

Efficiently Enumerating Minimal Triangulations

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ABSTRACT

We present an algorithm that enumerates all the minimal triangulations of a graph in incremental polynomial time. Consequently, we get an algorithm for enumerating all the proper tree decompositions, in incremental polynomial time, where “proper” means that the tree decomposition cannot be improved by removing or splitting a bag. The algorithm can incorporate any method for (ordinary, single result) triangulation or tree decomposition, and can serve as an anytime algorithm to improve such a method. We describe an extensive experimental study of an implementation on real data from different fields. Our experiments show that the algorithm improves upon central quality measures over the underlying tree decompositions, and is able to produce a large number of high-quality decompositions.

Keywords

Minimal triangulation; Tree decomposition; Enumeration algorithm; Minimal separators; Maximal independent sets; Maximal cliques

1. INTRODUCTION

Many intractable computational problems on graphs admit tractable algorithms when applied to trees or forests. A *tree decomposition* extracts a tree structure from a graph by grouping nodes into *bags* (each treated as a single node). The corresponding operation on hypergraphs is that of a *generalized hypertree decomposition* [16] that consists of a tree decomposition of the *primal* graph (which has the same set of nodes, and an edge between every two hyperedge neighbors), and an assignment of hyperedge labels (edge covers) to the tree nodes [17]. Tree decompositions and generalized hypertree decompositions have a plethora of applications, including optimization of (multi)join queries in databases [16, 24, 37], containment of database queries, constraint satisfaction problems [27], prediction of RNA secondary structure [40], computation of Nash equilibria in

games [16], inference in probabilistic graphical models [29], and weighted model counting [25].

Past research has focused on obtaining a “good” tree decompositions, where goodness is typically by means of the *width* [34]—the maximal cardinality of a bag (minus one). Nevertheless, finding a tree decomposition of the minimal width is NP-hard [2], as is the case for other common measures of goodness for tree decompositions such as *fill* [39], and in the case of hypergraphs *hypertree width* [18], *generalized hypertree width* [19], and *fractional hypertree width* [30]. Therefore, heuristic algorithms are often applied [3, 5]. The different measures of goodness are motivated by the fact that the needs of different applications are often different from (though related to) the width. Additional examples are the complexity of weighted model counting, induced by a parameter associated with the “CNF-tree” of the formula [17, 25], and the effectiveness of *adhesions* (parent-child intersection) for caching in terms of dimension and skew [24]. In fact, Kalinsky et al. [24] have illustrated how, in real-life scenarios, isomorphic tree decompositions of a minimal width may result in orders-of-magnitude difference in (join) performance.

The common approach is to devise a decomposition algorithm (exact, approximate or heuristic) to capture the desired measure of goodness per application. However, this is a nontrivial challenge that (to the least) requires high expertise in algorithms and tree decompositions. We propose an alternative approach—produce a large number of different tree decompositions, using a baseline decomposition method, and allow the application at hand to choose the best according to its internal measure function. Our approach brings together results and techniques from two seemingly unrelated areas, *chordal graphs* and *enumeration theory*, in order to establish a practical tool for enhancing decomposition algorithms and, by implication, the performance of various inference and optimization algorithms. Specifically, we explore the task of *enumerating* all (or a subset of) the tree decompositions. Such algorithms have been proposed in the past for small graphs (representing database queries), without complexity guarantees [37]. Our main result is an enumeration algorithm that runs in *incremental polynomial time* [22], that is, the time between producing the N th result and the $(N + 1)$ st result is polynomial in N and in the size of the input.

We first need to define which tree decompositions should be enumerated, as many of them are effectively useless. For example, if we take a graph that is already a tree, we do not wish to enumerate the tree decompositions that group nodes

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PODS’17, May 14–19, 2017, Chicago, IL, USA

© 2017 ACM. ISBN 978-1-4503-4198-1/17/05...\$15.00

DOI: <http://dx.doi.org/10.1145/3034786.3056109>

with no reason; in fact, the tree itself is the only reasonable decomposition in this case. Therefore, we consider only tree decompositions that cannot be “improved” by removing or splitting a bag, and we call such tree decompositions *proper*. We prove that the proper tree decompositions are in a bijective (and efficiently computable) correspondence to the *minimal triangulations* of the graph at hand, defined as follows. A *triangulation* of a graph g is a graph g' that is obtained from g by adding edges so that g' is *chordal*, that is, g' does not have any induced simple cycle of more than three nodes. A triangulation is *minimal* if no triangulation can be obtained using only a strict subset of the added edges.

So, the problem is reduced to the task of enumerating all of the minimal triangulations of a graph. In this paper we devise an algorithm for performing this task in incremental polynomial time. Our approach is as follows. Parra and Scheffler [32] have shown that there is a one-to-one correspondence between the minimal triangulations of a graph g and the maximal independent sets of a special graph \mathcal{G} . The nodes of \mathcal{G} are the so called *minimal separators of g* , and the edges are between *crossing* minimal separators. (Precise definitions are in Section 2.) So, enumerating the minimal triangulations of a graph boils down to enumerating these maximal sets. It is well known that all the maximal independent sets of a graph can be enumerated with polynomial delay [10, 22]. However, this is insufficient for us, since the graph \mathcal{G} is not given as input, and in fact, its number of nodes can be exponential in the size of the original graph g . Therefore, we cannot construct this graph ahead of time, and cannot directly use existing algorithms to establish incremental polynomial time.

We address this problem by defining an abstraction of the graph \mathcal{G} of minimal separators by means of a *Succinct Graph Representation* (SGR), which is represented compactly by two algorithms: one for enumerating the nodes and one for testing whether a given pair of nodes forms an edge. In particular, we can access the nodes of \mathcal{G} through a polynomial-delay iterator, due to a result by Berry et al. [4] (who show how to enumerate the minimal separators of a graph). Applying previous results, we prove that the SGR for the minimal separator graph (i.e., \mathcal{G}) meets certain tractability conditions termed *tractable expansion*, which enable the enumeration of its maximal independent sets (i.e., g 's minimal triangulations) in incremental polynomial time in the size of the representation (which can be logarithmic in the size of the graph itself).

In summary, we reduce the problem of enumerating the proper tree decompositions to that of enumerating the minimal triangulations, which we reduce to the problem of enumerating the maximal independent sets of an SGR with tractability properties, and we devise an algorithm for the latter task. An important feature of the algorithm is that it can incorporate any black-box procedure for expanding a given independent set into a maximal one. When applied to enumerating the proper tree decompositions, such a procedure can be any off-the-shelf algorithm for minimal triangulation or tree decomposition (e.g., Maximum Cardinality Search [3] and LB-Triang [5]). However, our algorithm executes this procedure on different versions of the original graph, each time with some new edges added. Hence, our algorithm has the potential of using a high-quality decomposition algorithm for producing *many* high-quality decompositions, enabling the user to choose the best one generated

according to the specific measures of her use case (may it be width or anything else).

After establishing our algorithm, we describe an experimental study where we have tested the ability of the algorithm to utilize the aforementioned triangulation algorithms. The experimental study covers graphs of a wide range of domains (where tree decomposition is needed for efficient analysis): join queries (from the TPC-H collection), Bayesian networks, Markov Random Fields, grids, and random graphs. We tested the execution time (delay) of the algorithm, its ability to reduce the width or fill (number of edges added to establish chordality), and the number of decompositions of quality (width/fill) the same or better than that of the original off-the-shelf algorithm. The results show that, indeed, our algorithm can effectively enhance the quality of the corresponding decomposition algorithm.

The rest of the paper is organized as follows. In Section 2 we give preliminary definitions and notation, and recall basic results from the literature. The SGR framework is presented in Section 3, along with the enumeration algorithm for maximal independent sets. In Section 4 we prove that the graph of minimal separating sets satisfies the tractability requirements needed for the SGR enumeration algorithm, and thereby establish an algorithm for enumerating the minimal triangulations. We show how this algorithm can enumerate the proper tree decompositions in Section 5. We present our experimental study in Section 6, and conclude in Section 7. Some of the proofs are in the appendix.

2. PRELIMINARIES

In this section we give some basic notation and terminology that we use throughout the paper. In addition, we recall some basic theory that we need in this paper.

2.1 Graphs

The graphs in this work are undirected. For a graph g , the set of nodes is denoted by $V(g)$, and the set of edges (pairs $\{u, v\}$ of distinct nodes) is denoted by $E(g)$. Let U be a set of nodes of a graph g . We denote by $g|_U$ the subgraph of g induced by U ; that is, $V(g|_U) = U$ and $E(g|_U) = \{\{u, v\} \in E(g) \mid \{u, v\} \subseteq U\}$. We denote by $g \setminus U$ the graph obtained from g by removing all the nodes in U (along with their incident edges), that is, the graph $g|_{V(g) \setminus U}$.

Let g be a graph and U a set of nodes of g . We say that U is an *independent set* if it does not contain both endpoints of any edge, and it is a *maximal independent set* if it is an independent set and it is not strictly contained in any other independent set. We denote by $MaxInd(g)$ the set of all the maximal independent sets of g . We say that U is a *clique* (of g) if every two nodes of U are connected by an edge, and it is a *maximal clique* (of g) if it is a clique that is not strictly contained in any other clique. We denote by $MaxClq(g)$ the set of all the maximal cliques of g . The operation of *saturating U* (in g) is that of connecting every non-adjacent pair of nodes in U by a new edge. Hence, if h is obtained from g by saturating U , then U is a clique of h .

