>2k</td>
<td>18</td>
<td>4</td>
</tr>
<tr>
<td>PTC-FR</td>
<td>121</td>
<td>2k</td>
<td>2k</td>
<td>19</td>
<td>4</td>
</tr>
<tr>
<td>PTC-MM</td>
<td>129</td>
<td>2k</td>
<td>2k</td>
<td>20</td>
<td>4</td>
</tr>
<tr>
<td>PTC-MR</td>
<td>152</td>
<td>2k</td>
<td>2k</td>
<td>18</td>
<td>4</td>
</tr>
<tr>
<td>UD-PUD-En</td>
<td>1000</td>
<td>21k</td>
<td>20k</td>
<td>17</td>
<td>46</td>
</tr>
</tbody>
</table>

**Settings.** We have developed a prototype of GraphMDL+ in Java 1.8, available as a git repository. We conducted the experiments on four different datasets (some of them having several sub-datasets). The AIDS dataset (AIDS-CA and AIDS-CM), Mutag, and PTC datasets (PTC-FM, PTC-FR, PTC-MM and PTC-MR) datasets are molecular datasets, where vertices are atoms and edges are bonds. These datasets have few labels and many cycles. The UD-PUD-En dataset is from the Universal Dependencies project. Each graph of the dataset represents a sentence: vertices are words, vertex labels are POS tags, and edge labels are dependency relationships. This dataset has many labels and no cycles. For datasets that have both a positive and a negative class, only the positive class was used for the evaluation. The characteristics of the used datasets are presented in Table 1.

GraphMDL needs an external approach to generate the candidate patterns that it filters. We used the algorithm gSpan for that task. This approach needs a support parameter: the lower the support, the less frequent the generated patterns can be (and therefore the more there are). We used the lowest value possible which allowed to terminate the experiments in a reasonable amount of time.

All experiments were conducted with a RAM limit of 10Gb on a laptop with an Intel Core i7-7600U@2.80Ghz cpu.

4.1 Comparison with GraphMDL

In order to compare the performances of GraphMDL and GraphMDL+ we ran some experiments, allowing each experiment a 4-hour maximum runtime. For GraphMDL, we chose a gSpan support as low as possible that would yield a set of candidate patterns which could be treated within the given time limit. The gSpan runtime is not included in the GraphMDL runtime. One first observation that we made while running these experiments is that it is difficult to control the runtime of GraphMDL; a small change in gSpan support can drastically change the number of candidates generated and therefore the GraphMDL runtime. On the

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3https://gitlab.inria.fr/Ibariatt/graphmdl/
4https://gitlab.inria.fr/Ibariatt/graphmdl/
5https://wiki.nci.nih.gov/display/NCIDTPdata/AIDS+Antiviral+/Screen+Data
6http://networkrepository.com/Mutag.php
7http://networkrepository.com/PTC-FM.php (also replace FM with FR, MM or MR)
8https://universaldependencies.org/
9https://sites.cs.ucsb.edu/~xyan/software/gSpan.htm
Table 2: Comparison of GraphMDL and GraphMDL+ results. $L\%$ is the ratio between the description length of the found code table and the singleton-only code table. $|CT|$ is the number of patterns in the code table found by the algorithm.

<table>
<thead>
<tr>
<th>Dataset</th>
<th>GraphMDL for best $L%$</th>
<th>GraphMDL+ for $L% \leq L_1$</th>
<th>GraphMDL+ for best $L%$</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>$L_1 \approx \text{best } L%$</td>
<td>time</td>
<td>$</td>
</tr>
<tr>
<td>AIDS-CA</td>
<td>19.15%</td>
<td>1h51m</td>
<td>148</td>
</tr>
<tr>
<td>AIDS-CM</td>
<td>20.71%</td>
<td>2h50m</td>
<td>212</td>
</tr>
<tr>
<td>Mutag</td>
<td>15.42%</td>
<td>2h38m</td>
<td>29</td>
</tr>
<tr>
<td>PTC-FM</td>
<td>22.87%</td>
<td>1h42m</td>
<td>77</td>
</tr>
<tr>
<td>PTC-FR</td>
<td>23.35%</td>
<td>2h54m</td>
<td>70</td>
</tr>
<tr>
<td>PTC-MM</td>
<td>23.65%</td>
<td>2h09m</td>
<td>75</td>
</tr>
<tr>
<td>PTC-MR</td>
<td>23.09%</td>
<td>1h43m</td>
<td>78</td>
</tr>
<tr>
<td>UD-PUD-En (undir.)</td>
<td>26.84%</td>
<td>1h41m</td>
<td>647</td>
</tr>
</tbody>
</table>

