

# Trap spaces of Boolean networks are conflict-free siphons of their Petri net encoding

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## Abstract

Boolean network modeling of gene regulation but also of post-transcriptomic systems has proven over the years that it can bring powerful analyses and corresponding insight to the many cases where precise biological data is not sufficiently available to build a detailed quantitative model. Besides simulation, the analysis of such models is mostly based on attractor computation, since those correspond roughly to observable biological *phenotypes*. The recent use of trap spaces made a real breakthrough in that field allowing to consider medium-sized models that used to be out of reach. However, with the continuing increase in model size and complexity of Boolean update functions, the state-of-the-art computation of minimal trap spaces based on *prime-implicants* shows its limits due to the difficulty of the prime-implicant computation.

In this article we explore and prove for the first time a connection between trap spaces of a general Boolean network and siphons of its Petri net encoding. Besides important theoretical applications in studying properties of trap spaces, the connection enables us to propose an alternative approach to compute minimal trap spaces, and hence complex attractors, of a general Boolean network. It replaces the need for prime-implicants by a completely different technique, namely the enumeration of maximal siphons in the Petri net encoding of the original model. We then demonstrate its efficiency and compare it to the state-of-the-art methods on a large collection of real-world

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and randomly generated models.

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## 1. Introduction

From the observation that the transcriptional regulation behaved in a sigmoid step-like way, came the original idea to represent models of gene regulation as discrete event systems. Those gene regulation networks use thresholds or equivalently logical functions to represent the different regulations [1, 2, 3, 4].

Boolean modeling made available some powerful analyses and corresponding insight for gene regulation models. Then, over the years, its use increased even for modelling post-transcriptional mechanisms, supported by the many cases where precise biological data was not sufficiently available to build a detailed quantitative model [5]. This lack of data is more frequent for large and very large models, which led to a steady increase in the size of logical models *à la* Thomas [6]. The main analysis tool for such models is the computation of its fixed and periodic attractors, since those correspond roughly to observable biological *phenotypes*. The recent use of trap spaces [7] made a real breakthrough in that field allowing to consider medium-sized models that used to be out of reach and for which only simulation was available. However, with the most recent models both being quite large and using rather complex update functions, the state-of-the-art computation of minimal trap spaces based on *prime-implicants* shows its limits. More specifically, the number of prime implicants of a Boolean function is in general exponential in the number of input nodes of this function [7]. Moreover, the computation of prime implicants is a demanding task, especially for complex Boolean functions.

It is worth noting that the recent method presented in [8] for computing minimal trap spaces avoids the prime-implicant computation by relying on the *most-permissive* semantics of Boolean networks. This method has been implemented in the tool `mpbn`<sup>1</sup> demonstrated in [9] for handling medium-sized models from the literature and very large synthetic models

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<sup>1</sup><https://github.com/bnediction/mpbn>

(up to 100,000 nodes). However, this method is only applicable for *locally-monotonic* Boolean networks, whereas the prime-implicants based method [7] is applicable for *general* Boolean networks (i.e., including both locally-monotonic and non-locally-monotonic ones). In addition, the bioLQM platform also provides another method using Binary Decision Diagrams (BDDs) in <http://colomoto.org/biolqm/doc/tools-trapSpace.html>. This method avoids the prime-implicant computation as it characterizes the set of generic trap spaces of a Boolean network by a BDD, then filters this set to get the set of all minimal trap spaces. By this approach, it requires the computation of all solutions, whereas the methods [7, 9] based on Answer Set Programming (ASP) can start enumerating them as they are found. Moreover, the main issue with the BDD-based method is that the number of generic trap spaces of a Boolean network may be extremely larger than its number of minimal trap spaces. This issue limits the efficiency of the BDD-based method. The study [10] highlights the need for non-locally-monotonic Boolean networks in both biological and theoretical aspects. Hence, it is still necessary to develop efficient methods for computing minimal trap spaces of large-scale general Boolean networks.

Petri nets were introduced in the 60s as simple formalism for describing and analyzing information-processing systems that are characterized as being concurrent, asynchronous, non-deterministic and possibly distributed [11, 12]. The use of Petri nets for representing biochemical reaction systems, by mapping molecular species to places and reactions to transitions, hinted at already in [11, 12] was used more thoroughly quite late in [13], together with some Petri net concepts and tools for the analysis of metabolic networks. Siphons are such a concept, but they have not been used a lot for the study of biochemical systems [14, 15] even if the practical cost of computing their minimal/maximal elements appear much more manageable than the theoretical complexity would indicate [16, 17].

In this article we explore and prove for the first time a connection between trap spaces of a general Boolean network and siphons of its Petri net encoding. Not only having important theoretical applications in studying properties of trap spaces in Boolean networks, the connection has important practical applications in the trap space computation. Specifically, based on the connection, we propose an alternative approach to compute minimal trap spaces, and hence complex attractors, of a general Boolean network. It replaces the need for prime-implicants by a completely different technique, namely the enumeration of maximal siphons in the Petri net encoding of the

original model. We then demonstrate its efficiency and compare it to the state-of-the-art methods for computing minimal trap spaces of Boolean networks on many real-world models from various sources in the literature and on randomly generated models.

Herein we revise and extend our previous work in [18] as follows. First, more formal definitions are given and the existing proofs are made more detailed. In particular, an updated proof provides another way to prove the independence of trap spaces of a Boolean network with respect to its update scheme, which was originally proved in [7]. Second, we showcase a theoretical application of the connection between trap spaces in Boolean networks and conflict-free siphons in Petri nets. Third, beyond the proposed ASP method implementing the alternative approach [18], we propose several other possible methods for computing minimal trap spaces using Maximum Satisfiability (MaxSAT), Constraint Programming (CP), and Integer Linear Programming (ILP). Fourth, we discuss in detail how to compute several special types of trap spaces in a Boolean network. Besides minimal trap spaces, these special types also play crucial roles in analyzing and controlling Boolean networks [19]. Fifth, regarding the implementation, we have developed a new converter that directly reads a `.bnet` file and builds the Petri net encoding, instead of using the PNML conversion of `bioLQM` [18]. Finally, we conduct a more extensive benchmark on more real-world models from various sources and randomly generated models to evaluate all the proposed methods (the benchmark conducted in [18] considers only a few dozens of representative real-world models), therefore obtaining more comprehensive insights.

The rest of this paper is organized as follows: Section 2 recalls the basic concepts including Boolean networks, attractors, trap spaces, Petri nets, and siphons. Section 3 presents the main finding, the connection between trap spaces in Boolean networks and siphons in Petri nets. Section 4 presents the alternative approach for computing minimal trap spaces and the four possible methods implementing it. Section 5 shows an important biological case study showing the applicability of the new approach. Section 6 reports the experimental results for evaluating the efficiency of the proposed methods. Finally, Section 7 concludes the paper and draws future work.

## 2. Preliminaries

We shall briefly recall here some preliminaries on Boolean networks related to trap spaces and Petri nets.

104 2.1. Boolean networks

105 **Definition 2.1.** A Boolean Network (BN) is a pair  $\mathcal{N} = (V, F)$  where:

- 106 •  $V = \{v_1, \dots, v_n\}$  is the set of nodes. We use  $v_i$  to denote both the node  
107  $v_i$  and its associated Boolean variable.
- 108 •  $F = \{f_1, \dots, f_n\}$  is the set of update functions. Each function  $f_i$  is  
109 associated with node  $v_i$  and satisfies  $f_i: \mathbb{B}^{|IN(v_i)|} \mapsto \mathbb{B}$  where  $\mathbb{B} = \{0, 1\}$   
110 and  $IN(v_i)$  denotes the set of input nodes of  $v_i$ . Note that a node  $v_i \in V$   
111 is called a source node if and only if  $f_i = v_i$ .

112 A Boolean function is *locally-monotonic* if it can be represented by a  
113 formula in disjunctive normal form in which all occurrences of any given  
114 literal are either negated or non-negated [9]. A Boolean network is said  
115 to be locally-monotonic if all its Boolean functions are locally-monotonic.  
116 Otherwise, this model is said to be non-locally-monotonic.

A state  $v \in \mathbb{B}^n$  is as a mapping  $v: V \mapsto \mathbb{B}$  that assigns either 0 (inactive)  
or 1 (active) to each node. We denote the set of all possible states of a Boolean  
network  $\mathcal{N}$  by  $\mathcal{S}_{\mathcal{N}} = \mathbb{B}^n$ . At each time step  $t$ , node  $v_i$  can, depending on the  
update scheme, update its state by

$$v_i(t+1) = \begin{cases} f_i(v(t)) \\ \text{or} & v_i(t) \end{cases}$$

117 where  $v(t)$  (resp.  $v_i(t)$ ) is the state of  $\mathcal{N}$  (resp. the state of node  $v_i$ ) at time  
118  $t$ . Note that for simplicity, we write  $f_i(v(t))$  even if  $IN(v_i) \subsetneq V$  (i.e.,  $IN(v_i)$   
119 does not contain some nodes of  $V$ ). An update scheme of a Boolean network  
120 specifies which nodes update their states, as defined above, through time  
121 evolution [4]. Following the update scheme, the Boolean network transits  
122 from a state to another state (possibly identical). This transition is called  
123 the *state transition* and denoted by  $\rightarrow \subseteq \mathcal{S}_{\mathcal{N}} \times \mathcal{S}_{\mathcal{N}}$ . Then the dynamics of  $\mathcal{N}$   
124 is captured by the directed graph  $(\mathcal{S}_{\mathcal{N}}, \rightarrow)$  called the State Transition Graph  
125 (STG). There are many different update schemes, but the two main types [4]  
126 are: *synchronous*, where all the nodes are update simultaneously, and *fully*  
127 *asynchronous*, where only one node is selected non-deterministically to be  
128 updated.

## 129 2.2. Traps spaces

130 We recall here some definitions from [7] for the introduction of *trap spaces*.  
 131 Minimal trap spaces prove to be a very good approximation of the attractors  
 132 of a Boolean network under asynchronous update schemes and have become  
 133 the *de facto* standard way to analyze models of a few tens of *genes* [20, 21].

134 A non-empty set  $T \subseteq \mathcal{S}_{\mathcal{N}}$  is a trap set with respect to  $\rightarrow$  if for every  
 135  $x \in T$  and  $y \in S$  with  $x \rightarrow y$  it holds that  $y \in T$  [7]. An attractor of  $\mathcal{N}$   
 136 with respect to  $\rightarrow$  can be defined as an inclusion-wise minimal trap set of  
 137  $(\mathcal{S}_{\mathcal{N}}, \rightarrow)$ . An attractor can be also seen as a terminal strongly connected  
 138 component of  $(\mathcal{S}_{\mathcal{N}}, \rightarrow)$  [22]. An attractor of size 1 is called a fixed point,  
 139 otherwise it is called a cyclic or complex attractor [7].

A subspace  $m$  of a Boolean network  $\mathcal{N} = (V, F)$  is a mapping  $m: V \mapsto \mathbb{B} \cup \{\star\}$ .  $m(v_i) \in \mathbb{B}$  means that the value of  $v_i$  is fixed in  $m$  and  $v_i$  is called a *fixed* variable.  $m(v_i) \in \star$  means that the value of  $v_i$  is free in  $m$  and  $v_i$  is called a *free* variable. We denote  $D_m$  the set of all fixed variables of  $m$ . A subspace  $m$  is equivalent to a set of states:

$$\mathcal{S}_{\mathcal{N}}[m] := \{s \in \mathcal{S}_{\mathcal{N}} \mid \forall v \in D_m: s(v) = m(v)\}.$$

140 For example,  $m = \star\star 1$  (for simplicity, we shall write subspaces likes states as  
 141 a sequence of values) means that  $D_m = \{v_3\}$ ,  $m(v_3) = 1$ , and it is equivalent  
 142 to the set of states  $\{001, 011, 101, 111\}$ . We denote  $\mathcal{S}_{\mathcal{N}}^{\star} = (\mathbb{B} \cup \{\star\})^n$  the set  
 143 of all possible subspaces of  $\mathcal{N}$ . Note that  $|\mathcal{S}_{\mathcal{N}}^{\star}| = 3^n$  and  $\mathcal{S}_{\mathcal{N}} \subset \mathcal{S}_{\mathcal{N}}^{\star}$  [7].