2.2 Minimal Separators

Let g be a graph, and let S be a subset of $V(g)$. Let u and v be two nodes of g . We say that S is a (u, v) -separator if u and v belong to distinct connected components of $g \setminus S$. We say that S is a *minimal (u, v) -separator* if no strict subset of S is a (u, v) -separator. We say that S is a *minimal separator*

if there are two nodes u and v such that S is a minimal (u, v) -separator. We denote by $\text{MinSep}(g)$ the set of all the minimal separators of g . We mention that the number of minimal separators (i.e., $|\text{MinSep}(g)|$) may be exponential in the number of nodes (i.e., $|V(g)|$).

Let g be a graph, and let S and T be two minimal separators of g . We say that S *crosses* T , in notation $S \bowtie_g T$, if there are nodes u and v in T such that S is a (u, v) -separator. If g is clear from the context, we may omit it and write simply $S \bowtie T$. It is known that \bowtie is a symmetric relation: if S crosses T then T crosses S [26, 32]. Hence, if $S \bowtie T$ then we may also say that S and T are *crossing*. When S and T are non-crossing, then we also say that S and T are *parallel*.

2.3 Chordality and Triangulation

Let g be a graph. A *cycle* of g is a path that starts and ends with the same node. A *chord* of a cycle c of g is an edge $e \in E(g)$ that connects two nodes that are non-adjacent in c . We say that g is *chordal* if every cycle of length greater than three has a chord. Whether a given graph is chordal can be decided in linear time [36]. Dirac [12] has shown a characterization of chordal graphs by means of their minimal separators.

THEOREM 2.1. (Dirac [12]) *A graph g is chordal if and only if every minimal separator of g is a clique.*

Rose [35] has shown that a chordal graph g has fewer minimal separators than nodes (that is, if g is chordal then $|\text{MinSep}(g)| < |V(g)|$), and Kumar and Madhavan [28] have shown that we can find all of these minimal separators in linear time.

THEOREM 2.2. (Kumar and Madhavan [28]) *Let g be a chordal graph. The set $\text{MinSep}(g)$ can be computed in linear time.*

A *triangulation* of a graph g is a graph h such that $V(g) = V(h)$, $E(g) \subseteq E(h)$, and h is chordal. A *minimal triangulation* of g is a triangulation h of g with the following property: for every graph h' with $V(g) = V(h')$, if $E(g) \subseteq E(h') \subsetneq E(h)$ then h' is non-chordal (or in other words, h' is not a triangulation of g). In particular, if g is already chordal then g is the only minimal triangulation of itself. We denote by $\text{MinTri}(g)$ the set of all the minimal triangulations of g .

2.4 Tree Decomposition

Let g be a graph. A *tree decomposition* d of g is a pair (t, β) , where t is a tree and $\beta : V(t) \rightarrow 2^{V(g)}$ is a function that maps every node of t into a set of nodes of g , so that all of the following hold.

- Nodes are covered: for every node $u \in V(g)$ there is a node $v \in V(t)$ such that $u \in \beta(v)$.
- Edges are covered: for every edge $e \in E(g)$ there is a node $v \in V(t)$ such that $e \subseteq \beta(v)$.
- *Junction-tree* (or *running-intersection*) property: for all nodes $u, v, w \in V(t)$, if v is on the path between u and w , then $\beta(v)$ contains $\beta(u) \cap \beta(w)$.

Let g be a graph, and let $d = (t, \beta)$ be a tree decomposition of g . For a node v of t , the set $\beta(v)$ is called a *bag* of d . We denote by $\text{bags}(d)$ the set $\{\beta(v) \mid v \in V(t)\}$, and we denote

by $\text{saturate}(g, d)$ the graph obtained from g by saturating (i.e., adding an edge between every pair of nodes in) every bag of d .

Jordan [23] shows the following characterization of chordal graphs by means of tree decompositions.

THEOREM 2.3. (Jordan [23]) *A graph g is chordal if and only if it has a tree decomposition d such that every bag of d is a clique of g .*

2.5 Enumeration

An *enumeration problem* P is a collection of pairs (x, Y) where x is an *input* and Y is a finite set of *answers* for x , denoted by $P(x)$. A *solver* for an enumeration problem P is an algorithm that, when given an input x , produces (or *prints*) a sequence of answers such that every answer in $P(x)$ is printed precisely once. A solver for an enumeration problem is also referred to as an *enumeration algorithm*.

Johnson, Papadimitriou and Yannakakis [22] introduced several different notions of *efficiency* for enumeration algorithms, and we recall these now. Let P be an enumeration problem, and let A be solver for P . We say that A runs in:

- *polynomial total time* if the total execution time of A is polynomial in $(|x| + |P(x)|)$;
- *polynomial delay* if the time between printing every two consecutive answers is polynomial in $|x|$;
- *incremental polynomial time* if, after printing N answers, the time to print the next $(N + 1)$ st answer is polynomial in $(|x| + N)$.¹

Observe that a solver that enumerates with polynomial delay also enumerates with incremental polynomial time, which, in turn, implies polynomial total time.

3. ENUMERATING MAXIMAL INDEPENDENT SETS ON SUCCINCT GRAPHS

The main result of this paper is an algorithm for enumerating the minimal triangulations of a graph g . As we explain in the next section, this problem amounts to enumerating the maximal independent sets of a graph h . It is known that the maximal independent sets of a graph can be enumerated with polynomial delay [22]. However, we cannot instantiate h , since the number of nodes of h can be exponential in the size of g . Hence, known algorithms for enumerating maximal independent sets cannot be applied to solve our problem. Nevertheless, h possesses some tractability properties that, in fact, allow us to efficiently enumerate the maximal independent sets of h . In this section we identify these properties within an abstract framework of *succinct graph representations*, where a graph may be exponentially larger than its representation, and we have access to the nodes and edges through efficient algorithms. Mainly, we devise an algorithm for enumerating the maximal independent sets for such graphs.

¹The definition of Johnson et al. [22] requires the delay to be polynomial in the size of the input and the *size* of the previously produced results (not just their *number* N as we define here). However, the definitions are equivalent when the size of each answer is polynomial in that of the input, as in our case.

Algorithm EnumMIS(x)

```
1:  $J := \text{Extend}(x, \emptyset)$ 
2: print  $J$ 
3:  $Q := \{J\}$ 
4:  $\mathcal{P} := \emptyset$ 
5:  $\mathcal{V} := \emptyset$ 
6:  $\text{iterator} := A_V(x)$ 
7: while  $Q \neq \emptyset$  do
8:    $J := Q.\text{pop}()$ 
9:    $\mathcal{P}.\text{push}(J)$ 
10:  for all  $v \in \mathcal{V}$  do
11:     $J_v := \{v\} \cup \{u \in J \mid \neg A_E(x, v, u)\}$ 
12:     $K := \text{Extend}(x, J_v)$ 
13:    if  $K \notin Q \cup \mathcal{P}$  then
14:      print  $K$ 
15:       $Q := Q \cup \{K\}$ 
16:  while  $Q = \emptyset$  and  $\text{iterator}.\text{hasNext}()$  do
17:     $v := \text{iterator}.\text{next}()$ 
18:     $\mathcal{V} := \mathcal{V} \cup \{v\}$ 
19:    for all  $J' \in \mathcal{P}$  do
20:       $J'_v := \{v\} \cup \{u \in J' \mid \neg A_E(x, v, u)\}$ 
21:       $K := \text{Extend}(x, J'_v)$ 
22:      if  $K \notin Q \cup \mathcal{P}$  then
23:        print  $K$ 
24:         $Q := Q \cup \{K\}$ 
```

The algorithm maintains two collections, \mathcal{Q} and \mathcal{P} , for storing answers (which are maximal independent sets of the graph $\mathcal{G}(x)$). The algorithm inserts answers into \mathcal{Q} , and repeatedly *removes* (or *pops*) an answer from \mathcal{Q} and *processes* that answer (while possibly inserting new answers into \mathcal{Q}), until \mathcal{Q} is empty. The set \mathcal{P} stores the answers that have already been removed from \mathcal{Q} and processed. Importantly, both collections feature membership testing, element removal and element insertion with a number of comparisons logarithmic in their cardinality (i.e., the number of answers they hold at the time of the operation). In addition, the algorithm maintains a collection \mathcal{V} of the nodes of $\mathcal{G}(x)$ generated thus far. The collection \mathcal{Q} is initialized with a single result (which is printed after generated), which is an arbitrary maximal independent set. This result is obtained through the procedure `Extend(x, I)` that extends a given independent set I into a maximal one. Note that this procedure can be implemented in polynomial time, since (\mathcal{G}, A_V, A_E) has a tractable expansion. The sets \mathcal{P} and \mathcal{V} are initialized empty.

The algorithm accesses the nodes of $\mathcal{G}(x)$ through an iterator object that is obtained by executing $A_V(x)$, and features two polynomial-time operations:

- Boolean `hasNext()` determines whether there are additional nodes of $\mathcal{G}(x)$ to enumerate.
- `next()` returns the next node in the iteration.