opposite, since GraphMDL+ is an anytime algorithm, it can be easily stopped at a chosen time limit. Table 2 presents the results of these experiments. For each dataset we present the description length of the best code table found by GraphMDL (as a percentage of the length of a singleton-only code table), the time it took to find it, and the number of patterns it contains. We then present the time it takes GraphMDL+ to find a code table with an equivalent description length and the number of patterns in that code table. Finally we present the description length of the best code table that can be found by GraphMDL+ within the given time limit, the time it took to find it, and the number of patterns it contains.

We observe that GraphMDL+ manages in all cases to find a code table resulting in the same description length and a similar amount of patterns (between -29% and +14%) than GraphMDL. It does so in significantly less time. For instance, for the UD-PUD-En dataset, GraphMDL+ only takes 3 minutes to reach the same description length than GraphMDL, which takes 1h41m. We attribute this to the fact that the latter needs to process all candidate patterns, and most of them will not be useful for decreasing the description length (since they are generated by an external approach with no knowledge of the MDL principle), while the former generates less candidates of higher quality for an MDL approach. A consequence of this speed increase is that GraphMDL+ can find code tables that have a description length even lower than the best ones found by GraphMDL. For instance, for the Mutag dataset, the best description length computed by GraphMDL is 15.42% whereas the best description length computed by GraphMDL+ is 10.73%. We think that given enough time and candidate patterns, GraphMDL would eventually find those code tables, but in such a long time that it would impair the practicality of the approach. Note that for most experiments the GraphMDL+ algorithm was not actually stopped at the 4 hours time limit, but completed before. This is because it reached a rewritten graph where no candidate improved the description length (see Section 3.4). The number of patterns selected for the best GraphMDL+ code table is higher, but remains significantly smaller than gSpan’s (at least 10k on all datasets).
4.2 Candidate Ranking Heuristic Evaluation

In Section 3.3 we give a heuristic (the usage estimate) that GraphMDL+ uses to choose which candidate to test first for inclusion in the code table (line 7 in Alg. 1). In order to evaluate this heuristic, we ran three versions of GraphMDL+ which used different candidate ranking functions. The “test all candidates” version sorts all possible candidates by the actual description length gain, which is costly to compute. The “random ranking” version randomly sorts the candidates. The “GraphMDL+ ranking” version sorts the candidates using the usage estimate heuristic. All versions after ranking the candidates then proceed through the list and select the first candidate that when added to the code table produces a description length which is better than the current best one (See Section 3.4). This experiment does not question the greedy approach of GraphMDL+, but evaluates the heuristic that guides this approach.

Fig. 8 and Fig. 9 show the results of this experiment on the AIDS-CA dataset. Results on the other datasets follow the same behaviour. We stopped the “test all” version after 18 hours, the others terminated. We observe in Fig. 8 that testing all candidates takes a significant amount of time and that a heuristic is needed in order for the approach to complete in a reasonable amount of time. The ranking that we propose is the fastest approach of the three, faster even than the random ranking. We assume that the cost of computing the usage estimate is negligible (it can be computed during the candidate generation phase), and the proposed candidates are efficient in reducing the description length. We observe in Fig. 9 that the “test all” version always selects the candidate that improves the description length the most, as expected. The ranking that we propose is close to it, meaning that it is a good approximation of the exact gain given by each candidate. The random ranking is the worst from this point of view, as expected, which has the consequence of needing to test more candidates in order to converge to similar description lengths as our ranking, since candidates improve less.

In conclusion this experiment shows that a heuristic is needed in order for GraphMDL+ to complete in a reasonable time, and that the one that we propose in Section 3.3 is both fast and efficient in finding good candidates.

4.3 Advantages of Controlling Generation

Since GraphMDL+ directly controls the generation of patterns, it has more freedom than GraphMDL over the shape of patterns.