144 A *trap space* is defined as a subspace that is also a trap set. It is noted  
 145 that trap spaces of a Boolean network are independent of the update scheme  
 146 of this model [7]. Then, we define a partial order  $<$  on  $\mathcal{S}_{\mathcal{N}}^{\star}$  as:  $m < m'$  if and  
 147 only if  $\mathcal{S}_{\mathcal{N}}[m] \subseteq \mathcal{S}_{\mathcal{N}}[m']$  and  $\mathcal{S}_{\mathcal{N}}[m] \neq \mathcal{S}_{\mathcal{N}}[m']$ . Consequently, a trap space  $m$   
 148 is minimal if and only if there is no trap space  $m' \in \mathcal{S}_{\mathcal{N}}^{\star}$  such that  $m' < m$ .

149 For example, let us consider the Boolean network shown in Example 2.1.  
 150 Figure 1(a) shows the dynamics of this model under the fully asynchronous  
 151 update (i.e., only one node is updated at each time step). The model has  
 152 all two trap spaces,  $m_1 = 11$  and  $m_2 = \star\star$ . Since  $m_1 < m_2$ ,  $m_1$  is the only  
 153 minimal trap space of the Boolean network.

154 **Example 2.1.** We give a Boolean network  $\mathcal{N} = (V, F)$ , where  $V = (x_1, x_2)$   
 155 and  $F = (f_1, f_2)$  with  $f_1 = (x_1 \wedge x_2) \vee (\neg x_1 \wedge \neg x_2)$ ,  $f_2 = (x_1 \wedge x_2) \vee (\neg x_1 \wedge \neg x_2)$ .  
 156 Herein,  $\wedge$ ,  $\vee$ , and  $\neg$  denote the logical conjunction, disjunction, and negation  
 157 operators, respectively.



Figure 1: Dynamics and encoding of the Boolean network of Example 2.1.

### 2.3. Petri net encoding of Boolean networks

**Definition 2.2.** A Petri net is a weighted bipartite directed graph  $(P, T, W)$ , where  $P$  is a non-empty finite set of vertices called places,  $T$  is a non-empty finite set of vertices called transitions,  $P \cap T = \emptyset$ , and  $W : (P \times T) \cup (T \times P) \mapsto \mathbb{N}$  is a weight function attached to the arcs.

A marking for a Petri net is a mapping  $m : P \mapsto \mathbb{N}$  that assigns a number of tokens to each place. A place  $p$  is marked by a marking  $m$  if and only if  $m(p) > 0$ . Marking  $m$  can be seen as a subset of  $P$  that contains all marked places by  $m$ . We shall write  $\text{pred}(x)$  (resp.  $\text{succ}(x)$ ) to represent the set of vertices that have a (non-zero weighted) arc leading to (resp. coming from)  $x$ . In this work, we consider a class of Petri nets called 1-safe Petri nets where every place has at most 1 token and all arcs are of weight 1. In this case, weights are implicitly omitted in the arcs of a Petri net. Then, a transition  $t \in T$  is *enabled* at a marking  $m$  if and only if  $\text{pred}(t) \subseteq m$ . A marking  $m$  is called a *deadlock* if there are no enabled transitions at  $m$ . The firing of  $t$  leads to a new marking  $m'$  specified by  $m' = (m \setminus \text{pred}(t)) \cup \text{succ}(t)$ . Note that when multiple transitions are enabled, we need to embed one firing scheme (similar to the update scheme of a Boolean network) to the Petri net. The classical firing scheme is that only one of the enabled transition is non-deterministically chosen to fire [12].

The link between Boolean networks *à la* Thomas and Petri nets was originally established in [23] in order to make available formal methods like model-checking for the analysis of such systems. The basic encoding into 1-safe (i.e., never more than one token in each place) nets only holds for purely Boolean networks but was later extended to multivalued logical models in two ways, either in [24] with non 1-safe Petri nets or more recently in [22] with 1-safe nets but many more places.

185 Since our study is focused on Boolean networks, we briefly recall the orig-  
186 inal encoding here. Its basis is that every node (*gene*)  $v$  of the original model  
187  $\mathcal{N} = (V, F)$  is represented by two separate places ( $p_v$  and  $\bar{p}_v$ ), corresponding  
188 to its two states, active, and inactive, respectively. Each conjunct of the  
189 logical function that activates the *gene* will lead to a transition  $t$ , consuming  
190 the inactive place (i.e., a directional arc from  $\bar{p}_v$  to  $t$ ), producing the active  
191 place (i.e., a directional arc from  $t$  to  $p_v$ ), and with all other literals both  
192 consumed and produced (i.e., a bidirectional arc). And conversely for the  
193 inactivation. Let  $s$  be a state of the Boolean network and  $m_s$  be its corre-  
194 sponding marking in the encoded Petri net. It holds that  $\forall v \in V, s(v) = 0$  if  
195 and only if  $m_s(\bar{p}_v) = 1$  and  $s(v) = 1$  if and only if  $m_s(p_v) = 1$ . Note also that  
196 at any marking  $m$  of the Petri net encoding a Boolean network, it always  
197 holds that  $m(p_v) + m(\bar{p}_v) = 1$ .

198 The main property of this encoding is that it is completely faithful with  
199 respect to the update scheme of the original Boolean network. For each node  
200  $v$  of  $\mathcal{N}$ , only transitions corresponding to  $v$  can change the current marking  
201 of  $p_v$  or  $\bar{p}_v$ . In addition, at any marking at most one of such transitions is en-  
202 abled because  $m(p_v) + m(\bar{p}_v) = 1$  holds. Hence, for any update scheme in  $\mathcal{N}$ ,  
203 we have a corresponding firing scheme in  $\mathcal{P}$ , which preserves the equivalence  
204 between the dynamics of  $\mathcal{N}$  and  $\mathcal{P}$  [25].

205 For illustration, let us reconsider the Boolean network shown in Exam-  
206 ple 2.1. Figure 1(b) shows the Petri net encoding of this Boolean network.  
207 Place  $p_{x_1}$  (resp.  $\bar{p}_{x_1}$ ) in  $\mathcal{P}$  represents the activation (resp. the inactivation) of  
208 node  $x_1$  in  $\mathcal{N}$ . Marking  $\{p_{x_1}, \bar{p}_{x_2}\}$  in  $\mathcal{P}$  represents state 10 in  $\mathcal{N}$ . Transitions  
209  $t_{x_1}^1$  and  $t_{x_1}^2$  represent the update of node  $x_1$ . Of course, in any marking  $t_{x_1}^1$   
210 and  $t_{x_1}^2$  cannot be both enabled. Then, the fully asynchronous update scheme  
211 in  $\mathcal{N}$  corresponds to the classical firing scheme in  $\mathcal{P}$  where only one of the  
212 enabled transitions for a given marking will be fired [12].

213 Note that given a Boolean network in the standard **SBML-Qual** format [26],  
214 i.e., the package of SBML v3 [27] for such models, one can easily obtain its  
215 Petri net encoding in the Petri Net Markup Language (PNML)<sup>2</sup> standard  
216 using the **bioLQM**<sup>3</sup> library. This piece of software extracted from **GINsim** [28]  
217 and part of the **CoLoMoTo**<sup>4</sup> [29] software suite allows for easy conversion

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<sup>2</sup><https://www.pnml.org/>

<sup>3</sup><http://www.colomoto.org/biolqm/>

<sup>4</sup><http://colomoto.org/>



218 between standard formats. It also accepts many other common formats for  
 219 Boolean networks, notably the `.bnet` files of the BoolNet [30, 20] tools. The  
 220 conversion is executed as follows:

```
221 java -jar GINsim.jar -lqm <input.{sbml,bnet,...}> <output.pnml>
```

222 Note that transforming a Boolean network defined by its functions into its  
 223 Petri net encoding roughly relies on obtaining conditions for the activation  
 224 and inactivation of the states. In [23] this took the form of the whole truth  
 225 table of the Boolean functions, but as shown in Appendix 1 of [22] comput-  
 226 ing Disjunctive Normal Forms (DNF) of each Boolean function is enough.  
 227 Though this might appear quite computationally intensive it is important to  
 228 remark first that contrary to the prime-implicants case, there is no need to  
 229 find *minimal* DNFs. One way to look at this is to consider that this amounts  
 230 to a similar approach as that used in [8] but with the encoding of both activa-  
 231 tion and inhibition functions as DNFs in order to take into account possible  
 232 non-local-monotonicity. This does not change the worst-case-complexity (ob-  
 233 taining a single DNF being exponential) but might matter a lot in practice.  
 234 As such, we will explore how this transformation, here using BDDs in `bioLQM`  
 235 or directly in our tool using the `pyeda`<sup>5</sup> library, and the one based on the  
 236 most-permissive semantics compare with each other in Section 6.

#### 237 2.4. Siphons

238 Siphons are a static and classical property of Petri nets [11]. Note how-  
 239 ever that the use of siphons for the analysis of biological models, though it is  
 240 not new, has been mostly relevant to the ODE-based continuous semantics  
 241 of chemical reaction networks [31, 32, 33]. We recall here the basic definition  
 242 establishing that to produce something in a siphon you must consume some-  
 243 thing from the siphon. This corresponds to the idea that a siphon is a set of  
 244 places that once unmarked remains unmarked.

**Definition 2.3.** *A siphon of a Petri net  $(P, T, W)$  is a set of places  $S$  such that:*

$$\forall t \in T, S \cap \text{succ}(t) \neq \emptyset \Rightarrow S \cap \text{pred}(t) \neq \emptyset.$$

245 *Note that  $\emptyset$  is trivially a siphon.*

246 Let  $\text{pred}(S) := \bigcup_{s \in S} \text{pred}(s)$  and  $\text{succ}(S) := \bigcup_{s \in S} \text{succ}(s)$ . If  $S = \emptyset$ , then  
 247 conventionally  $\text{pred}(S) = \text{succ}(S) = \emptyset$ . We have an important property on  
 248 siphons [34] as follows.

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<sup>5</sup><https://pyeda.readthedocs.io/en/latest/>

249 **Proposition 2.1.** *Let  $S$  be a siphon of a Petri net  $(P, T, W)$ . Then  $\text{pred}(S) \subseteq$*   
 250  *$\text{succ}(S)$ .*

### 251 3. Trap spaces as conflict-free siphons

252 First, we add a definition related to any set of places of a Petri net  
 253 encoding a Boolean network, and notably a siphon of such a net.

254 **Definition 3.1.** *A set of places of Petri net  $\mathcal{P}$  encoding Boolean network*  
 255  *$\mathcal{N}$  is conflict-free if it does not contain any two places corresponding to the*  
 256 *active and inactive states of the same node of  $\mathcal{N}$ . Then, a conflict-free siphon*  
 257  *$S$  is said to be maximal if and only if there is no other conflict-free siphon*  
 258  *$S'$  such that  $S \subset S'$ .*

259 Intuitively, a siphon is a set of places that once unmarked remains so.  
 260 If it is conflict-free then its dual corresponds to a subspace of the model  
 261 such that whatever update, the fixed values remain so (since the unmarked  
 262 places remain unmarked). This is precisely the definition of a trap space and  
 263 maximality of the siphon is equivalent to as many fixed values as possible,  
 264 hence minimality of the trap space. For example, the Boolean network given  
 265 in Example 2.1 has two trap spaces,  $m_1 = 11$  and  $m_2 = \star\star$ . The Petri net  
 266 encoding of this Boolean network has five generic siphons,  $S_1 = \emptyset$ ,  $S_2 =$   
 267  $\{p_{x_1}, \bar{p}_{x_1}\}$ ,  $S_3 = \{p_{x_2}, \bar{p}_{x_2}\}$ ,  $S_4 = \{\bar{p}_{x_1}, \bar{p}_{x_2}\}$ , and  $S_5 = \{p_{x_1}, \bar{p}_{x_1}, p_{x_2}, \bar{p}_{x_2}\}$ .  
 268 However, only  $S_1$  and  $S_4$  are conflict-free siphons and correspond to  $m_2$  and  
 269  $m_1$ , respectively. Since  $S_1 \subset S_4$ ,  $S_4$  is a maximal siphon corresponding to  
 270 the minimal trap space  $m_1$ . Hereafter, we formally prove that a (maximal)  
 271 conflict-free siphon is equivalent to a (minimal) trap space.