The algorithm applies the iteration of line 7 until \mathcal{Q} becomes empty, and then terminates. In every iteration, the algorithm pops an element from \mathcal{Q} , stores it in \mathcal{P} (lines 8–9), and then processes it. The algorithm iterates through the nodes in \mathcal{V} , and for each node v it applies (in lines 11–15) what we call *extension of J in the direction of v* :

1. Generate the set J_v that consists of v and all the nodes in J that are non-neighbors of v , using the algorithm A_E for testing adjacency;
2. Extend J_v into an arbitrary maximal independent set K , again using `Extend(x, J_v)`;
3. If K is in neither \mathcal{Q} nor \mathcal{P} (meaning it was not printed before), then print K and add it to \mathcal{Q} .

Observe that J_v is an independent set, and hence, it is valid to invoke `Extend(x, J_v)` with J_v .

Up to this point, the algorithm is very similar to the algorithm of Cohen et al. [9] for computing full disjunctions, except that \mathcal{V} does not hold all nodes but only the nodes generated so far. The twist (and the source of extra challenge in proving correctness and efficiency) is in lines 16–24, where we generate additional nodes and compensate for them being missing in the previous iterations. In these lines, the algorithm tests whether it is the case that \mathcal{Q} is empty and the node iterator has additional nodes to process (line 16). While this is the case, the algorithm repeats the following procedure (lines 17–24): generate the next node using the iterator of $A_V(x)$, add it to \mathcal{V} , and extend *every* previously processed result (i.e., the results in \mathcal{P}) in the direction of the newly generated node v (as previously described).

3.2.2 Correctness and Efficiency

The following lemma states the correctness of the algorithm. That is, the algorithm enumerates *every* element in $\text{MaxInd}(\mathcal{G}(x))$, *only* elements in $\text{MaxInd}(\mathcal{G}(x))$, and every element is printed exactly once.

LEMMA 3.2. `EnumMIS(x)` enumerates $\text{MaxInd}(\mathcal{G}(x))$.

PROOF. The algorithm prints only elements that are created by invoking the procedure `Extend`. Therefore, the algorithm prints only elements in $\text{MaxInd}(\mathcal{G}(x))$. The tests of lines 13 and 22 ensure that whenever an element is printed, this element has not been seen before. Hence, no element is printed more than once. It is left to prove that every maximal independent set of $\mathcal{G}(x)$ is printed by the algorithm.

Observe the following. When the algorithm terminates we have $\mathcal{Q} = \emptyset$. Therefore, in the previous iteration the loop of line 16 could only have terminated due to `iterator.hasNext()` returning false. Therefore, upon termination $\mathcal{V} = V(\mathcal{G}(g))$.

Suppose, by way of contradiction, that there is some maximal independent set H that is not printed by the algorithm. Let J be a maximal independent set of $\mathcal{G}(x)$, among all the printed ones, that contains a maximal number of elements from H . The set J must exist, since the algorithm prints at least one maximal independent set. Let H_m be the intersection $H \cap J$. Since $H \neq H_m$ (or else H is not maximal), there is at least one node in $H \setminus J$; let v be such a node.

At this point we have established that before the algorithm terminated, (a) the node v has been generated, and (b) J has been printed. We now branch into two cases, as follows.

1. The set J was inserted into \mathcal{P} before the node v was generated. Immediately after v is generated (in line 17), the set $J_v = \{v\} \cup \{u \in J \mid \neg A_E(x, v, u)\}$ will be constructed (in line 20) and expanded to a maximal independent set K that contains J_v .
2. The node v was generated before J was inserted into \mathcal{P} . At the iteration when J is inserted into \mathcal{P} , we have $v \in \mathcal{V}$, and so the set $J_v = \{v\} \cup \{u \in J \mid \neg A_E(x, v, u)\}$ will be constructed (in line 11) and expanded to a maximal independent set K that contains J_v .

So, we have established that before the algorithm terminates, the set J_v is generated and expanded to a maximal independent set K that contains J_v . Furthermore, $H_m \cup \{v\} \subseteq J_v$ (since $H_m \subseteq J$, and does not contain any neighbor of v), and therefore $H_m \cup \{v\} \subseteq K$. According to the algorithm, one of the following options must hold: (1) K is inserted into \mathcal{Q} , (2) K is already in \mathcal{Q} (3) K was in \mathcal{Q} in the past and is now in \mathcal{P} . Since the algorithm prints every maximal independent set that is inserted into \mathcal{Q} , we get a contradiction to the maximality of H_m . \square

We now prove that the algorithm `EnumMIS` enumerates with incremental polynomial time. We do so in two steps. We first define an algorithm that is similar to `EnumMIS`, but with a small twist that makes it easier to prove incremental polynomial time. Then, we prove a general result that will imply that, if the new algorithm enumerates in incremental polynomial time then so does `EnumMIS`.

The new algorithm is similar to `EnumMIS`, except that each of the print commands (lines 2, 14 and 23) is replaced with an operation that takes the time of the printing, but is actually void (e.g., printing to `/dev/null` in Unix). Instead, each maximal independent set is printed immediately after being removed from \mathcal{Q} (line 8). Hence, answers are *held* until removed from \mathcal{Q} . Next, we prove that `EnumMISHold` enumerates in incremental polynomial time. Observe that to bound the delay `EnumMISHold`, we only need to bound the time between two executions of line 8 of `EnumMIS`.

LEMMA 3.3. `EnumMISHold`(x) enumerates with incremental polynomial time.

PROOF. We begin by showing that the size of the node set \mathcal{V} is polynomial in the size of the printed result set \mathcal{P} . Whenever a new node v is inserted into \mathcal{V} (line 18), the set \mathcal{Q} is empty. The following calls to `Extend` (line 21) will generate maximal independent sets containing v . Each of these maximal independent sets is either already in \mathcal{P} , or it is inserted into \mathcal{Q} (line 24). Therefore, at the end of the iteration of the main loop in which v was inserted into \mathcal{V} , all maximal independent sets in \mathcal{Q} contain v . In the next iteration of the main loop, if such an iteration exists, one of these newly generated independent sets will be printed and inserted into \mathcal{P} (line 9). That is, at the beginning of every iteration of the algorithm (specifically, line 10), every node $v \in \mathcal{V}$ belongs to some maximal independent set that has already been printed (and thus part of \mathcal{P}). Since we assume tractable expansion, each independent set in \mathcal{P} contains at most $p(|x|)$ nodes, and we can conclude that $|\mathcal{V}| \leq p(|x|) \cdot |\mathcal{P}|$.

We now bound the time between two executions of line 8 of `EnumMIS`. Line 9 takes polynomial time in $|x|$ (since there are at most exponentially many independent sets, (\mathcal{G}, A_v, A_E) has a tractable expansion, and operations on \mathcal{P} require a logarithmic number of comparisons in the cardinality). The number of iterations of line 10 is at most the size of \mathcal{V} , which is polynomial in the number of answers printed so far (due to the above observation). Each operation in that iteration takes time polynomial in $|x|$.

The loop of line 16 repeats (at most) until a node that belongs to none of the printed answers is generated. Hence, the observation that this number is polynomial in the size of the output, along with the tractable expansion, again implies that we iterate a number of times that is polynomial in the number of answers printed so far. The loop of line 19 repeats at most as many times as the number of answers in \mathcal{P} , and all of these have been printed before. Besides the loops, each of lines 17–24 takes polynomial time in $|x|$. \square

Lemma 3.3 shows that `EnumMISHold` enumerates with incremental polynomial time. Next, we show the same for `EnumMIS`. The key point is that every answer is printed in `EnumMIS` earlier than it is printed in `EnumMISHold`. We will prove that this suffices to conclude that if `EnumMISHold` enumerates in incremental polynomial time, then so does `EnumMIS`. We prove here a general result. Let P be an enumeration problem, and let A be a solver for P . For input x and answer $y \in P(x)$, we denote by $\text{time}_{A,x}(y)$ the time in which y is printed. We prove the following theorem.

THEOREM 3.4. Let P be an enumeration problem, and let A and B be two solvers for P . Suppose that for all instances x and for all answers $y \in P(x)$ we have $\text{time}_{A,x}(y) \leq \text{time}_{B,x}(y)$. If B enumerates in incremental polynomial time, then so does A .

Theorem 3.4 is not a vacuous statement, since the order of results may differ between A and B . Furthermore, the corollary no longer holds when substituting “incremental polynomial time” with “polynomial delay.”

Using the algorithms `EnumMIS` and `EnumMISHold` as A and B in Theorem 3.4, respectively, the combination with Lemma 3.3 implies that `EnumMIS` enumerates in incremental polynomial time, as claimed.

4. ENUMERATING MINIMAL TRIANGULATIONS

In Section 3.1.1 we introduced `MSGraph` and claimed that it is an SGR. In this section, we will use known results to reduce the problem of enumerating the minimal triangulations of a graph to the problem of enumerating the maximal independent sets for `MSGraph`. We will describe how to enumerate the nodes of `MSGraph` with polynomial delay, concluding that it is in fact an SGR. We will further show that `MSGraph` has a tractable expansion (Definition 2), and therefore Theorem 3.1 can be applied to conclude that the minimal triangulations can be enumerated in incremental polynomial time.

4.1 Reduction

We use the following notation. Let g be a graph. We denote by $\text{ClqMinSep}(g)$ the set of minimal separators S of g , such that S is a clique of g . Let φ be a subset of $\text{MinSep}(g)$. We denote by $g_{[\varphi]}$ the graph that results from saturating the minimal separators in φ .