Patterns without labels. GraphMDL allows for vertices to have any number of labels, including none, however gSpan requires each vertex to have exactly one label, which means that when GraphMDL is used to select between patterns generated by gSpan, it can only select patterns which have a label on each vertex. GraphMDL+ does not have this limitation. Fig. 10 shows one of the patterns extracted by GraphMDL+ on the UD-PUD-En dataset: this pattern can be interpreted as “an adverb that is the adverbial modifier of something”. Since its second vertex does not have a label, it can be anything. And in fact, this pattern is used by GraphMDL+ for describing adverbial modifiers of many different entities: nouns, auxiliaries, determiners, pronouns, etc. GraphMDL (coupled with gSpan) could not have such a pattern and would instead have more specific patterns such as “an adverb that is the adverbial modifier of a noun”, “…of an auxiliary”, “…of a pronoun”, etc. Having the control over the pattern generation step gives to GraphMDL+ a greater generalisation power.

Directed graphs. GraphMDL has the potential to handle directed graph patterns. However graph pattern mining algorithms that can handle directed graphs are rare in the literature, which makes it difficult to apply GraphMDL on directed sources of data. While it is possible to interpret a directed graph as undirected, doing so removes part of the information from the generated patterns and can therefore hinder the interpretation for the users of GraphMDL. GraphMDL+ does not have this limitation, since it directly controls the pattern generation.

Handling automorphisms. Fig. 11 shows one of the patterns extracted by GraphMDL+ on the AIDS-CA dataset. This pattern is a benzene cycle, and has many automorphisms that reflect the rotation and mirror symmetries: every vertex is equivalent to every other. Table 3 shows what is the usage of each port and its associated code length when automorphisms are handled —as in GraphMDL+— (on the left) and what those port usages and code lengths would be if the approach did not handle automorphisms (on the right). Every time
Table 4: Difference in description length given by the best code table found by GraphMDL+ with and without automorphisms (4 hours maximum runtime).

<table>
<thead>
<tr>
<th>Dataset</th>
<th>Without automorphisms</th>
<th>With automorphisms</th>
<th>Ratio without / standard</th>
</tr>
</thead>
<tbody>
<tr>
<td>AIDS-CA</td>
<td>11191 bits</td>
<td>107207 bits</td>
<td>1.037</td>
</tr>
<tr>
<td>AIDS-CM</td>
<td>287482 bits</td>
<td>267101 bits</td>
<td>1.001</td>
</tr>
<tr>
<td>Mutag</td>
<td>12756 bits</td>
<td>12388 bits</td>
<td>1.030</td>
</tr>
<tr>
<td>PTC-FM</td>
<td>17905 bits</td>
<td>17900 bits</td>
<td>1.000</td>
</tr>
<tr>
<td>PTC-FR</td>
<td>16088 bits</td>
<td>16704 bits</td>
<td>1.017</td>
</tr>
<tr>
<td>PTC-MM</td>
<td>16191 bits</td>
<td>16215 bits</td>
<td>0.999</td>
</tr>
<tr>
<td>PTC-MR</td>
<td>19582 bits</td>
<td>19509 bits</td>
<td>1.004</td>
</tr>
<tr>
<td>UD-PUD-En</td>
<td>298812 bits</td>
<td>299073 bits</td>
<td>1.001</td>
</tr>
</tbody>
</table>

In order to analyze the impact of handling automorphisms on the performances of GraphMDL+, we ran some experiments with and without it. Table 4 presents the description length attained by the best code table found by the algorithm on each dataset for a maximum runtime of 4h. We observe that the impact of handling automorphisms is quantitatively small but positive. Indeed, the resulting description length without it is increased by 4% and 3% in AIDS-CA and Mutag respectively, and not significantly changed for the other datasets. From a qualitative point of view, handling automorphisms gives a guarantee that GraphMDL+ will not consider as different patterns or vertices that are actually equal.

5 CONCLUSION

In this paper we propose GraphMDL+, an MDL-based graph pattern mining approach that generates and selects a descriptive set of graph patterns from labeled graphs. GraphMDL+ tightly interleaves pattern generation and selection to quickly generate descriptive patterns in an anytime manner. Our experiments show that GraphMDL+ is faster than its main competitor, GraphMDL, and can extract patterns that attain better description lengths. Additionally, the handling of automorphisms allows to precisely detect whether two patterns or vertices are equivalent. Thanks to the control that GraphMDL+ gives to the pattern generation, we plan to extend this approach to other kinds of graph datasets, e.g. knowledge graphs, which are directed multi-graphs.

REFERENCES

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