**Definition 3.2.** *Let  $m$  be a subspace of Boolean network  $\mathcal{N} = (V, F)$ . A*  
*mirror of  $m$  is a set of places  $S$  in the Petri net encoding  $\mathcal{P}$  of  $\mathcal{N}$  such that:*

$$\forall v \in D_m, m(v) = 0 \Leftrightarrow p_v \in S, m(v) = 1 \Leftrightarrow \bar{p}_v \in S$$

and

$$\forall v \in V \setminus D_m, p_v \notin S, \bar{p}_v \notin S.$$

272 **Theorem 3.1.** *Let  $\mathcal{N} = (V, F)$  be a Boolean network and  $\mathcal{P}$  be its Petri net*  
 273 *encoding. A subspace  $m$  is a trap space of  $\mathcal{N}$  if and only if its mirror  $S$  is a*  
 274 *conflict-free siphon of  $\mathcal{P}$ .*

275 *Proof.* First, we show that if  $m$  is a trap space of  $\mathcal{N}$ , then  $S$  is a conflict-free  
 276 siphon of  $\mathcal{P}$  (\*). If  $D_m = \emptyset$ , then  $S = \emptyset$  is trivially a conflict-free siphon of  
 277  $\mathcal{P}$ . Thus, we consider the case that  $D_m \neq \emptyset$  (resp.  $S \neq \emptyset$ ). Assume that  $S$   
 278 is not a siphon of  $\mathcal{P}$ . Then, there is a transition  $t \in T$  such that  $S \cap \text{succ}(t) \neq \emptyset$   
 279 but  $S \cap \text{pred}(t) = \emptyset$ . This implies that there is a place  $p \in S$  such that  
 280  $p \in \text{succ}(t)$  but  $p \notin \text{pred}(t)$ . Let  $v$  be the node in  $\mathcal{N}$  corresponding to  $p$ . By  
 281 the characteristics of the encoding [23], there is a directional arc from  $t$  to  $p$   
 282 and a directional arc from the complementary place of  $p$  to  $t$ . Without loss  
 283 of generality, we assume that  $p = p_v$ , then there is a directional arc from  $t$   
 284 to  $p_v$  and a directional arc from  $\bar{p}_v$  to  $t$ . We follow the following procedure  
 285 to find a state  $s \in \mathcal{S}_{\mathcal{N}}[m]$  such that  $m_s(p') = 1, \forall p' \in \text{pred}(t)$  where  $m_s$  is  
 286 the corresponding marking in  $\mathcal{P}$  of  $s$ . For every place  $p' \in \text{pred}(t)$ , let  $p''$  be  
 287 the complementary place of  $p'$  and  $v'$  be the corresponding node in  $\mathcal{N}$  of  $p'$   
 288 and  $p''$ . If  $p'' \notin S$ , then  $v' \notin D_m$  and we can always set a Boolean value to  
 289  $s(v')$  such that  $s \in \mathcal{S}_{\mathcal{N}}[m]$  and  $m_s(p') = 1$ . If  $p'' \in S$ , then  $v' \in D_m$  and we  
 290 set  $s(v') = m(v')$ . In this case, if  $p' = p_v$  then  $s(v') = m(v') = 1$  leading to  
 291  $m_s(p') = 1$ , if  $p' = \bar{p}_v$  then  $s(v') = m(v') = 0$  leading to  $m_s(p') = 1$ . For  
 292 the remaining nodes of  $\mathcal{N}$ , we can always set Boolean values to these nodes  
 293 to preserve that  $s \in \mathcal{S}_{\mathcal{N}}[m]$ . We also have  $m_s(p_v) = 0$  by the characteristics  
 294 of the encoding [23]. Now,  $t$  is enabled at marking  $m_s$ . Its firing leads to  
 295 a new marking  $m'_s$  such that  $m'_s(p_v) = 1$  and  $m'_s(\bar{p}_v) = 0$ . Let  $s'$  be the  
 296 corresponding state in  $\mathcal{N}$  of  $m'_s$ . We have  $s'(v) = 1$  because  $m'_s(p_v) = 1$  and  
 297  $m(v) = 0$  because  $p_v \in S$ . This implies that  $s' \notin \mathcal{S}_{\mathcal{N}}[m]$ . For any firing  
 298 scheme of  $\mathcal{P}$ , the firing of  $t$  always happens. Since a firing scheme of  $\mathcal{P}$   
 299 is equivalent to an update scheme of  $\mathcal{N}$ ,  $s$  can escape from the trap space  $m$   
 300 for any update scheme of  $\mathcal{N}$ , which contradicts to the property of a trap  
 301 space. Hence,  $S$  is a siphon of  $\mathcal{P}$ . By the definition of a mirror,  $S$  is also a  
 302 conflict-free one.

303 Second, we show that if  $S$  is a conflict-free siphon of  $\mathcal{P}$ , then  $m$  is a trap  
 304 space of  $\mathcal{N}$  (\*\*). By the definition of a mirror,  $m$  is a subspace of  $\mathcal{N}$ . Let  
 305  $s$  be an arbitrary state in  $\mathcal{S}_{\mathcal{N}}[m]$  and  $m_s$  be its corresponding marking in  
 306  $\mathcal{P}$ . Assume that there is a place  $p \in S$  such that  $m_s(p) = 1$ . Let  $v$  be the  
 307 corresponding node in  $\mathcal{N}$  of  $p$ . Since  $p \in S$ ,  $v \in D_m$  and  $m(v) = s(v)$ . If  
 308  $p = p_v$ , then  $m_s(p_v) = 1$  leading to  $m(v) = s(v) = 1$  by the characteristics of  
 309 the encoding [23]. By the definition of a mirror,  $m(v) = 0$  because  $p_v \in S$ ,  
 310 which is a contradiction. It is symmetric for the case that  $p = \bar{p}_v$ . Hence,  
 311  $m_s(p) = 0, \forall p \in S$ . In any marking  $m'_s$  reachable from  $m_s$  regardless of the  
 312 firing scheme of  $\mathcal{P}$ , we have  $m'_s(p) = 0, \forall p \in S$  by the dynamical property on

313 markings of a siphon [34]. Let  $s'$  be the corresponding state in  $\mathcal{N}$  of  $m'_s$ . For  
 314 every node  $v \in D_m$ , we have all two cases as follows. Case 1:  $p_v \in S$ , then  
 315  $m'_s(p_v) = 0$ , thus  $s'(v) = 0 = m(v)$ . Case 2:  $\bar{p}_v \in S$ , then  $m'_s(\bar{p}_v) = 0$ , thus  
 316  $s'(v) = 1 = m(v)$ . Hence,  $s'(v) = m(v)$  for every  $v \in D_m$ . Then,  $s' \in \mathcal{S}_{\mathcal{N}}[m]$ .  
 317 By the definition of a trap space and the arbitrariness of  $s$ ,  $m$  is a trap space  
 318 of  $\mathcal{N}$ .

319 From (\*) and (\*\*), we can conclude the proof.  $\square$

320 From the proof of Theorem 3.1, we can see that the theorem holds for  
 321 any update scheme associated to the Boolean network. Since the Petri net  
 322 encoding of a Boolean network is independent of its update scheme and  
 323 siphons are a static property of a Petri net, we can imply that trap spaces of a  
 324 Boolean network are independent of its update scheme. Note that the original  
 325 proof for this property of trap spaces (see Theorem 1 of [7]) only considers  
 326 the two popular update schemes (i.e., synchronous and fully asynchronous).  
 327 Theorem 3.1 exhibits the very first theoretical application of the connection  
 328 between trap spaces of Boolean networks and siphons of Petri nets.

329 **Theorem 3.2.** *Let  $\mathcal{N}$  be a Boolean network and  $\mathcal{P}$  be its Petri net encoding.*  
 330 *A subspace  $m$  is a minimal trap space of  $\mathcal{N}$  if and only if its mirror  $S$  is a*  
 331 *maximal conflict-free siphon of  $\mathcal{P}$ .*

332 *Proof.* First, we show that if  $m$  is a minimal trap space of  $\mathcal{N}$ , then  $S$  is  
 333 a maximal conflict-free siphon of  $\mathcal{P}$  (\*). Since  $m$  is a trap space of  $\mathcal{N}$ ,  
 334  $S$  is a conflict-free siphon of  $\mathcal{P}$  by Theorem 3.1. Assume that  $S$  is not  
 335 maximal. Then, there is another conflict-free siphon  $S'$  such that  $S \subset S'$ .  
 336 By Theorem 3.1, there is a trap space  $m'$  corresponding to  $S'$ . Following the  
 337 definition of a mirror,  $D_m \subset D_{m'}$  and  $m(v) = m'(v), \forall v \in D_m$ . It follows  
 338 that  $\mathcal{S}_{\mathcal{N}}[m'] \subset \mathcal{S}_{\mathcal{N}}[m]$ , thus  $m' < m$ . This contradicts to the minimality of  
 339  $m$ . Hence,  $S$  is a maximal conflict-free siphon of  $\mathcal{P}$ .

340 Second, we show that if  $S$  is a maximal conflict-free siphon of  $\mathcal{P}$ , then  
 341  $m$  is a minimal trap space of  $\mathcal{N}$  (\*\*). Since  $S$  is a conflict-free siphon of  $\mathcal{P}$ ,  
 342  $m$  is a trap space of  $\mathcal{N}$  by Theorem 3.1. Assume that  $m$  is not minimal.  
 343 Then, there is another trap space  $m'$  such that  $m' < m$ . By the definition of  
 344 the partial order  $<$  on subspaces,  $\mathcal{S}_{\mathcal{N}}[m'] \subset \mathcal{S}_{\mathcal{N}}[m]$ . Let  $S'$  be the mirror of  
 345  $m'$ .  $S'$  is a conflict-free siphon by Theorem 3.1. Following the definition of  
 346 a mirror,  $S \subset S'$ , which contradicts to the maximality of  $S$ . Hence,  $m$  is a  
 347 minimal trap space of  $\mathcal{N}$ .

348 From (\*) and (\*\*), we can conclude the proof.  $\square$

349 We here showcase a theoretical application of the connection between  
 350 trap spaces in Boolean networks and conflict-free siphons in Petri nets. We  
 351 use it to prove a property of minimal trap spaces, which has surprisingly  
 352 not been formally proved. Specifically, all minimal trap spaces of a Boolean  
 353 network are mutually disjoint. This property is important because we can  
 354 use it to approximate the set of attractors of the Boolean network under  
 355 any update scheme [7] or to compute exactly the set of complex attractors  
 356 of the Boolean network under the fully asynchronous update scheme [35].  
 357 Note that it would be not difficult to obtain a direct proof on trap spaces  
 358 for this property, which follows the same structure as the proof on siphons.  
 359 However, we emphasize here the potential of using the connection between  
 360 Boolean networks and Petri nets to explore and prove properties of trap  
 361 spaces in Boolean networks.

362 **Theorem 3.3.** *Let  $\mathcal{N} = (V, F)$  be a Boolean network. For any two distinct*  
 363 *minimal trap spaces  $m_1$  and  $m_2$  of  $\mathcal{N}$ , we have that  $\mathcal{S}_{\mathcal{N}}[m_1] \cap \mathcal{S}_{\mathcal{N}}[m_2] = \emptyset$ .*

364 *Proof.* Let  $\mathcal{P}$  be the Petri net encoding of  $\mathcal{N}$ . If  $\mathcal{N}$  has only one minimal  
 365 trap space, then the theorem trivially holds. Note that by Theorem 3.2,  
 366  $\mathcal{N}$  always has at least one minimal trap space because  $\mathcal{P}$  has at least one  
 367 maximal conflict-free siphon. Hence, we consider the case that  $\mathcal{N}$  has at least  
 368 two minimal trap spaces.