Parra and Scheffler [32] have shown the following connection between minimal triangulations and maximal sets of pairwise-parallel minimal separators (that is, every two minimal separators in the set are non-crossing).

THEOREM 4.1. (Parra and Scheffler [32]) Let g be a graph.

1. If φ is a maximal set of pairwise-parallel minimal separators of g , then $g_{[\varphi]}$ is a minimal triangulation of g , and $\text{MinSep}(g_{[\varphi]}) = \varphi$.
2. If h is a minimal triangulation of g , then the set $\varphi = \text{MinSep}(h)$ is a maximal set of pairwise-parallel minimal separators in g , and $h = g_{[\varphi]}$.

Theorem 4.1, combined with Theorem 2.2, gives the desired reduction in the following corollary. Recall that the graph $\mathcal{G}^{\text{ms}}(g)$ is defined in Section 3.1.1, as part of the SGR $\text{MSGraph} = (\mathcal{G}^{\text{ms}}, A_V^{\text{ms}}, A_E^{\text{ms}})$.

COROLLARY 4.2. For a graph g , there is a polynomial-time-computable bijection between the following two sets:

- $\text{MaxInd}(\mathcal{G}^{\text{ms}}(g))$, that is, the set of all maximal sets of pairwise-parallel minimal separators of g .
- $\text{MinTri}(g)$, that is, the set of all minimal triangulations of g .

Hence, it suffices to prove that `MSGraph` has a tractable expansion, which we do next.

4.2 Enumerating Minimal Separators

We now describe a variation of the algorithm of Berry et al. [4] that, given a graph g , enumerates its set $\text{MinSep}(g)$ of minimal separators. Their algorithm enumerates with polynomial total time, and with a simple change (that we explain next) can enumerate with polynomial delay. Our variation is depicted in Figure 2. There, for $v \in V(g)$ we denote by $N(v)$ the set of neighbors of v . For $U \subseteq V(g)$ we denote by $N(U)$ the set of neighbors of nodes in U , excluding the nodes of U themselves; that is,

$$N(U) \stackrel{\text{def}}{=} \left(\bigcup_{v \in U} N(v) \right) \setminus U.$$

Algorithm PDelayAllMinSep(g)

```

1:  $\mathcal{Q} := \emptyset$ 
2:  $\mathcal{P} := \emptyset$ 
3: for all  $v \in V(g)$  do
4:   for all  $C \in \mathcal{C}(\{v\} \cup N(v))$  do
5:      $\mathcal{Q} := \mathcal{Q} \cup \{N(C)\}$ 
6: while  $\mathcal{Q} \neq \emptyset$  do
7:    $S := \mathcal{Q}.\text{pop}()$ 
8:   for all  $x \in S$  do
9:      $S' := \{N(C) \mid C \in \mathcal{C}(S \cup N(x))\}$ 
10:    if  $S' \notin \mathcal{P}$  then
11:       $\mathcal{Q} := \mathcal{Q} \cup \{S'\}$ 
12:     $\mathcal{P} := \mathcal{P} \cup \{S\}$ 
13: print  $S$ 

```

Figure 2: Enumerating $\text{MinSep}(g)$ with polynomial delay (a variation of the algorithm by Berry et al. [4])

We also denote by $\mathcal{C}(U)$ the set of connected components of the graph $g \setminus U$ (the graph obtained from g by removing all the nodes of U).

The algorithm remains intrinsically the same as that of Berry et al. [4]. Minimal separators are considered as neighborhoods of connected components. The algorithm finds minimal separators contained in a set $U \subseteq V(g)$ by taking the neighborhoods of the connected components of $g \setminus U$, that is, $N(C)$ for all $C \in \mathcal{C}(U)$. Initially, the minimal separators that are contained in the neighborhoods of single nodes are generated (lines 3–5). Then, every previously generated minimal separator S is processed to produce more minimal separators that are *close* to S (lines 7–12). For every node v in the minimal separator S , it produces minimal separators that are contained in $S \cup N(v)$.

Our modification is in the data structures and the time of printing answers. In Figure 2, \mathcal{Q} and \mathcal{P} play the role of $\mathcal{S} \setminus \mathcal{T}$ and \mathcal{T} of the original algorithm [4], respectively. There, \mathcal{S} holds all minimal separators generated, and \mathcal{T} is a subset that holds the separators that were processed. The easy access to the separators yet to be processed (i.e. $\mathcal{S} \setminus \mathcal{T}$), along with printing answers when processed (in line 13, rather than when revealed in line 11), provides the polynomial delay. Correctness is derived directly by the correctness of the original algorithm, and the polynomial delay can be easily verified. In particular, the time between two consecutive results is $O(|V(g)|^3)$.

4.3 Tractable Expansion

Recall that Rose [35] proved that a chordal graph has fewer minimal separators than nodes. Combined with this result, Theorem 4.1 gives the first of the two conditions of Definition 2.

COROLLARY 4.3. *Let g be a graph. If I is a (maximal) independent set of $\mathcal{G}^{\text{ms}}(g)$, then $|I| < V(g)$.*

PROOF. Suppose that I is a maximal set of pairwise-parallel minimal separators of g . Then by Theorem 4.1, $h = g_{[I]}$ is a minimal triangulation of g , and $\text{MinSep}(h) = I$. The graph h is chordal, hence from Rose [35] we get that $|\text{MinSep}(h)| < |V(h)| = |V(g)|$. \square

Algorithm Extend(g, φ)

```

1:  $g_t := \text{Triangulate}(g_{[\varphi]})$ 
2:  $h := \text{MinTriSandwich}(g_{[\varphi]}, g_t)$ 
3: return  $\text{ExtractMinSeps}(h)$ 

```

Figure 3: An algorithm for extending a set φ of pairwise-parallel minimal separators

We now turn to proving the second condition of Definition 2. We do so by describing a general procedure for extending a set of pairwise-parallel minimal separators of a graph g to a maximal such set. Algorithm **Extend** of Figure 3 can apply any known polynomial time triangulation heuristic, referred to as **Triangulate**, as a black box. It uses the following procedures as subroutines.

- **Saturate(g, S)** receives a graph g and a set $S \subseteq V(g)$ of vertices, and saturates S (i.e., modifies g such that S becomes a clique).
- **Triangulate(g)** receives a graph g and returns a (not necessarily minimal) triangulation g' of g . We assume that this procedure runs in polynomial time. (For example, a naïve implementation would be to add every possible edge; later we discuss smarter alternatives.)
- **MinTriSandwich(g, g')** receives a graph g and a triangulation g' of g , and returns a *minimal* triangulation of g . We note that, using one of the known algorithms [6, 11, 33], this procedure runs in time that is polynomial in the size of the graph.
- **ExtractMinSeps(h)** receives a chordal graph h and returns its set of minimal separators. Using the algorithm of Kumar [28], the execution time of this procedure is linear in h .

Extend takes as input a graph g and a set φ of pairwise-parallel minimal separators. It then proceeds by saturating the separators in φ , resulting in $g_{[\varphi]}$. At this stage it passes $g_{[\varphi]}$ to the triangulation heuristic **Triangulate**. We note that **Triangulate** does not have to produce a minimal triangulation. This is important since it allows us to incorporate *any* method for triangulation or tree decomposition. (We discuss in detail the translation between triangulations and tree decompositions in Section 5.)

The problem of transforming a non-minimal triangulation into a minimal one is called the *minimal triangulation sandwich problem* [20]. Various polynomial-time algorithms for this problem exist [11, 33], and these were reported to perform well in practice [6].

So, at this stage we have a minimal triangulation h of $g_{[\varphi]}$. Theorem 4.4 (that we give in the next section) shows that h is also a minimal triangulation of g . Lemma 4.5 (also in the next section) shows that the set of minimal separators of h contains φ , which is essential as we need to *extend* φ . Finally, we can apply the algorithm of Kumar [28] to extract the minimal separators of the (chordal) graph h in linear time.

4.3.1 Correctness.

To prove correctness of the algorithm `Extend` of Figure 3, we need the following result by Heggernes [20].

THEOREM 4.4. (Heggernes [20]) *Given a graph g , let φ be an arbitrary set of pairwise-parallel minimal separators of g . Obtain a graph $g_{[\varphi]}$ by saturating each separator in φ .*

1. $\varphi \subseteq \text{ClqMinSep}(g_{[\varphi]})$, that is, φ consists of clique minimal separators of $g_{[\varphi]}$.
2. $\text{ClqMinSep}(g) \subseteq \text{MinSep}(g_{[\varphi]})$; that is, every clique minimal separator of g is a (clique) minimal separator of $g_{[\varphi]}$.
3. Every minimal triangulation of $g_{[\varphi]}$ is a minimal triangulation of g .

The next lemma builds on Theorems 4.1 and 4.4.

LEMMA 4.5. *Let g be a graph, and φ a set of pairwise-parallel minimal separators of g . Let h be a minimal triangulation of $g_{[\varphi]}$. Then $\varphi \subseteq \text{MinSep}(h)$.*

PROOF. By Part 1 of Theorem 4.4 we have that $\varphi \subseteq \text{ClqMinSep}(g_{[\varphi]})$. Since h is a minimal triangulation of $g_{[\varphi]}$ then by Part 2 of Theorem 4.1, h is the result of saturating a maximal set, say φ' , of pairwise-parallel minimal separators of $g_{[\varphi]}$. Therefore, by Part 2 of Theorem 4.4 we have $\text{ClqMinSep}(g_{[\varphi]}) \subseteq \text{MinSep}(h)$. This implies that $\varphi \subseteq \text{MinSep}(h)$, as claimed. \square

We then conclude the correctness of the algorithm.