369 Consider two any distinct minimal trap spaces  $m_1$  and  $m_2$ . Assume that  
 370  $\mathcal{S}_{\mathcal{N}}[m_1] \cap \mathcal{S}_{\mathcal{N}}[m_2] \neq \emptyset$ . Let  $S_1$  and  $S_2$  be the mirrors of  $m_1$  and  $m_2$ , re-  
 371 spectively. By Theorem 3.2,  $S_1$  and  $S_2$  are maximal conflict-free siphons  
 372 of  $\mathcal{P}$ . We have that  $S = S_1 \cup S_2$  is also a siphon because of Proposi-  
 373 tion 2.1. For every node  $v \in V$ , assume that  $p_v \in S$  and  $\bar{p}_v \in S$  hold.  
 374 Since  $S_1$  and  $S_2$  are conflict-free, there are all two cases. Case 1:  $p_v \in S_1$   
 375 and  $\bar{p}_v \in S_2$ . Case 2:  $p_v \in S_2$  and  $\bar{p}_v \in S_1$ . These two cases lead to  
 376  $m_1(v) \neq m_2(v)$ ,  $m_1(v) \neq \star$ ,  $m_2(v) \neq \star$ , then  $\mathcal{S}_{\mathcal{N}}[m_1] \cap \mathcal{S}_{\mathcal{N}}[m_2] = \emptyset$ . This is a  
 377 contradiction. Hence, for every node  $v \in V$ ,  $p_v \in S$  and  $\bar{p}_v \in S$  cannot hold  
 378 together. Therefore,  $S$  is conflict-free. Now, we have that  $S$  is a conflict-free  
 379 siphon but  $S_1 \subset S$  or  $S_2 \subset S$  holds because  $S_1 \neq S_2$ . This contradicts to the  
 380 maximality of  $S_1$  and  $S_2$ . Hence,  $\mathcal{S}_{\mathcal{N}}[m_1] \cap \mathcal{S}_{\mathcal{N}}[m_2] = \emptyset$  holds.

381

□

382 A natural computational application of Theorem 3.1 is that we can effi-  
 383 ciently decide whether a subspace  $m$  is a trap space. In `PyBoolNet` [20], this  
 384 is checked by using the percolation on the prime-implicants of the Boolean

385 functions. As we have mentioned at the beginning of this article, the com-  
 386 putation of prime-implicants is a demanding task for complex Boolean net-  
 387 works, even is sometimes intractable. Hence, the checking method in [20]  
 388 shows its limitations. Instead, we can first compute the mirror  $S_m$  of  $m$  in  
 389 the Petri net encoding. Then, by Proposition 2.1 and Theorem 3.1, we can  
 390 check if  $\text{pred}(S_m) \subseteq \text{succ}(S_m)$ . Note that the Petri net construction is less  
 391 computationally demanding than the prime-implicant computation because  
 392 it only requires computing generic (not prime) implicants of the Boolean  
 393 functions [22]. In addition, the worst case time complexity of the above  
 394 checking method is quadratic in the number of transitions of the Petri net.

395 Furthermore, by Theorem 3.2, we can reduce the problem of computing  
 396 all minimal trap spaces of a Boolean network to the problem of computing  
 397 all maximal conflict-free siphons of its Petri net encoding. Note that in the  
 398 case of special types of trap spaces (e.g., fixed points), this can be put in  
 399 regard to special types of siphons in Petri nets. See Subsection 4.5 for more  
 400 discussions about many special types of trap spaces. It might actually be  
 401 possible to generalize our result to any 1-safe place-complementary Petri net  
 402 to define a notion of trap spaces that might be useful for the analysis of Petri  
 403 nets, but this is out of the scope of the present article.

404 Note that there are no existing methods specifically designed for comput-  
 405 ing maximal conflict-free siphons (even maximal generic siphons) of a Petri  
 406 net. The reason might be that researchers mainly focus on minimal generic  
 407 siphons [34] in the field of Petri nets. Hence, we here propose several meth-  
 408 ods for computing maximal conflict-free siphons of a Petri net. The details  
 409 of the proposed methods shall be given in the next section.

## 410 4. Computation methods

### 411 4.1. Characterization

First, we show the characterization of all conflict-free siphons of the en-  
 coded Petri net  $\mathcal{P} = (P, T, W)$ . Suppose that  $S$  is a generic siphon of  $\mathcal{P}$ .  
 If a place  $p$  should belong to  $S$ , then by Proposition 2.1 all the transitions  
 in  $\text{pred}(p)$  must belong to  $\text{succ}(S)$ . A transition  $t$  belongs to  $\text{succ}(S)$  if and  
 only if there is at least one place  $p'$  in  $S$  such that  $p' \in \text{pred}(t)$ . Hence, for  
 each transition  $t \in \text{pred}(p)$ , we can state that

$$p \in S \Rightarrow \bigvee_{p' \in \text{pred}(t)} p' \in S. \quad (1)$$

The system of all the rules of the above form with respect to all pairs  $(p, t)$  where  $p \in P, t \in T, t \in \text{pred}(p)$  fully characterizes all generic siphons of a Petri net and has been used with SAT solvers in [16, 17]. To make  $S$  to be a conflict-free siphon, we need to add to the system the rule

$$p_v \in S \Rightarrow \bar{p}_v \notin S \wedge \bar{p}_v \in S \Rightarrow p_v \notin S \quad (2)$$

412 for each node  $v \in V$ . By definition, the final system fully characterizes all  
 413 conflict-free siphons of the encoded Petri net.

#### 414 4.2. Constraint satisfaction problem

415 The following Boolean Constraint Satisfaction Problem (CSP) directly  
 416 derives from the above characterization:

417 **Definition 4.1.** *Given a Petri net  $\mathcal{P} = (P, T, W)$  encoding a Boolean net-*  
 418 *work  $\mathcal{N} = (V, F)$ . The CSP  $\mathcal{C}(\mathcal{P})$  is the triple  $(R, D, C)$  where*

- 419 •  $R = P$ , i.e., a variable is introduced for each place of  $\mathcal{P}$ ,
- 420 •  $D(p) = \mathbb{B}$  for all  $p \in R$ , i.e., the variables are Boolean,
- 421 •  $C = \{\neg p_v \vee \neg \bar{p}_v = 1 \mid \forall v \in V\} \wedge \{(p = 1 \rightarrow \bigvee_{p' \in \text{pred}(t)} p' = 1) \mid p \in$   
 422  $P, t \in \text{pred}(p)\}$ .

**Proposition 4.1.**  $\mathcal{C}(\mathcal{P})$  is satisfied by a valuation  $r$  if and only if

$$\{p \in P \mid r(p) = 1\}$$

423 is a conflict-free siphon of  $\mathcal{P}$ .

424 *Proof.* By the former part  $\neg p_v \vee \neg \bar{p}_v = 1$  of  $C$ , the conflict-freeness is imposed  
 425 because for any satisfiable valuation  $r$ ,  $r(p_v) = r(\bar{p}_v) = 1$  is impossible for all  
 426  $v \in V$ . As shown in [17], the latter part of  $C$  can characterize the set of all  
 427 generic siphons of  $\mathcal{P}$ . Hence, we can conclude the proof.

428 □

429 In [17], the set of all siphons of a given Petri net is characterized by a sim-  
 430 ilar Boolean CSP except the conflict-freeness constraint. From the encoded  
 431 CSP, the set of all *minimal* siphons of the Petri net can be enumerated in the  
 432 set inclusion order. For enumerating siphons in the set inclusion order, the  
 433 proposed method by [17] uses the technique that labels directly the Boolean

434 variables with increasing value selection (i.e., to test first the absence, then  
 435 the presence of a place in the candidate solution). The method has two  
 436 implementations, one uses an iterated SAT procedure and the other uses  
 437 Constraint Programming (CP) with backtracking.

438 One natural question is that how to use the CSP-based method for enu-  
 439 merating all the maximal conflict-free siphons of a Petri net encoding a  
 440 Boolean network? Of course, the set of all conflict-free siphons of the Petri  
 441 net can easily be characterized by the CSP model presented in [17] along with  
 442 the additional constraint  $\neg p_v \vee \neg \bar{p}_v = 1$ , for each  $v \in V$ , which represents  
 443 the conflict-freeness. However, the main concern is to enumerate all the  
 444 *maximal* ones, which is not trivial to adapt from the CSP-based method.  
 445 By Proposition 4.1, the set of all maximal conflict-free siphons of  $\mathcal{P}$  can be  
 446 enumerated in the (maximality) set inclusion order, by restarting the search  
 447 each time a conflict-free siphon  $S$  is found, with the following additional con-  
 448 straint for disallowing any subset of that conflict-free siphon:  $\bigvee_{p \notin S} p = 1$ .  
 449 For enumerating conflict-free siphons in the set inclusion order, we can use  
 450 the same technique as used in [17] but with the opposite setting, i.e., labeling  
 451 directly the Boolean variables with decreasing value selection. The correct-  
 452 ness of this technique comes from the fact that once  $S$  is found, it is the  
 453 conflict-free siphon of maximum cardinality among all the remaining feasible  
 454 conflict-free siphons. Similar to [17], the newly CSP-based method can also  
 455 be implemented with SAT and CP solvers.

456 This method was implemented using the state-of-the-art CP solver Chuffed<sup>6</sup> [36]  
 457 via its MiniZinc [37] interface. Because it is a high-level interface, the  
 458 backtrack-and-replay method of [17] was not used but rather the alterna-  
 459 tive implementation with two global constraints for lexicographic ordering  
 460 (ensuring enumeration of solutions) and iterated non-subset of each already  
 461 found solution (for maximality).

For the SAT-based method, however a more direct method is to use a  
 MaxSAT solver. We construct a MaxSAT problem with the following hard  
 clauses:

$$(\neg p_v \vee \neg \bar{p}_v), \forall v \in V$$

and

$$(\neg p \vee \bigvee_{p' \in \text{pred}(t)} p'), \forall p \in P, \forall t \in \text{pred}(p).$$

---

<sup>6</sup><https://github.com/chuffed/chuffed>



462 We set a soft clause for each variable of the CSP and then use a “minimal cor-  
 463 rection subset” blocking strategy, which will ensure set-inclusion maximality  
 464 of the solutions. We implement this approach by using the RC2 MaxSAT  
 465 solver [38] available through the `python-sat` package<sup>7</sup>.

#### 466 4.3. Answer set programming-based method

Another possible method is to translate the characterization shown in Subsection 4.1 into the ASP  $\mathcal{L}$  as follows. We introduce atom  $\mathbf{p-v}$  (resp.  $\mathbf{n-v}$ ) to denote place  $p_v$  (resp.  $\bar{p}_v$ ),  $\forall v \in V$ . The set of all atoms in  $\mathcal{L}$  is given as  $\mathcal{A} = \bigcup_{v \in V} \{\mathbf{p-v}, \mathbf{n-v}\}$ . For each pair  $(p, t)$  where  $p \in P, t \in T, t \in \text{pred}(p)$ , we translate the rule (1) into the ASP rule

$$\mathbf{a\_1}; \dots ; \mathbf{a\_k} :- \mathbf{a}.$$

where  $\mathbf{a} \in \mathcal{A}$  is the atom representing place  $p$  and  $\{\mathbf{a\_1}, \dots, \mathbf{a\_k}\} \subseteq \mathcal{A}$  is the set of atoms representing places in  $\text{pred}(t)$ . The rule (2) is translated into the ASP rule

$$:- \mathbf{p-v}, \mathbf{n-v}.$$

for each  $v \in V$ . This ASP rule guarantees that two places representing the same node in  $\mathcal{N}$  never belong to the same siphon of  $\mathcal{P}$ , representing the conflict-freeness. Naturally, a Herbrand model (see, e.g., [39]) of  $\mathcal{L}$  is equivalent to a conflict-free siphon of  $\mathcal{P}$ . To guarantee that a Herbrand model is also a stable model (an answer set), we need to add to  $\mathcal{L}$  the two choice rules

$$\{\mathbf{p-v}\}. \{\mathbf{n-v}\}.$$

467 for each  $v \in V$ . Note that the number of atoms of  $\mathcal{L}$  is only  $2n$ , whereas  
 468 the ASP encoding shown in [7] has as many atoms as the number of prime-  
 469 implicants of the Boolean network and that number might be exponential in  
 470  $n$ . In [8], there is an ASP characterization of trap spaces that does not rely  
 471 on minimal DNFs either and thus seems very similar to our ASP encoding.  
 472 Remarkably it only requires the DNF for the *activation* part, using the in-  
 473 formation that it will only be used for locally-monotonic Boolean networks.  
 474 We would therefore expect that, when available, it will have comparable per-  
 475 formance on the ASP part (the ASP program would be approximately twice  
 476 smaller, though redundancy is not always bad in that field), but can also

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<sup>7</sup><https://pysathq.github.io/docs/html/api/examples/rc2.html>

477 avoid combinatorial explosion of the Petri net encoding for some formula  
 478 where the activation DNF is simple but the inhibition is not. Since `mpbn` is  
 479 included in our benchmark this will be evaluated in our experiments.

480 Now, a solution (simply an answer set)  $A \subseteq \mathcal{A}$  of  $\mathcal{L}$  is equivalent to a  
 481 conflict-free siphon  $S$  of  $\mathcal{P}$ , thus a trap space  $m$  of  $\mathcal{N}$ . The conversion from  $A$   
 482 to  $m$  is straightforward. If  $\mathbf{p-v} \in A$  then  $v \in D_m$  and  $m(v) = 0$ . Conversely,  
 483 if  $\mathbf{n-v} \in A$  then  $v \in D_m$  and  $m(v) = 1$ . Otherwise,  $v \notin D_m$ . Comput-  
 484 ing multiple answer sets is built into ASP solvers and the solving collection  
 485 `POTASSCO` [39] also features the option to find set-inclusion maximal answer  
 486 sets with respect to the set of atoms. Naturally, a set-inclusion maximal  
 487 answer set of  $\mathcal{L}$  is equivalent to a maximal conflict-free siphon of  $\mathcal{P}$ , thus a  
 488 minimal trap space of  $\mathcal{N}$ . By using this built-in option, we can compute all  
 489 the set-inclusion maximal answer sets of  $\mathcal{L}$  (resp. all the minimal trap spaces  
 490 of  $\mathcal{N}$ ) in one execution.

#### 491 4.4. Integer linear programming-based method

We first show how an Integer Linear Programming (ILP)  $\mathcal{I}$  can define  
 a set of all conflict-free siphons of the encoded Petri net  $\mathcal{P}$ . We introduce  
*binary* variable  $\mathbf{p-v}$  (resp.  $\mathbf{n-v}$ ) to denote place  $p_v$  (resp.  $\bar{p}_v$ ),  $\forall v \in V$ . The  
 set of all binary variables in  $\mathcal{I}$  is  $\bigcup_{v \in V} \{\mathbf{p-v}, \mathbf{n-v}\}$ . For each pair  $(p, t)$  where  
 $p \in P, t \in T, t \in \text{pred}(p)$ , we translate the rule (1) into the ILP inequality

$$\mathbf{a} \leq \mathbf{a\_1} + \dots + \mathbf{a\_k}$$

where  $\mathbf{a}$  is the binary variable representing place  $p$  and  $\{\mathbf{a\_1}, \dots, \mathbf{a\_k}\}$  is  
 the set of binary variables representing places in  $\text{pred}(t)$ . The rule (2) is  
 translated into the ILP inequality

$$\mathbf{p-v} + \mathbf{n-v} \leq 1$$

for each  $v \in V$ . This inequality forbids both  $\mathbf{p-v}$  and  $\mathbf{n-v}$  receive the value  
 1, thus representing the conflict-freeness. Since we only consider feasible  
 solutions, the objective function is set to  $\max \mathbf{p-v}$  for some  $v \in V$ . Naturally,  
 a solution  $I$  of  $\mathcal{I}$  is equivalent to a conflict-free siphon  $S$  of  $\mathcal{P}$ . The conversion  
 is that

$$S = \{p \in P \mid I(\mathbf{a-p}) = 1\}$$

492 where  $\mathbf{a-p}$  is the binary variable presenting place  $p$ .

493 We can see the similarity between  $\mathcal{I}$  and the encoded ASP shown in the  
 494 previous subsection. However, due to the nature of solutions of an ILP, it is

495 hard to compute all the set-inclusion maximal solutions of  $\mathcal{I}$  in one execution  
 496 of an ILP solver. Hence, we propose an iterative approach as follows.

The conflict-free siphon of maximum cardinality is of course maximal. Therefore, we impose the following objective function:

$$\max \sum_{v \in V} (p-v + n-v).$$

Now,  $\mathcal{I}$  can be solved using a general purpose ILP solver. If it admits any solution  $I^*$ , the corresponding conflict-free siphon (say  $S^*$ ) is maximal. Hence, it makes sense that it does not need to find any other conflict-free siphon of the net that is strictly contained in  $S^*$ . To do this, we add to  $\mathcal{I}$  a new inequality

$$1 \leq \sum_{p \in P \setminus S^*} a-p$$

497 where  $a-p$  is the binary variable presenting place  $p$ . Now, we solve  $\mathcal{I}$  again to  
 498 find a new solution. If a new solution  $I'$  exists, then let  $S'$  be its corresponding  
 499 conflict-free siphon. Indeed, abide by the newly added inequality, we have  
 500  $S' \cap (P \setminus S^*) \neq \emptyset$  because there is some  $a-p$  with  $p \in P \setminus S^*$  such that  
 501  $I'(a-p) = 1$ . This implies that it is impossible that  $S' = S^*$  or  $S' \subset S^*$ .  
 502 By the objective function, it means that  $S'$  is the conflict-free siphon of  
 503 maximum cardinality among the conflict-free siphons that are not contained  
 504 in  $S^*$ . Hence,  $S'$  is also a maximal conflict-free siphon. Again, we add to  $\mathcal{I}$   
 505 a new inequality with respect to the newly found siphon. The above process  
 506 is iterated until  $\mathcal{I}$  becomes unfeasible, this means that there is no further  
 507 maximal conflict-free siphon. Thus, all the maximal conflict-free siphons of  
 508 the Petri net have been found.

509 Since we used the MiniZinc framework to interface with the CP solver, it  
 510 was simple to make the slight modifications described above and to use that  
 511 same interface to call the Coin-OR CBC solver<sup>8</sup> [40].

#### 512 4.5. Computation of special types of trap spaces

513 In the field of systems biology, biologists may want to compute more  
 514 special types of trap spaces beyond minimal trap spaces [20], which also play  
 515 crucial roles in analysis and control of Boolean networks [21, 19]. We shall  
 516 show that our proposed methods can be easily adjusted to compute such

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<sup>8</sup><https://github.com/coin-or/Cbc>

517 popular types of trap spaces. We illustrate the adjustments via the ASP-  
 518 based method (see Subsection 4.3) because ASP is declarative by nature,  
 519 but these adjustments are completely applicable for other approaches such  
 520 as MaxSAT, CP, and ILP.

521 First, the work by [19] uses the concept of *stable motifs* to build the suc-  
 522 cession diagram of a Boolean network, a summary of the decisions in the  
 523 network dynamics that lead to successively more restrictive nested stable  
 524 motifs. The succession diagram is useful for control and decision making  
 525 on this Boolean network. In particular, the proposed control methods are  
 526 independent to the update scheme. It has been shown that a stable motif of  
 527 a Boolean network is equivalent to a maximal trap space of this Boolean net-  
 528 work [19]. Hence, it is necessary to develop an efficient method for computing  
 529 maximal trap spaces of a Boolean network. We shall show how to adjust the  
 530 ASP-method presented in Subsection 4.3 to compute maximal trap spaces.

We first provide the definition of maximal trap spaces. Let  $\varepsilon$  be the special  
 trap space of  $\mathcal{N}$  where all the nodes are free. Of course,  $\varepsilon$  corresponds to the  
 special conflict-free siphon  $\emptyset$ . A trap space  $m$  is called maximal if  $m \neq \varepsilon$  and  
 there is no other trap space  $m'$  such that  $m' \neq \varepsilon$  and  $m < m'$ . Analogously,  
 a conflict-free siphon  $S$  is called minimal if  $S \neq \emptyset$  and there is no other  
 trap space  $S'$  such that  $S' \neq \emptyset$  and  $S' \subset S$ . By using the reasoning similar  
 to the proof of Theorem 3.2, we can easily conclude that a maximal trap  
 space of  $\mathcal{N}$  is equivalent to a minimal conflict-free siphon of its encoded  
 Petri net  $\mathcal{P}$ . Let  $\mathcal{L}$  be the ASP characterizing all conflict-free siphons of  $\mathcal{P}$   
 (see Subsection 4.3). Naturally, we need to exclude  $\emptyset$  from the solution space  
 of  $\mathcal{L}$  (equivalently exclude  $\varepsilon$  from the set of trap spaces). To do this, we add  
 to  $\mathcal{L}$  the ASP rule

$$\mathbf{p-v\_1; n-v\_1; \dots; p-v\_n; n-v\_n.}$$

531 that ensures that every answer set of  $\mathcal{L}$  cannot be empty. Then a set-inclusion  
 532 minimal answer set of  $\mathcal{L}$  is equivalent to a minimal conflict-free siphon of  $\mathcal{P}$ ,  
 533 thus a maximal trap space of  $\mathcal{N}$ .

Second, we consider *fixed points* in Boolean networks. To date, the anal-  
 ysis of the fixed points of a Boolean network remains a very useful tool in  
 understanding the behavior of complex biological models not only due to the  
 fact that in some cases the full computation of complex attractors remains  
 intractable, but also because for many biological systems, the expected long-  
 term behavior is not cyclic [41]. Furthermore, the fixed point computation is

also the crucial starting point for several state-of-the-art methods for computing complex attractors of Boolean networks [35]. Let  $s$  be a fixed point of a Boolean network  $\mathcal{N}$ . We have a subspace  $m$  corresponding to  $s$  as follows:  $\forall v \in V, m(v) = s(v)$ , i.e., all nodes are fixed in  $m$ . Clearly,  $s$  is a trap set of  $\mathcal{N}$  regardless of the update scheme. Hence,  $m$  is a trap space of  $\mathcal{N}$ . In addition, since  $|S_{\mathcal{N}}[m]| = 1$ ,  $m$  is also a minimal trap space. To compute all fixed points of  $\mathcal{N}$ , we can add more constraints to the encoded ASP characterizing all conflict-free siphons (equivalently trap spaces). For every  $v \in V$ , we add to the encoded ASP the rule

$$\mathbf{p-v}; \mathbf{n-v}.$$

534 that ensures that for every conflict-free siphon  $S$ , it contains either  $\mathbf{p-v}$  or  $\mathbf{n-v}$   
 535 for every  $v \in V$ . Equivalently, the trap space corresponding to  $S$  is always  
 536 a fixed point. Now, the set of answer sets of the encoded ASP is equivalent  
 537 to the set of fixed points of  $\mathcal{N}$ . In particular, when solving the encoded ASP  
 538 using an ASP solver, we do not need to use the built-in option for computing  
 539 set-inclusion maximal answer sets. Note that we can also build another ASP  
 540 characterizing all fixed points of  $\mathcal{N}$  based on the equivalence between a fixed  
 541 point of  $\mathcal{N}$  and a deadlock of its Petri net encoding [22]. This approach may  
 542 give a more compact ASP.

Third, we consider the trap spaces *intersecting* a given subspace  $m^*$  of a Boolean network. Such trap spaces are used in the trap space-based control method [21]. A trap space  $m$  intersects  $m^*$  if and only if  $S_{\mathcal{N}}[m] \cap S_{\mathcal{N}}[m^*] \neq \emptyset$ . It follows that for every  $v$ , if  $m^*(v) = 0$  then  $m(v) = 0$  or  $m(v) = \star$ , if  $m^*(v) = 1$  then  $m(v) = 1$  or  $m(v) = \star$ . For the former case, we add to  $\mathcal{L}$  the ASP rule

$$:- \mathbf{n-v}.$$

that ensures that  $m(v)$  cannot be 1. For the latter case, we add to  $\mathcal{L}$  the ASP rule

$$:- \mathbf{p-v}.$$

543 that ensures that  $m(v)$  cannot be 0. Now  $\mathcal{L}$  characterizes all trap spaces that  
 544 intersect  $m^*$ .