LEMMA 4.6. *Let φ be a set of pairwise-parallel minimal separators of a graph g . `Extend`(g, φ) returns a maximal set I of pairwise-parallel minimal separators of g such that $\varphi \subseteq I$. Furthermore, the algorithm terminates in polynomial time.*

PROOF. Assuming correctness of procedures `Triangulate`, and `MinTriSandwich`, the graph h is a minimal triangulation of $g_{[\varphi]}$. By Part 3 of Theorem 4.4, we have that h is a minimal triangulation of g . Consequently, from Part 2 of Theorem 4.1 we get that $\text{MinSep}(h) = I$ is a maximal set of pairwise-parallel minimal separators of g . By Lemma 4.5 it holds that $\varphi \subseteq \text{MinSep}(h)$, making I an extension of φ . All of the procedures in Figure 3 run in time that is polynomial in the size of the graph making it polynomial as well. \square

From Corollary 4.3 and Lemma 4.6 we get the main result of this part.

THEOREM 4.7. *The SGR `MSGraph` has a tractable expansion of independent sets.*

This theorem allows us to establish the main result of this paper.

4.4 Main Result

From Theorems 4.7 and 3.1 we conclude that it is possible to enumerate the maximal independent sets of `MSGraph` in incremental polynomial time. Applying the bijection of Corollary 4.2, we get the main result of this paper.

COROLLARY 4.8. *Given a graph, the minimal triangulations can be enumerated in incremental polynomial time.*

In the next section we will use this result for enumerating tree decompositions.

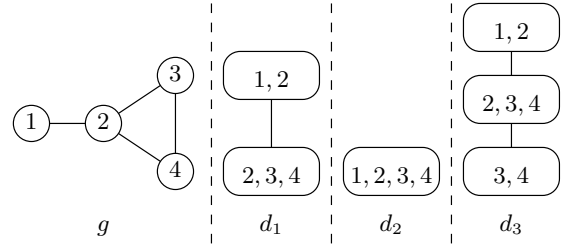


Figure 4: A graph g and tree decompositions d_1 , d_2 and d_3 of g . The decomposition d_1 is proper, but d_2 and d_3 are subsumed by d_1 , and hence, improper.

5. ENUMERATING THE PROPER TREE DECOMPOSITIONS

In this section we define the notion of a *proper* tree decomposition, which is essentially a tree decomposition that is, intuitively, not deemed redundant due to another tree decomposition. Our ultimate goal is to enumerate *only* the proper tree decompositions, and we will show that this translates to enumerating the minimal triangulations.

5.1 Proper Tree Decompositions

Let d_1 and d_2 be two tree decompositions of a graph g . We say that d_1 and d_2 are *bag equivalent*, denoted $d_1 \equiv_b d_2$, if $\text{bags}(d_1) = \text{bags}(d_2)$. We denote by $d_1 \sqsubseteq d_2$ the fact that for every bag $b_1 \in \text{bags}(d_1)$ there exists a bag $b_2 \in \text{bags}(d_2)$ such that $b_1 \subseteq b_2$.

Let g be a graph, and let d and d' be tree decompositions of g . We say that d' *strictly subsumes* d if $d' \sqsubseteq d$ and $\text{bags}(d) \not\subseteq \text{bags}(d')$. A tree decomposition is *proper* if it is not strictly subsumed by any tree decomposition, and it is *improper* otherwise.

Figure 4 shows examples of proper and improper tree decompositions. It can be shown that d_1 is proper (e.g., since every clique of g is contained in some bag of d , as we prove in Proposition A.2 in the appendix). But d_2 is not proper, since it is subsumed by d_1 ; that is, every bag of d_1 is contained in some bag of d_2 , but the bag $\{1, 2, 3, 4\}$ is not a bag of d_1 . For the same reason, d_2 is subsumed also by d_3 . Finally, d_3 is subsumed by d_1 since every bag of d_1 is a bag of d_3 , but the bag $\{3, 4\}$ is not a bag of d_1 .

5.2 Enumeration

The main result of this section is the following, showing that enumerating the proper tree decompositions reduces to enumerating the minimal triangulations.

THEOREM 5.1. *Let g be a graph. There is a bijection M between $\text{MinTri}(g)$ and the equivalence classes of \equiv_b over the proper tree decompositions of g . Moreover, given a minimal triangulation h of g , the proper tree decompositions in the class $M(h)$ can be enumerated with polynomial delay.*

Combined with Corollary 4.8, we get the following.

COROLLARY 5.2. *The set of proper tree decompositions of a given graph can be enumerated in incremental polynomial time.*

Next, we discuss the proof of Theorem 5.1, and in particular show how M is defined. The definition of M is based on the following lemma.

LEMMA 5.3. *If g is a chordal graph and d is a proper tree decomposition of g , then $\text{bags}(d) = \text{MaxClq}(g)$.*

Based on Lemma 5.3, we define M to be the function that maps every $h \in \text{MinTri}(g)$ to the equivalence class of the proper tree decomposition of h . The following lemma states the M has the required properties.

LEMMA 5.4. *Let g be a graph. The mapping M is a bijection between $\text{MinTri}(g)$ and the equivalence classes of \equiv_b over the proper tree decompositions of g .*

To complete the proof of Theorem 5.1, we explain how the proper tree decompositions in the class $M(h)$ can be enumerated with polynomial delay for $h \in \text{MinTri}(g)$. Jordan [23] shows that, given a chordal graph h , a tree over the bags that represent the maximal cliques of h is a tree decomposition if and only if it is a maximal spanning tree, where the weight of an edge between two bags is the size of their intersection. Hence, this enumeration problem is reduced to enumerating all maximal spanning trees, which can be solved in polynomial delay [38]. Since Gavril [14] has shown that in chordal graphs the number of maximal cliques of h is at most the number of nodes of h , we have a polynomial delay algorithm for enumerating the tree decompositions. This concludes the proof.

6. EXPERIMENTAL EVALUATION

We now describe an experimental study over an implementation of our enumeration algorithm for minimal triangulations, namely the algorithm EnumMIS of Figure 1 for the SGR ($\mathcal{G}^{\text{ms}}, A_V^{\text{ms}}, A_E^{\text{ms}}$), calling the procedure Extend of Figure 3. The goal of the experimental study is twofold. First, we wish to understand how practical the execution cost of the algorithm is for enumerating many minimal triangulations (and tree decompositions). Second, we wish to study the ability of the algorithm to produce many *high-quality* triangulations, given an underlying triangulation algorithm (for Extend), and even to improve upon standard quality measures of the underlying algorithm itself. In Section 6.1 we describe the experimental setup, in Section 6.2 we report on the efficiency of the algorithm in terms of its delay, and in Sections 6.3 and 6.4 we study the quality of the results.

6.1 Experimental Setup

We first describe the general setup for our study.

Implementation and Hardware. We implemented all algorithms in C++, with STL data structures.² All experiments were carried out on a 2.6GHz dual-core laptop with 8GB of RAM running Windows 10 professional.

Triangulation Algorithms. We implemented two well known triangulation algorithms as the procedure `Triangulate` in line 1 of the procedure `Extend` (Figure 3). Both algorithms apply the general technique of *node-elimination ordering* [31], where nodes are eliminated from the graph in turn, by adding a subset of edges (called *fill* edges) between the eliminated node and its neighbors in the (leftover) graph. Both algorithms guarantee a minimal triangulation (hence there was no need to call `MinTriSandwich($g_{[\varphi]}, g_t$)` in line 2 of `Extend`).

²The code is available online: <https://github.com/NofarCarmeli/MinTriangulationsEnumeration>

- **MCS_M** [3]. This is an extension of the *Maximum Cardinality Search* (MCS) algorithm for recognizing chordal graphs [36], which finds a minimal elimination ordering along with its corresponding minimal triangulation.
- **LB_TRIANG** [5]. This algorithms guarantees minimality of the triangulation by adding only a subset of the fill edges at each of the elimination steps, and allows for complete flexibility in determining the elimination order. We applied the *min fill* heuristic that selects, at each iteration, the node whose elimination results in the smallest number of edges to add.

Datasets. We used three types of datasets: probabilistic graphical models, database queries, and random (synthetic) graphs. For the first type, we used the following benchmark networks from the UAI probabilistic inference challenge.³ The datasets *Alchemy* and *DBN* from the challenge are not described here as each of their graphs had only one or two minimal triangulations, and the enumeration ended instantaneously.

- **Promedas**: “PRObabilistic MEDical Diagnostic Advisory System.” The Promedas Markov networks represent medical diagnosis cases, and consist of binary variables that were converted from layered noisy-or Bayesian networks. The dataset includes 33 graphs with 26-1039 nodes and 36-1696 edges, and many of them are considered too difficult for exact inference.⁴
- **Object detection**: Markov Random Fields for object-detection tasks in computer vision. It includes 79 instances of connected networks, each containing 60 nodes and between 135 to 180 edges.
- **Image segmentation**: Bayesian networks generated from image-segmentation tasks. It includes 6 graphs with 226-235 nodes and 617-647 edges.
- **Grids**: An $N \times N$ grid network. Such networks that are common in image processing [7], and networks that model problems such as medical diagnosis and object detection. This dataset includes 8 grids with $N = 10$ and $N = 20$, resulting in graphs with 100 or 400 nodes, and 180-760 edges.
- **Pedigree**: Bayesian networks used to model genetic information [13]. The data set includes 3 graphs, each has 385 nodes and 930 edges.
- **CSP**: Constraint-satisfaction problems. There are 3 instances in the dataset, with 67-100 nodes and 226-619 edges.