Finally, we consider the trap spaces that are *inside* a given subspace  $m^*$  of a Boolean network. Such trap spaces are used in the iterative procedure of building the succession diagram of a Boolean network [19], which is hierarchical. We first adjust  $\mathcal{L}$  to characterize all such trap spaces. A trap space

$m$  is inside  $m^*$  if and only if  $m(v) = m^*(v)$  for every  $v \in D_{m^*}$ . If  $m^*(v) = 0$ , we add to  $\mathcal{L}$  the ASP rule

$$\mathbf{p-v.}$$

that ensures that  $m(v) = 0$ . If  $m^*(v) = 1$ , we add to  $\mathcal{L}$  the ASP rule

$$\mathbf{n-v.}$$

that ensures that  $m(v) = 1$ . It is noted that if we want to compute maximal trap spaces inside  $m^*$ , we need to exclude the conflict-free siphon corresponding  $m^*$  from the solution space. Specifically, we need to add to  $\mathcal{L}$  the ASP rule

$$\mathbf{p-v_{i1}; n-v_{i1}; \dots; p-v_{ik}; n-v_{ik}.}$$

545 where  $\{v_{i_1}, \dots, v_{i_k}\}$  is the set of free nodes of  $m^*$ . This rule ensures that  
 546  $m \neq m^*$ . In the case that  $m^* = \varepsilon$ , we have all maximal trap spaces of the  
 547 original Boolean network.

## 548 5. Motivating example

549 For a few years now we have been collaborating with biologists who build  
 550 very large detailed and annotated maps and now wish to analyze the dy-  
 551 namics of the corresponding models. One of the main maps studied this way  
 552 represents knowledge about the Rheumatoid Arthritis [42], and was the main  
 553 motivation for the development of a tool to automatically transform it into  
 554 an executable Boolean network [6]. In the supplementary material of the pa-  
 555 per, an excerpt of the map, focused around the apoptosis (cell death) module  
 556 is transformed into a model of *reasonable* size, namely 180 Boolean variables  
 557 (model `F5_RA_apoptosis_executable_module.sbml` of supplementary ma-  
 558 terial S3, and model “RA\_apoptosis” of Subsection 6.3). The study of such  
 559 model, though, is a big hurdle. Indeed, as stated in the article about another  
 560 model of the same size: “*The size of the CaSQ-inferred MAPK model (181*  
 561 *nodes) made the calculation of stable states a non-realistic endeavour.*”

562 In practice, even if there is a huge number of attractors in such a model,  
 563 obtaining a sample of those can reveal very useful to invalidate the model and  
 564 lead to further refinement. In particular, it provides a feature-rich alternative  
 565 to random simulations for this type of very non-deterministic model. Being  
 566 able to detect that there are inconsistencies with published experimental data  
 567 in some of the first 1000 attractors, for instance, can lead to a much quicker  
 568 Systems Biology loop: model, invalidate, refine.

569 However, using a state-of-the-art tool like `PyBoolNet` [7] on that model  
570 actually fails at the phase of prime-implicant generation. `mpbn` [9] can return  
571 the first 1000 solutions within 1.43s, but indeed, it limits the modeling range  
572 of the modelers as it does not permit using non-locally-monotonic Boolean  
573 functions. This is also true for the Alzheimer model also mentioned in that  
574 same article and originally from [43] (F4 file in the original supplementary  
575 material, and “Alzheimer” in Table 2), where `PyBoolNet` also fails at the  
576 prime-implicant computation and `mpbn` does not give any answer because  
577 this model is actually non-locally-monotonic. The current practice usually  
578 revolves then around fixing some source nodes to plausible values and re-  
579 ducing the model accordingly. While this approach makes sense, it relies  
580 on potentially arbitrary decisions, and *hides away* critical modelling choices  
581 that were actually not part of the original Boolean network or even of the  
582 starting map.

583 For the “RA\_apoptosis” model, using the ASP-based method presented  
584 in Subsection 4.3, it is possible to obtain the first 1000 minimal trap spaces  
585 (including ones that contain more than one state) within 0.19s, which is  
586 much quicker than `mpbn`. The needed time for the “Alzheimer” model is  
587 0.79s. Unfortunately since this method was not available at the time, the  
588 analysis of the model remained very high-level and qualitative, instead of  
589 being able to use the rich information of computed minimal trap spaces.

## 590 6. Evaluation

591 To evaluate the performance of the newly proposed methods (imple-  
592 mented as a Python package named `Trappist` and available on the Python  
593 package index<sup>9</sup>) and the state-of-the-art methods (`bioLQM`<sup>10</sup>, `PyBoolNet` [7,  
594 20], and `mpbn` [9]), we compared them on both `PyBoolNet`’s own model repos-  
595 itory and many real-world models from various sources in the literature. To  
596 our knowledge, these models are a highly representative sample of Boolean  
597 models currently available. It is worth noting that `mpbn` [9] only handles  
598 locally-monotonic models, whereas the other methods can handle general  
599 models. To obtain a more comprehensive comparison, we also used random  
600 models generated by a third-party software `BoolNet R` package [30]. As ex-  
601 plained in Section 5, in our benchmarks, we only searched for the first 1000

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<sup>9</sup><https://pypi.org/project/trappist/>

<sup>10</sup><http://colomoto.org/biolqm/doc/tools-trap-space.html>

minimal trap spaces for each model. It is worth noting that unlike existing analysis shown in the literature, we did not fix specific values for source nodes in all the considered models.

To solve the ASP problems, we used the same ASP solver `Clingo` [39] and the same configuration as that used in `PyBoolNet` [7, 20] and `mpbn` [9]. Specifically, we used the configuration `-heuristic=Domain -enum-mod=domRec -dom-mod=3` (subset maximality, equivalent to the deprecated `--dom-pref=32 --heuristic=domain --dom-mod=7` used by `PyBoolNet`). We ran all the benchmarks on a machine whose environment is CPU: Intel® Core™ i9-11950H 2.60GHz  $\times$  16, 16 GB DDR4 RAM, Ubuntu 20.04.5 LTS. Finally, we set a time limit of three minutes for each model.

All the models and some Jupyter notebooks realizing the benchmarks (and named `TCS-Benchmark-<...>.ipynb`) can be found at <https://github.com/soli/trap-spaces-as-siphons/>. These can be run on a Docker image in the cloud by clicking the “Binder” button.

### 6.1. *PyBoolNet* repository

Table 1 shows the experimental results on the models from the official `PyBoolNet` repository<sup>11</sup>. Column  $n$  denotes the number of nodes of each model. Column  $|M|$  denotes the number of minimal trap spaces and for each method is given the computation time in seconds, asking only for the first 1000 minimal trap spaces. “DNF” means that the method did not finish the computation within the time limit of three minutes. In the case of `bioLQM`, “N/A” means that the number of all minimal trap spaces of the model is larger than 1000 and we did not recorded the running time of `bioLQM` because it always requires to compute all minimal trap spaces. A number in bold indicates a ratio greater than three compared to the best result. “NM” indicates a non-locally-monotonic model. There are four variants of `Trappist: SAT` (i.e., `Trappist-MaxSAT`, the MaxSAT-based method shown in Subsection 4.2), `CP` (i.e., `Trappist-CP`, the CP-based method shown in Subsection 4.2), `ILP` (i.e., `Trappist-ILP`, the ILP-based method shown in Subsection 4.4), and `ASP` (i.e., `Trappist-ASP`, the ASP-based method shown in Subsection 4.3).

We first analyze the results of the four variants of `Trappist`. We can see that `Trappist-MaxSAT` and `Trappist-ASP` are comparable in most mod-

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<sup>11</sup><https://github.com/hklarner/pyboolnet/tree/master/pyboolnet/repository>



Table 1: Timing comparisons (in seconds) between bioLQM (LQM), PyBoolNet (PBN), mpbn and the four variants of Trappist on the PyBoolNet repository.

model	$n$	$ M $	LQM	PBN	mpbn	Trappist			
						SAT	CP	ILP	ASP
1 arellano_rootstem	9	4	<b>0.13</b>	0.01	0.00	0.00	<b>0.97</b>	<b>0.96</b>	0.01
2 calzone_cellfate	28	27	<b>0.12</b>	0.02	0.01	0.01	<b>5.59</b>	<b>6.03</b>	0.01
3 dahlhaus_neuroplastoma	23	32	<b>0.11</b>	0.03	0.01	0.01	<b>6.56</b>	<b>6.99</b>	0.01
4 davidich_yeast	10	12	<b>0.11</b>	0.02	0.01	0.01	<b>2.56</b>	<b>2.21</b>	0.01
5 dinwoodie_life	15	7	<b>0.11</b>	0.01	0.00	0.01	<b>1.68</b>	<b>1.39</b>	0.01
6 dinwoodie_stomatal	13	1	<b>0.10</b>	0.01	0.00	0.00	<b>0.39</b>	<b>0.29</b>	0.01
7 faure_cellcycle	10	2	<b>0.11</b>	0.02	0.01	0.01	<b>0.58</b>	<b>0.46</b>	0.01
8 grieco_mapk	53	18	<b>0.19</b>	0.03	0.02	0.03	<b>3.93</b>	<b>10.46</b>	0.02
9 irons_yeast	18	1	<b>0.12</b>	0.03	0.01	0.01	<b>0.37</b>	<b>0.39</b>	0.02
10 jaoude_thdiff	103	1000 <sup>+</sup>	N/A	<b>0.85</b>	<b>0.45</b>	<b>0.56</b>	DNF	DNF	0.09
11 klamt_tcr	40	8	<b>0.11</b>	0.01	0.01	0.01	<b>1.98</b>	<b>1.22</b>	0.02
12 krumsiek_myeloid	11	6	<b>0.10</b>	0.01	0.00	0.00	<b>1.48</b>	<b>1.26</b>	0.01
13 multivalued	13	4	<b>0.10</b>	0.01	0.00	0.00	<b>0.93</b>	<b>0.86</b>	0.01
14 n12c5	11	5	<b>0.11</b>	<b>17.83</b>	0.01	0.01	<b>1.21</b>	<b>1.10</b>	0.01
15 n3s1c1a	2	2	<b>0.10</b>	0.01	0.00	0.00	<b>0.63</b>	<b>0.49</b>	0.01
16 n3s1c1b	2	2	<b>0.09</b>	0.02	0.00	0.00	<b>0.56</b>	<b>0.49</b>	0.01
17 n5s3	4	3	<b>0.10</b>	0.02	NM	0.00	<b>0.74</b>	<b>0.69</b>	0.01
18 n6s1c2	5	3	<b>0.10</b>	0.02	0.00	0.00	<b>0.91</b>	<b>0.59</b>	0.01
19 n7s3	6	3	<b>0.11</b>	0.02	0.00	0.00	<b>0.79</b>	<b>0.68</b>	0.01
20 raf	3	2	<b>0.10</b>	0.01	0.00	0.00	<b>0.55</b>	<b>0.39</b>	0.01
21 randomnet_n15k3	15	3	<b>0.10</b>	0.02	NM	0.01	<b>0.77</b>	<b>0.67</b>	0.01
22 randomnet_n7k3	7	10	<b>0.10</b>	0.01	NM	0.00	<b>2.07</b>	<b>1.46</b>	0.01
23 remy_tumorigenesis	34	25	<b>0.15</b>	<b>0.94</b>	0.02	0.02	<b>5.98</b>	<b>7.98</b>	0.02
24 saadatpour_guardcell	13	1	<b>0.10</b>	0.06	0.00	0.00	<b>0.53</b>	<b>0.45</b>	0.02
25 selvaggio_emt	56	1000 <sup>+</sup>	N/A	<b>0.48</b>	<b>0.28</b>	<b>0.28</b>	DNF	DNF	0.09
26 tournier_apoptosis	12	3	<b>0.10</b>	0.01	0.00	0.00	<b>0.74</b>	<b>0.75</b>	0.01
27 xiao_wnt5a	7	4	<b>0.10</b>	0.01	0.00	0.00	<b>1.00</b>	<b>0.89</b>	0.01
28 zhang_tlgl	60	156	<b>0.60</b>	0.09	0.09	0.07	<b>37.26</b>	DNF	0.04
29 zhang_tlgl_v2	60	258	<b>0.64</b>	0.04	0.08	0.11	<b>69.95</b>	DNF	0.04

els, but Trappist-ASP is much faster for the jaoude\_thdiff and selvaggio\_emt models where the number of minimal trap spaces is greater than 1000. The latter can be explained by the fact that Trappist-MaxSAT follows an iterative approach, i.e., it restarts the search with a new constraint each time a solution is found (see Subsection 4.2). This iterative approach may be less efficient than the way ASP solvers use to enumerate multiple solutions

(answer sets), which is an advantage of ASP solvers [39]. Hence, when the number of solutions increases, the inferiority of **Trappist-*MaxSAT*** compared to **Trappist-*ASP*** will be exhibited more clearly. The two remaining variants, **Trappist-*CP*** and **Trappist-*ILP***, are much less efficient than **Trappist-*MaxSAT*** and **Trappist-*ASP*** in every model, even are more than three orders of magnitude slower in some models. The first reason for their bad performance is that they are also iterative methods like **Trappist-*MaxSAT***, thus they are not efficient for "enumeration" problems. Upon closer inspection, for the Boolean CSP characterizing conflict-free siphons, **CP** seems to be something that is a "less-efficient-SAT", handling mostly Boolean constraints and making little use of the global constraints only added for the iterative part. For **ILP**, it may be even worse, since the problem is purely Boolean (no real or integer numbers whatsoever). This is confirmed by the observation that for some quite large models (e.g., the *grieco\_mapk*, *zhang\_tlg1*, and *zhang\_tlg1.v2* models), **Trappist-*ILP*** is much slower than **Trappist-*CP***. Note that the inferiority of **ILP** compared to **ASP** with respect to the trap space enumeration has been reported in [7]. Hereafter, we shall compare the best variant of **Trappist** (i.e., **Trappist-*ASP***) with other methods.