The datasets of second and third types are as follows.

- **TPC-H**: Graphs induced from TPC-H. These are the Gaifman (primal) graphs of joins for implementing the TPC-H benchmark queries in LogiQL, the Datalog variant of LogicBlox [1].⁵ The queries include up to 22 nodes, and up to 46 edges, and their treewidth is up to 7.

³<http://www.cs.huji.ac.il/project/PASCAL/showNet.php>

⁴<http://graphmod.ics.uci.edu/uai08/Evaluation/Report/Benchmarks>

⁵The queries, provided to us by LogicBlox, are used for benchmarking the engine.

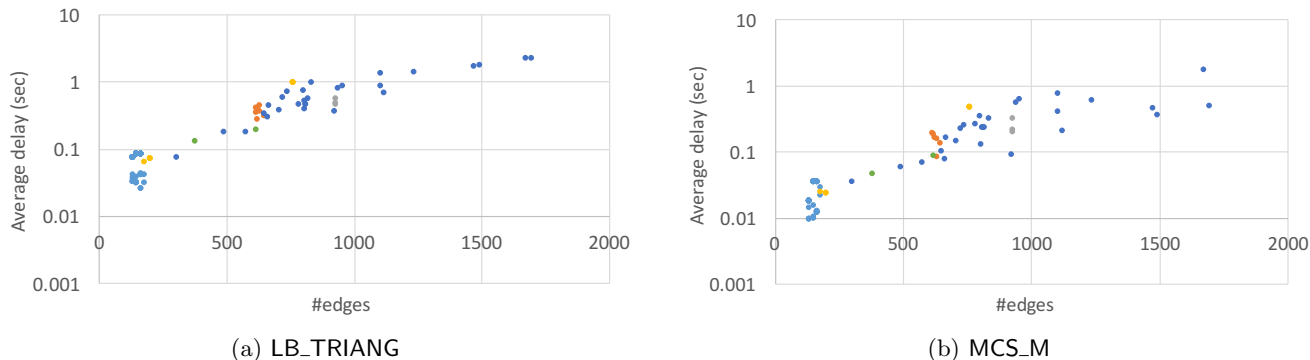


Figure 5: Average delay (in seconds) for the two triangulation algorithms over the probabilistic-graphical-model benchmarks: Object Detection (●), Segmentation (●), Pedigree (●), Grids (●), Promedas (●), CSP (●)

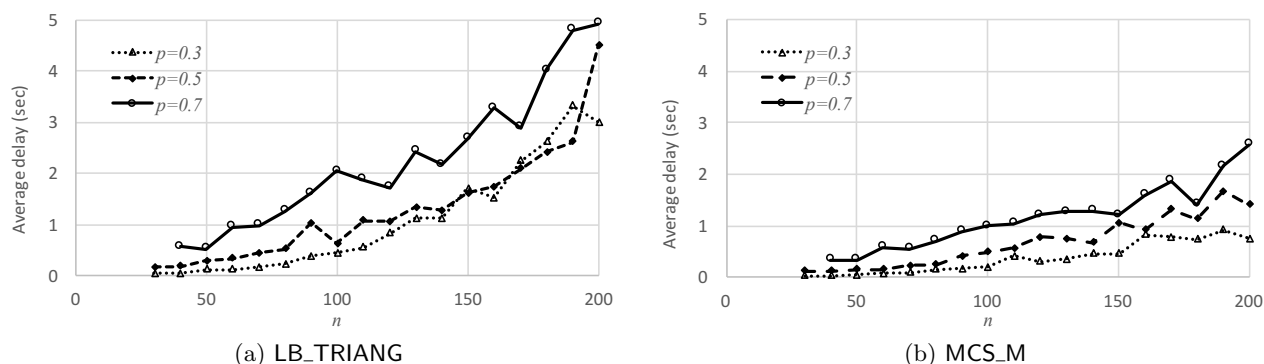


Figure 6: Average delay over 54 graphs randomly generated from the Erdős-Rényi $G(n, p)$ for varying n and p

- **Random:** Random $G(n, p)$ graphs in the Erdős-Rényi model. The number of nodes is n and every pair of nodes is connected by an edge with probability p (independently). We generated 54 random graphs for varying n between 30 and 200, and three values of p : 0.3 (sparsest), 0.5 and 0.7 (densest).

As a baseline approach, we implemented the algorithm of DuncCap [37] for generating all of the generalized hypertree decompositions (each involving an underlying tree decomposition). However, this algorithm is designed to handle small join queries and to span a much greater space of objects (namely, the generalized hypertree decompositions). In particular, on the TPC-H dataset we observed that on the smaller queries our algorithm is faster by 3 to 4 orders of magnitude, and on some of the larger queries (Q7 and Q9) we could not get their algorithm to terminate in less than two hours (while our algorithms terminated in a few seconds, as we later discuss). Therefore, we decided to exclude comparisons to this implementation. As of today, we are not aware of any other published algorithms for enumerating (minimal) triangulations or tree decompositions with guarantees of correctness (completeness).

6.2 Execution Cost

In what follows we report on the delay of the two variants of the implementation, corresponding to the two triangulation algorithms LB_TRIANG and MCS_M.

Probabilistic graphical models. We measured the average delay between minimal triangulation printouts for the network datasets from the UAI challenge. The measurements were conducted during 30 minutes executions. 5 of the graphs in Promedas, and one graph of CSP completed the enumeration within this time. We plotted the delay of the other graphs against the number of their edges. The plots, corresponding to the two minimal triangulation algorithms LB_TRIANG and MCS_M, are presented in Figures 5a and 5b, respectively. Overall, we see an exponential relationship between the number of edges and the average delay. However, this trend widely varies between the different benchmarks. While this dependency is apparent for the Promedas data set, the average delay for object detection has little correlation with the number of edges in the graph.

Random graphs. We measured the average delay (in seconds) between the printout of consecutive minimal triangulations during a 30 minute execution. The plots in Figures 6a and 6b show the average delay vs. the size of the graph for the two variants. We can see that the delay increases with the size of the graph, and that the general trend is that the delay is larger for denser graphs. We also see that for LB_TRIANG the delay is generally longer than for MCS_M.

Database queries. We evaluated our enumeration algorithm over a set of 22 queries from the TPC-H dataset. The graphs of these queries are quite small when compared to

Dataset	#trng	min-w	# $\leq w_1$ (%)	%w \downarrow (max)	min-f	# $\leq f_1$ (%)	%f \downarrow (max)
MCS_M							
Promedas (28)	11064.5	25.8	3713.6 (33.6%)	2.2 (15.2)	3353.4	8136.0 (73.5%)	18.1 (49.9)
Grids (8)	40319.8	18.4	93.6 (0.2%)	0.0 (0.0)	2752.6	15771.4 (39.1%)	4.2 (28.1)
Obj. Detection (79)	100349.9	6.1	42743.9 (42.6%)	0.4 (12.5)	30.0	27614.1 (27.5%)	19.9 (47.1)
Segmentation (5)	12836.5	23.0	20.5 (0.2%)	0.0 (0.0)	2555.2	5269.7 (41.1%)	5.9 (12.5)
Pedigree (3)	7789.0	31.7	3087.3 (39.6%)	0.0 (0.0)	3525.7	743.0 (9.5%)	2.8 (3.5)
CSP (2)	29450.5	16.5	26741.5 (90.8%)	13.2 (26.3)	46.0	18815.5 (63.9%)	35.2 (55.8)
LB_TRIANG							
Promedas (28)	4220.7	18.6	2352.0 (55.7%)	1.9 (16.7)	1239.4	175.0 (4.1%)	0.2 (11.1)
Grids (8)	13881.3	24.5	1273.0 (9.2%)	3.0 (8.7)	1600.3	1.0 (0.0%)	0.0 (0.0)
Obj. Detection (79)	33295.4	5.8	15709.3 (47.2%)	0.0 (0.0)	27.6	5110.7 (15.3%)	10.4 (27.6)
Segmentation (5)	5174.2	21.8	2141.8 (41.4%)	10.3 (20.7)	1402.0	130.2 (2.5%)	1.2 (4.2)
Pedigree (3)	3646.0	23.7	3227.7 (88.5%)	5.3 (14.8)	1491.0	1.0 (0.0%)	0.0 (0.0)
CSP (2)	11772.0	16.5	3760.5 (31.9%)	0.0 (0.0)	34.5	664.0 (5.6%)	1.4 (3.0)

Table 1: Statistics on generated triangulations following 30 minutes execution

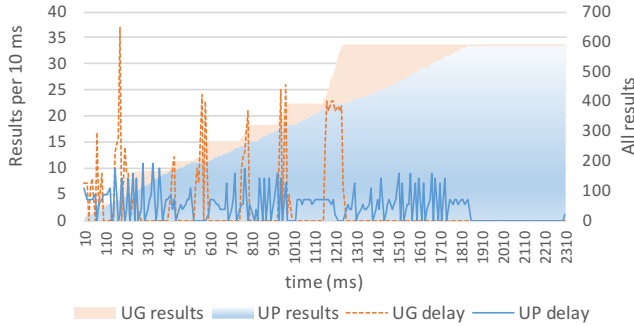


Figure 7: Delay behavior in two printing modes: UG (Upon Generation, as in EnumMIS), and UP (Upon Pop, as in EnumMISHold)

the UAI datasets (< 23 nodes). Moreover, half of these graphs are chordal to begin with (i.e., have only one minimal triangulation—the graph itself), and hence, irrelevant for us. Except for two queries, all of the rest had at most 5 minimal triangulations. The remaining two queries are Q7 (Volume shipping Query) and Q9 (Product Type Profit Measure Query), and they have a considerable number of minimal triangulations: 700 and 588, respectively. When considering the minimum-width tree decomposition for each of the queries, the largest bag was of size 8; this is due to a relation of arity 8 in the query. In fact the largest bag in each of the queries had at most two variables more than the size of the largest relation. The execution for all 22 queries completed within 5 seconds.