As shown in Table 1, for most of the models of the **PyBoolNet** repository, the results are comparable with all minimal trap spaces found very fast. However upon closer inspection, we can see some notable differences. First, **Trappist-*ASP*** is far more efficient than **bioLQM** in every model with speedups between  $5\times$  and  $16\times$ . Second, for small models, **PyBoolNet** and **mpbn** are comparable to **Trappist-*ASP***. However, on every model that was a bit challenging for **PyBoolNet** or **mpbn**, **Trappist-*ASP*** is far more efficient with speedups between  $3\times$  and  $5\times$  for the case of **mpbn**, and between  $5\times$  and  $1783\times$  for the case of **PyBoolNet**. In particular, the second best variant of **Trappist** (i.e., **Trappist-*MaxSAT***) is even far more efficient than **bioLQM** and **PyBoolNet**, and is comparable to **mpbn** on every model. It is worth noting that for 3 of the 29 models, **mpbn** did not give any answer because these models are locally-monotonic but all the other methods did, which confirms the limit of **mpbn** on the applicable class of models.

## 6.2. *BBM repository*

Currently, a research group has made a great effort for building a collection (called **BBM**) of real-world Boolean models from various sources used in systems biology. It aims to be a comprehensive collection suitable for benchmarking and testing new tools and methods. **BBM** consists of 211 models (24

679 out of them are non-locally-monotonic), peaking at 321 nodes, 1100 regula-  
680 tions among the nodes, and 133 source nodes, respectively. It is released and  
681 maintained at <https://github.com/sybila/biodivine-boolean-models>.  
682 We here tested all the compared methods on this model repository.

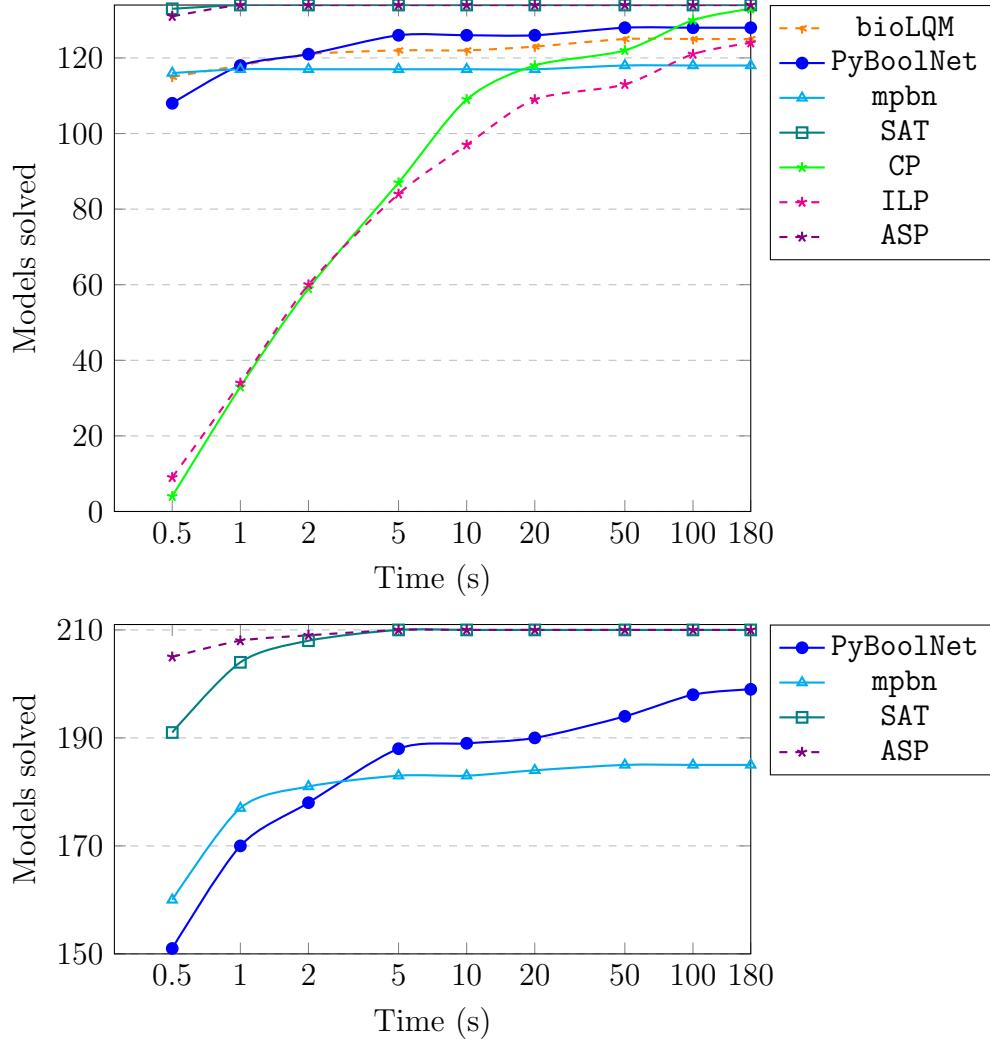


Figure 2: Cumulative numbers of the BBM models that have less than 1000 minimal trap spaces (upper panel) and BBM models solved by the compared methods with respect to enumerating the first 1000 minimal trap spaces (lower panel).

683 Figure 2 (upper panel) shows cumulative numbers of the BBM models that  
684 have less than 1000 minimal trap spaces solved by the compared methods

with respect to enumerating the first 1000 minimal trap spaces. The number of such models is 134 (per all 211 models), and 15 of them are non-locally-monotonic. This model set allows us to fairly consider **bioLQM** for comparison, since **bioLQM** always requires to compute all minimal trap spaces. We can first see that **Trappist-ASP** and **Trappist-MaxSAT** are still the two best methods as they can handle every model within 1s as well as they always can handle more models than all the remaining methods on every time limit. Second, **Trappist-CP** is better than **Trappist-ILP**, which is consistent with their comparison shown in the previous subsection. Third, one notable remark is that for the time limit of 100s or 180s, **Trappist-CP** can handle more models than all **bioLQM**, **PyBoolNet**, and **mpbn**. This remark shows that even with a not best implementation, our alternative approach is still better than the state-of-the-art methods on a certain set of real-world models. This is supported by the fact that our alternative approach avoids the need for computing prime implicants (as opposed to **PyBoolNet**) and can handle non-locally-monotonic Boolean networks (as opposed to **mpbn**).

Figure 2 (lower panel) shows cumulative numbers of the **BBM** models solved by the compared methods (except **bioLQM**, **Trappist-CP**, and **Trappist-ILP**) with respect to enumerating the first 1000 minimal trap spaces. We omit the results of **Trappist-CP** and **Trappist-ILP** because they can handle no model with more than 1000 minimal trap spaces. Again, we can see that **Trappist-ASP** and **Trappist-MaxSAT** are the two best methods as they can handle every but one model within 5s. They also always handle many more models than both **PyBoolNet** and **mpbn** on every time limit. Note that with the time limit of 0.5s, **Trappist-ASP** can handle 14 more models than **Trappist-MaxSAT**, which is opposed to the case of models with less than 1000 minimal trap spaces (see Figure 2 (upper panel)). This observation confirms the disadvantage of **Trappist-MaxSAT** compared to **Trappist-ASP** for the case of many minimal trap spaces.

### 6.3. Selected models

We used a set of real-world Boolean networks lying in various scales collected from numerous bibliographic sources in the literature. Most of these models are quite big (in size), complex (i.e., having high average in-degree, which is related to the number of prime-implicants), and have never been fully analyzed. Note that these models are not included in the **PyBoolNet** and **BBM** repositories. We then applied **bioLQM**, **PyBoolNet**, **mpbn**, and the

four variants of **Trappist** to computing minimal trap spaces of these real-world models. Table 2 shows the obtained experimental results. A number in bold indicates a ratio greater than or equal to 10 compared to the best result. The remaining notations are similar to those in Table 1. Hereafter, we analyze in detail the results with respect to minimal trap space computation.

Table 2: Timing comparisons (in seconds) between **bioLQM** (LQM), **PyBoolNet** (PBN), **mpbn** and the four variants of **Trappist** on selected models from the literature.

model	$n$	$ M $	LQM	PBN	mpbn	Trappist			
						SAT	CP	ILP	ASP
1 metastatic [44]	10	4	<b>0.10</b>	0.04	NM	0.01	<b>1.15</b>	<b>0.89</b>	0.02
2 Arabidopsis.thaliana [44]	15	8	<b>0.10</b>	0.06	NM	0.01	<b>2.06</b>	<b>1.83</b>	0.02
3 p53_high_dna [44]	16	1	0.38	<b>1.76</b>	NM	0.08	0.53	0.43	0.14
4 p53_low_dna [44]	16	1	0.41	<b>1.76</b>	NM	0.07	0.58	0.48	0.14
5 FT-GRN [45]	23	32	<b>DNF</b>	<b>DNF</b>	NM	0.03	<b>8.41</b>	<b>12.38</b>	0.19
6 DNA_damage [44]	26	16	<b>0.24</b>	<b>0.33</b>	NM	0.02	<b>3.91</b>	<b>5.33</b>	0.05
7 Rho-GTPases [44]	33	2	0.17	0.57	<b>40.39</b>	0.07	<b>0.74</b>	0.56	0.11
8 Pluripotency [46]	36	440	<b>DNF</b>	<b>DNF</b>	NM	0.16	<b>138.92</b>	<b>DNF</b>	0.28
9 Pluripotent [44]	36	276	0.37	0.43	NM	0.07	<b>72.40</b>	<b>DNF</b>	0.06
10 Pancreatic.Cancer [44]	43	1000+	N/A	0.11	0.36	0.17	<b>DNF</b>	<b>DNF</b>	0.06
11 Drosophila [47]	52	128	0.33	0.05	0.07	0.06	<b>32.66</b>	<b>126.22</b>	0.05
12 Cacace.TdevModel [48]	61	28	<b>1.29</b>	<b>5.67</b>	NM	0.06	<b>7.51</b>	<b>23.15</b>	0.08
13 hedgehog [44]	65	1000+	N/A	<b>DNF</b>	0.50	0.34	<b>DNF</b>	<b>DNF</b>	0.33
14 EMT [19]	69	268	<b>39.22</b>	<b>1.01</b>	0.20	0.12	<b>75.81</b>	<b>DNF</b>	0.05
15 Bcell [49]	73	72	0.23	0.04	0.08	0.06	<b>18.95</b>	<b>81.85</b>	0.05
16 mast_cell [6]	73	1000+	N/A	0.09	0.55	0.37	<b>DNF</b>	<b>DNF</b>	0.15
17 Corral.ThIL17diff [41]	92	1000+	N/A	<b>107.57</b>	0.76	0.56	<b>DNF</b>	<b>DNF</b>	0.16
18 Adhesion.CIP [50]	121	78	<b>56.81</b>	<b>4.25</b>	0.23	0.17	<b>25.20</b>	<b>DNF</b>	0.19
19 EMT_Mech [51]	136	82	<b>DNF</b>	<b>14.01</b>	0.27	0.20	<b>27.55</b>	<b>DNF</b>	0.25
20 macrophage [44]	136	1000+	N/A	0.54	1.09	0.84	<b>DNF</b>	<b>DNF</b>	0.27
21 angiogenesis [44]	141	1000+	N/A	0.16	1.07	1.06	<b>DNF</b>	<b>DNF</b>	0.16
22 angiofull [52]	142	1000+	N/A	0.17	1.06	0.88	<b>DNF</b>	<b>DNF</b>	0.23
23 EMT_Mech_TGFbeta [51]	150	492	<b>DNF</b>	<b>11.28</b>	0.78	0.69	<b>DNF</b>	<b>DNF</b>	0.35
24 RA_apoptosis [6]	180	1000+	N/A	<b>DNF</b>	1.43	1.55	<b>DNF</b>	<b>DNF</b>	0.19
25 MAPK [6]	181	1000+	N/A	<b>13.58</b>	1.76	1.51	<b>DNF</b>	<b>DNF</b>	0.27
26 Snf1-pathway [53]	202	1000+	N/A	1.13	1.47	1.43	<b>DNF</b>	<b>DNF</b>	0.31
27 T-cell-co-receptor [44]	206	1000+	N/A	<b>DNF</b>	1.52	2.26	<b>DNF</b>	<b>DNF</b>	0.35
28 TcellCheckPoint [54]	218	1000+	N/A	<b>4.99</b>	NM	1.96	<b>DNF</b>	<b>DNF</b>	0.28
29 Mycobacterium [44]	317	1000+	N/A	0.42	2.36	<b>4.91</b>	<b>DNF</b>	<b>DNF</b>	0.44
30 Leishmania [44]	342	1000+	N/A	<b>DNF</b>	2.56	<b>5.62</b>	<b>DNF</b>	<b>DNF</b>	0.46
31 Cholocystokinin [6]	383	1000+	N/A	0.36	2.99	<b>4.81</b>	<b>DNF</b>	<b>DNF</b>	0.37
32 Alzheimer [6]	762	1000+	N/A	<b>DNF</b>	NM	<b>18.21</b>	<b>DNF</b>	<b>DNF</b>	0.79