In one of the queries we compared the delays for two modes of printing: the one of EnumMIS and the one of EnumMISHold that prints upon extraction from the queue, as described in Section 3.2.2. We refer to the former as UG (Upon Generation) and to the latter as UP (Upon Pop). Recall that both modes guarantee incremental polynomial time (Theorem 3.4). The results are in Figure 7. While the dotted line (of UG) has bursts of high-frequency prints followed by

periods where no new triangulation is created, the solid line (UP) has a more steady pace as can be seen by the constant slope in Figure 7. As expected, despite the fact that the last result of UG is printed earlier than that of UP, termination is at the same time in both modes, as the algorithm still needs to check that there are no additional minimal triangulations.

6.3 Quality

In what follows we report on the quality of the generated minimal triangulations in terms of two standard measures of quality for triangulations and tree decompositions: *fill* and *width*. *Fill* refers to the total number of edges added in order to make the resulting graph chordal, while *width* refers to the size of the largest clique in the generated triangulation (minus one).⁶ The natural benchmark for the quality of the triangulations is the first result our enumeration returns, as it is the result we would get by running the minimal triangulation algorithm we used, on the original input graph.

For each graph of the probabilistic inference dataset, we executed the enumeration algorithm for 30 minutes. The results in Table 1 include only the experiments where the enumeration did not complete. For each graph we measured the following: the number of generated triangulations (**#trng**), the minimum observed width over all printed triangulations (**min-w**), the number of printed triangulations of width at most that of the first (**# $\leq w_1$**), the average reduction in width (over the dataset) and the maximum improvement in parentheses (**w \downarrow** (%)), and the same results for fill instead of width (**min-f**, **# $\leq f_1$** and **f \downarrow** (%)).

We can see that the algorithm, in both variants, is able to generate a significant number of triangulations of high quality, in terms of both width and fill. Moreover, it amplifies the quality of the underlying triangulation, by means of width, and much more by means of fill. According to the number of triangulations printed, MCS_M enables generating twice as many triangulations as LB_TRIANG. However, with the exception of only a handful of the graphs tested,

⁶Recall that is NP-hard to find a triangulation that minimizes the fill [39] or the width [2].

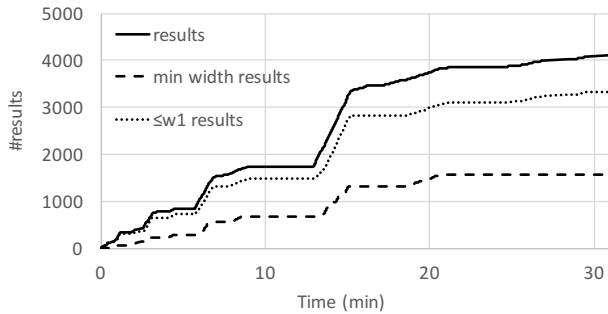


Figure 8: Cumulative number of triangulations

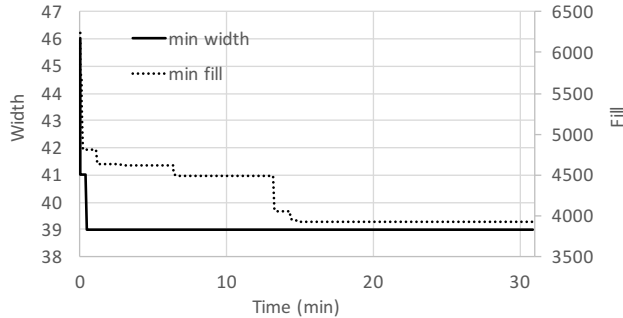


Figure 9: Minimum width and fill over time

the triangulations generated by LB_TRIANG are superior in both the width and fill metrics (this is especially apparent for the Promedas and Pedigree datasets). Furthermore, this set of superior triangulations accounts for a larger portion of the total number of triangulations that generated.

6.4 Case Study

In this section we take a closer look at the behaviour of the enumeration during a single execution. We use a graph from the Promedas dataset. In Figure 8 we show the cumulative number of results generated over time. We consider three types of results: (a) all minimal triangulations, (b) minimal triangulations of the minimum width (where the minimum is taken over the printed triangulations), and (c) those with a width at most that of the first triangulation ($\leq w_1$), which is the one that we would obtain by using only the triangulation algorithm at hand. The reduction in the number of new triangulations over time is consistent with the increase in the delay entailed in the guarantee of incremental polynomial time, rather than polynomial delay.

Figure 9 presents the reduction in the minimum width and minimum fill obtained during the execution of the algorithm. Each time slice records the minimum width (solid curve) and minimum fill (dotted curve) observed up to that time. We can see that both the width and the fill reduce over time, but the minimum observed width is reached very quickly, while attaining the minimum observed fill takes longer.

7. CONCLUDING REMARKS

We introduced the concept of a succinct graph representation (SGR), and presented an enumeration algorithm for its maximal independent sets. The algorithm enumerates in

incremental polynomial time under complexity assumptions: the SGR is tractably accessible, and it has a tractable expansion. Consequently, we established an algorithm for enumerating the minimal triangulations of a graph by reducing the problem to the enumeration of the maximal independent sets of an SGR, and showing that the complexity assumptions hold. We also proved that enumerating the minimal triangulations enables the enumeration of the proper tree decompositions. Our experimental study showed that the algorithm is effective on graphs of various domains, and is able to enhance off-the-shelf algorithms for triangulation (or tree decomposition) by generating many (rather than just one) high-quality different triangulations, and even improve standard quality measures such as width and fill.

This work opens up quite a few directions for future work. On the theoretical side, it is left open whether the enumeration of the minimal triangulations can be carried out with polynomial delay. It is clearly possible when the number of minimal separators is polynomial in the size of the input graph, using known polynomial-delay enumerations of maximal independent sets [10, 22]. Bouchitté and Todinca [8] have shown that, in this case, we can find in polynomial time a tree decomposition of a minimal width. A question we wish to explore is whether we can extend that result to enumerating the proper tree decomposition by *increasing width* (or finding the top- k decompositions of a restricted version of the problem). From the practical aspect, we believe that there are many interesting opportunities for optimizing the implementation, both in its execution cost (e.g., applying techniques for enumeration parallelization [15]) and the quality of results (e.g., heuristics for queue selections).

Acknowledgements

This work was supported in part by the US-Israel Binational Science Foundation (BSF) Grant No. 2014391, and by the Israel Science Foundation (ISF) Grant No. 1295/15. Benny Kimelfeld is a Taub Fellow, supported by the Taub Foundation. The authors are greatly thankful to LogicBlox, and in particular Hung Ngo, for insightful discussions and for providing test data.

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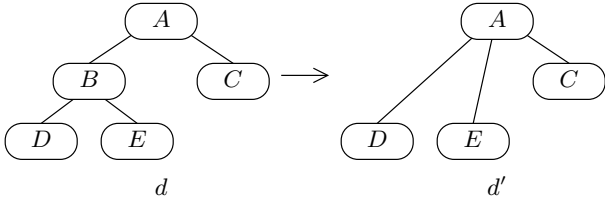


Figure 10: Obtaining a strictly subsuming tree decomposition d' given a tree decomposition d with $B \subseteq C$.

APPENDIX

A. ADDITIONAL PROOFS

In this section we give proofs that are missing from the body of the paper.

A.1 Proof of Theorem 3.4

Let P be an enumeration problem, let A be a solver for P , and let x be input for A . If τ is a time tick during the execution of $A(x)$, then we denote by $\text{out}_{A,x}(\tau)$ the answers $y \in P(x)$ that have been printed before time τ is reached. We have the following lemma.

LEMMA A.1. *Let P be an enumeration problem, and A a solver for P . The following are equivalent.*

1. *A enumerates in incremental polynomial time.*
2. *There is a polynomial p such that for all x and τ we have $p(|x| + |\text{out}_{A,x}(\tau)|) > \tau$.*

PROOF. Denote the time of the N th result by t_N .

1 \Rightarrow 2. If A enumerates in incremental polynomial time, there exists a polynomial p_1 such that $t_{N+1} - t_N \leq p_1(|x| + N)$. Without loss of generality, we assume that p_1 is monotone (as every polynomial is upper bounded by some monotone polynomial, and we can replace p_1 with such polynomial). We get the following on the printing time of the N th result.

$$t_N = \sum_{i=1}^N t_i - t_{i-1} \leq \sum_{i=1}^N p_1(|x| + i - 1) \leq N \cdot p_1(|x| + N - 1)$$

In this case we get that for any time τ there exists a polynomial p_2 such that the following holds.

$$\begin{aligned} \tau &< t_{|\text{out}_{A,x}(\tau)|+1} \\ &\leq (|\text{out}_{A,x}(\tau)| + 1) \cdot p_1(|x| + |\text{out}_{A,x}(\tau)|) \\ &\leq p_2(|x| + |\text{out}_{A,x}(\tau)|) \end{aligned}$$

2 \Rightarrow 1. Assume now that $p_3(|x| + |\text{out}_{A,x}(\tau)|) > \tau$ for any time τ . Consider the delay after the N th answer.

$$t_{N+1} - t_N \leq t_{N+1} < p_3(|x| + N + 1)$$

This shows that there exists a polynomial p_4 such that $t_{N+1} - t_N < p_4(|x| + N)$, meaning that A enumerates in incremental polynomial time. \square

We can now prove the theorem.

THEOREM 3.4. *Let P be an enumeration problem, and let A and B be two solvers for P . Suppose that for all instances x and for all answers $y \in P(x)$ we have $\text{time}_{A,x}(y) \leq \text{time}_{B,x}(y)$. If B enumerates in incremental polynomial time, then so does A .*

PROOF. Using the characterization of Lemma A.1, let p be a polynomial such that for all x and τ we have $p(|x| + |\text{out}_{B,x}(\tau)|) > \tau$. The condition of the theorem implies that at every time tick τ , the set of answers printed by B is a subset of the set of answers printed by A , and therefore, $|\text{out}_{A,x}(\tau)| \geq |\text{out}_{B,x}(\tau)|$. Again since we can assume monotonicity, we conclude that $p(|x| + |\text{out}_{A,x}(\tau)|) > \tau$ as well. We use Lemma A.1 to conclude that A enumerates in incremental polynomial time. \square

A.2 Proof of Lemma 5.3

LEMMA 5.3. *If g is a chordal graph and d is a proper tree decomposition g , then $\text{bags}(d) = \text{MaxClq}(g)$.*

PROOF. According to Proposition A.2, every clique of g is contained in some bag of d , and according to Theorem 2.3, g has some tree decomposition, say d' , where all the bags are cliques of g . So we have that $d' \sqsubseteq d$. If $\text{bags}(d) \not\subseteq \text{bags}(d')$, then d' strictly subsumes d , in contradiction to the fact that d is proper. Hence $\text{bags}(d) \subseteq \text{bags}(d')$, meaning that the bags of d are cliques of g . It thus follows that every maximal clique is a bag of d , or in notation, $\text{MaxClq}(g) \subseteq \text{bags}(d)$. Finally, Proposition A.3 states that the bags of d are an antichain w.r.t. set inclusion, and hence, $\text{bags}(d) \subseteq \text{MaxClq}(g)$. We conclude that $\text{bags}(d) = \text{MaxClq}(g)$, as claimed. \square

A.3 Proof of Lemma 5.4

In this section we prove Lemma 5.4. We first need some propositions. The following proposition is a folklore, and it is using a result by Heggernes [21], showing that every collection of subtrees of a tree satisfies the *Helly property*.

PROPOSITION A.2. *If d is a tree decomposition of a graph g , then every clique of g is contained in some bag of d .*

PROOF. We use the fact that the junction-tree property of a tree decomposition is equivalent to the property that for every node v of the graph, the bags of the tree decomposition that contain v form a (connected) subtree. Denote $d = (t, \beta)$ and let C be a clique of g . Every node v in C defines a subtree of t that is induced by the bags that contain v . Since d covers the edges of g , every two nodes in C must share some bag in d , and hence, their subtrees must share a vertex. Heggernes [21] shows that every collection of subtrees of a tree satisfies the *Helly property*: if every two subtrees share a vertex, then there exists a vertex that is shared by all the subtrees. In particular, there exists a vertex in d common to all of these subtrees; this shared node corresponds to a bag that contains C . \square

The following proposition states that in a proper tree decomposition, there is no containment among bags.

PROPOSITION A.3. *If d is a proper tree decomposition of a graph g , then $\text{bags}(d)$ is an antichain w.r.t. set inclusion (that is, no bag contains another)*

PROOF. We need to show that a proper tree decomposition cannot have two bags with one contained in the other. Assume, by way of contradiction, that d is a proper tree decomposition of g with two bags $B, C \in \text{bags}(d)$ where $B \subseteq C$. Let A be the second bag in the path from B to C .

Since d is a tree decomposition and A is on the path from B to C , we get that $B = B \cap C \subseteq A$.

Define d' to be the graph obtained from d by removing B and connecting A to all other neighbors of B , as illustrated in Figure 10. We will show that d' is a tree decomposition for g . The first two properties of the tree decomposition still hold because A contains B . Consider the path between two bags α and β of d' . If the path between them is the same as in d , the third property still holds. If it changed, then the path used to go through B , and the only new bag that may appear in this path is A . In this case, $\alpha \cap \beta \subseteq B \subseteq A$, and the third property holds as well. We have found a tree decomposition d' for g that strictly subsumes d , hence d is improper, and this is a contradiction. \square

From Theorem 2.3, the following easily follows.

PROPOSITION A.4. *If d is a tree decomposition of a graph g , then $\text{saturate}(g, d)$ is a triangulation of g .*

PROOF. From Proposition A.2 it easily follows that d is a tree decomposition of $\text{saturate}(g, d)$. Hence, since every bag of d is a clique of $\text{saturate}(g, d)$, it follows from Theorem 2.3 that $\text{saturate}(g, d)$ is chordal. \square

The next proposition states that a chordal graph g has a single proper tree decomposition, up to the equivalence \equiv_b , with the set of bags being precisely the set of maximal cliques. We can now prove Lemma 5.4.

LEMMA 5.4. *Let g be a graph. The mapping M is a bijection between $\text{MinTri}(g)$ and the equivalence classes of \equiv_b over the proper tree decompositions of g .*

PROOF. We will show that M has the correct range, that it is surjective, and that it is bijective.

M has a proper range. Let h be a minimal triangulation of g , and let d be a proper tree decomposition of h in $M(h)$. Then d is also a tree decomposition of g , as the three properties of a tree decomposition still hold. We need to show that d is a *proper* tree decomposition of g . According to Lemma 5.3, we have $\text{bags}(d) = \text{MaxClq}(h)$, and therefore, $\text{saturate}(g, d) = h$. Assume, by way of contradiction, that d is improper. Then d is strictly subsumed by some tree decomposition d' of g , meaning that $d' \sqsubset d$ and $\text{bags}(d) \not\subseteq \text{bags}(d')$. Let h' be the graph $\text{saturate}(g, d')$.

From Proposition A.4 it follows that h' is a triangulation of g . From $d' \sqsubset d$ and the fact that every bag of d is a clique of h , we conclude that $E(h') \subseteq E(h)$. And since h is a minimal triangulation, we get that $h = h'$. We can now conclude that d' is also a tree decomposition of g : the junction-tree property holds and the nodes are covered since it is a tree decomposition of g , and the edges are covered since those are the edges of h' that are covered by its definition. We get that both d and d' are tree decompositions of h , and d is strictly subsumed by d' , which contradicts the fact that d is a proper tree decomposition of h .

M is injective. Let h_1 and h_2 be two minimal triangulations such that $h_1 \neq h_2$. Without loss of generality, assume that the edge $\{u, v\}$ is in h_1 but not in h_2 . The nodes u and v are part of some maximal clique of h_1 , so they share a bag in $M(h_1)$. But they are not part of any clique of h_2 , so they do not share any bag in $M(h_2)$. Therefore, $M(h_1) \neq M(h_2)$.

M is surjective. Given a proper tree decomposition d of g , we need to show that there exists a minimal triangulation h of g such that $d \in M(h)$. Consider the graph $h = \text{saturate}(g, d)$. We will show that h is a minimal triangulation, and that d belongs to $M(h)$.

We first show that h is a minimal triangulation of g . According to Proposition A.4, h is a triangulation of g . Assume, by way of contradiction, that h is not minimal. Then there exists a minimal triangulation h' of g that is obtained from h by removing some edges; denote one of these edges by e . Consider a tree decomposition $d' \in M(h')$. The clique containing e in h is not a clique in h' , and therefore $\text{bags}(d) \not\subseteq \text{bags}(d')$. Also note that since $h' \subseteq h$, every maximal clique of h' is contained in some maximal clique of h , and therefore $d' \sqsubset d$. Then d' strictly subsumes d , in contradiction to the fact that d is proper.

Finally, we need to show that d is a proper tree decomposition of h . The nodes of h are covered in d , and the junction-tree property holds, since d is a tree decomposition of g . The new edges of h are covered in d since they are all a result of saturation of the bags of d . So d is a tree decomposition of h , and we claim that it is proper. Assume, by way of contradiction, that d is not a proper tree decomposition of h , then the tree decomposition d' that strictly subsumes it is also a tree decomposition for g , contradicting the fact that d is a proper tree decomposition of g . \square