First, we obtained some observations on the four variants of **Trappist**

727 consistent with the observations obtained in the previous subsections. More  
728 specifically, **Trappist-ASP** is still the best variant with a running time below  
729 one second for every model, and followed by **Trappist-MaxSAT**. In particular,  
730 the difference in running time between **Trappist-ASP** and **Trappist-MaxSAT**  
731 is bigger for larger models or models with more than 1000 minimal trap  
732 spaces. **Trappist-CP** and **Trappist-ILP** still have a much worse perfor-  
733 mance, with **Trappist-CP** better than **Trappist-ILP**. They still can handle  
734 no model with more than 1000 minimal trap spaces. However, **Trappist-CP**  
735 or **Trappist-ILP** can handle the FT-GRN and Pluripotency models, whereas  
736 all **bioLQM**, **PyBoolNet**, and **mpbn** cannot.

737 Second, **Trappist-ASP** (even **Trappist-MaxSAT**) is far more efficient than  
738 both **bioLQM** and **PyBoolNet** on every model where the comparison is possi-  
739 ble. For most models, the speedups of **Trappist-ASP** compared to **bioLQM**  
740 and **PyBoolNet** are between one and three orders of magnitude. This again  
741 confirms the superiority of **Trappist-ASP** compared to the other methods  
742 that can handle general Boolean networks.

743 Third, for 11 of the 32 models (more than 34%), **mpbn** did not give any an-  
744 swer because these models are non-locally-monotonic. For 21 of the 32 mod-  
745 els where **mpbn** returned the answers, **mpbn** and **Trappist-ASP** are roughly  
746 comparable in computation time, but **mpbn** appears quite slower on aver-  
747 age. In particular, for the Rho-GTPases model, **mpbn** is  $577\times$  slower than  
748 **Trappist-ASP**. This observation along with the comparisons between **mpbn**  
749 and **Trappist-ASP** in the previous subsections are quite surprising because  
750 the ASP encoding of **mpbn** only requires the DNF for the activation part of a  
751 Boolean function, whereas that of **Trappist-ASP** requires both the activation  
752 and inhibition parts (see Subsection 4.3). However, the reason may lie on the  
753 differences in the ASP encoding characteristics of the two methods and the  
754 fact that **mpbn** needs to spend time checking the local-monotonicity of each  
755 Boolean function in a Boolean network. We expect that **mpbn** may outper-  
756 form **Trappist** for a certain set of models, but not for the set of real-world  
757 models considered in this article.

758 Fourth, regarding the comparison of the ASP-based methods (i.e., **PyBoolNet**,  
759 **mpbn**, and **Trappist-ASP**), we note that for all the models where **PyBoolNet**  
760 did not finish before the time limit, the timeout occurred during the compu-  
761 tation of the prime-implicants. Hence, not even a single minimal trap space  
762 was output by that method. For all the remaining models, once **PyBoolNet**  
763 went through the prime-implicant phase, its ASP solving phase quickly re-  
764 turned the first 1000 minimal trap spaces, all under one second. Hence,

765 with the experimental results shown in this subsection as well as the two  
766 previous subsections, the practical differences between the ASP encoding of  
767 **Trappist-ASP** and that of **PyBoolNet** are not distinctly exposed. The fact  
768 that our new ASP encoding is guaranteed to be linear in the number of nodes  
769 of the original model (see Subsection 4.3) does not seem to be crucial here,  
770 however a much deeper analysis of those cases shall be shown in the next  
771 subsection.

#### 772 6.4. Randomly generated models

773 We randomly generated a set of N-K models [1] with network size  $n$  in the  
774 set  $\{100, 150, 200, 250, 300, 350, 400\}$  and in-degree  $K = 3$  (i.e., each node  
775 has exactly three input nodes). We chose N-K models because they are a  
776 useful tool for studying the dynamics of Boolean networks [1, 7, 19]. For each  
777 network size, 50 instances were generated using the `generateRandomNKNetwork`  
778 function. In total, we have 350 random models. We then applied the com-  
779 pared methods to these models and recorded the running time of each method  
780 for each model. It is worth noting that N-K models usually have small num-  
781 bers of minimal trap spaces [7]. Hence, we searched for all solutions in  
782 each model, which makes the comparison to `bioLQM` more comprehensive.  
783 In addition, each node has only three input nodes, leading to the number  
784 of prime-implicants of the associated Boolean function is small. Hence,  
785 **PyBoolNet** always passed the phase of computing prime-implicants in ev-  
786 ery model even within one second, which enables us to compare the ASP  
787 encoding of **PyBoolNet** and that of **Trappist-ASP**.

788 Figure 3 shows cumulative numbers of random models solved by the com-  
789 pared methods with respect to enumerating all the minimal trap spaces. The  
790 number of succeeded models within three minutes for each method is: `bioLQM`  
791 (0), `PyBoolNet` (320), `mpbn` (0), **Trappist-maxSAT** (338), **Trappist-CP** (226),  
792 **Trappist-ILP** (39), **Trappist-ASP** (349). We can see that **Trappist-ASP** is  
793 the only method that can handle every model, but one. Note that none of  
794 the other methods can handle that only model failed by **Trappist-ASP**. We  
795 also obtained some observations consistent with those obtained for real-world  
796 models. More specifically, **Trappist-MaxSAT** is still the second best method  
797 and **Trappist-CP** is better than **Trappist-ILP**. Upon closer inspection, we  
798 obtained several notable observations as follows.

799 First, `mpbn` was not able to handle any model because all the models  
800 are non-locally-monotonic. Recall that a Boolean network is non-locally-  
801 monotonic if only one of its Boolean functions is non-locally-monotonic.

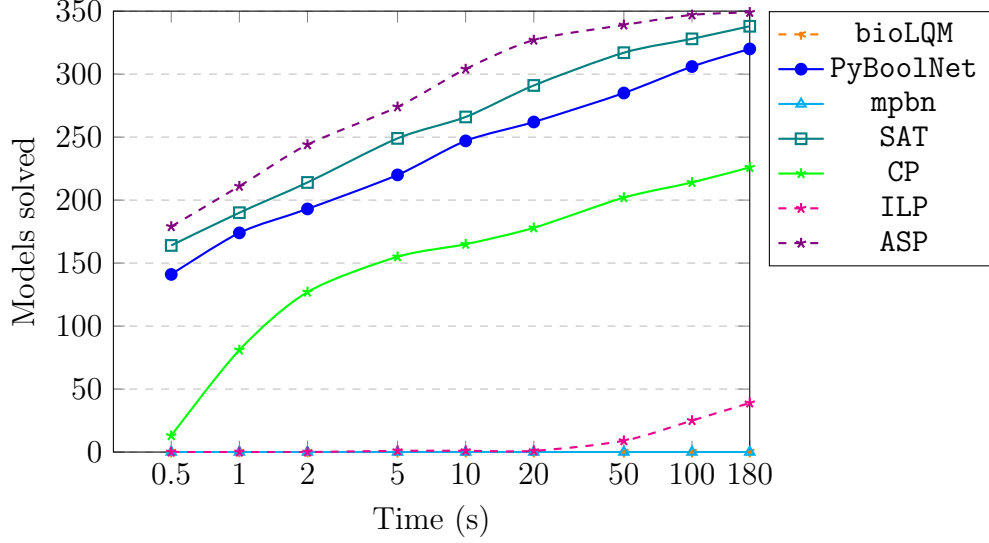


Figure 3: Cumulative numbers of random models solved by the compared methods with respect to enumerating all the minimal trap spaces.

Hence, it is apparent that all this type of randomly generated models are non-locally-monotonic because of the number of nodes is large ( $n \geq 100$ ). This observation confirms a limit on the applicable model class of `mpbn`.

Second, surprisingly `bioLQM` cannot handle any model. One of the reason may be that the BDD characterizing all trap spaces is too large, and its computation is slow. In addition, having too many generic trap spaces before the filtering process may be also a reason. It is apparent because the network size is large ( $n \geq 100$ ) and the Boolean functions are not simple.

Third, for every time limit, `Trappist-ASP` can always handle many more models than `PyBoolNet`, ranging from 29 to 65 more models. Since the time for the phase of computing prime-implicants of `PyBoolNet` is negligible in every model, most of the running time of `PyBoolNet` was spent for its ASP solving phase. Hence, we can easily see that the ASP encoding of `Trappist-ASP` is much better than that of `PyBoolNet`. This observation is consistent with the theoretical comparison in the ASP encoding between `Trappist-ASP` and `PyBoolNet` mentioned in Subsection 4.3.

### 6.5. Experimental summary

We have tested our alternative approach on many Boolean network models of various sizes and types (e.g., real-world models, randomly generated



models) on existing and newly created benchmarks. This indicates the high coverage and comprehensiveness of the experiments.

Among the four variants of the alternative approach, **Trappist-ASP** is the best method as it vastly outperforms all the other variants. The second best one is **Trappist-MaxSAT**. The two remaining variants (i.e., **Trappist-CP** and **Trappist-ILP**) give bad performance for most models. However, for certain cases, they are still better than all state-of-the-art methods (i.e., **bioLQM**, **PyBoolNet**, and **mpbn**). This is evidence for the advantages of an alternative approach compared to what preexisted.

Regarding general Boolean networks, **Trappist-ASP** (even **Trappist-MaxSAT**) is far more efficient than both **bioLQM** and **PyBoolNet**. The speedups of **Trappist-ASP** or **Trappist-MaxSAT** are large, even between one and three orders of magnitude for most models. In addition, the experimental results also confirm that the ASP encoding of **Trappist-ASP** is much more efficient than that of **PyBoolNet**.

Regarding locally-monotonic Boolean networks, the performance of **mpbn** is roughly comparable to that of **Trappist-ASP** or **Trappist-MaxSAT**. However, **mpbn** is quite slower than **Trappist-ASP** on average. This shows the practical advantage of **Trappist-ASP** compared to **mpbn**, though its ASP encoding may be more complex than that of **mpbn** in theory.

## 7. Conclusion

In this article we have explored and proved for the first time the equivalence between (minimal) trap spaces of a general Boolean network and (maximal) conflict-free siphons of its Petri net encoding. We have shown several useful applications of this finding to studying properties of trap spaces in Boolean networks. As an important practical application of the equivalence, we have proposed a new approach for the computation of minimal trap spaces in Boolean networks, based on the enumeration of maximal conflict-free siphons of Petri nets. We have also proposed four possible methods using MaxSAT, CP, ILP, and ASP for implementing the new approach. In particular, we have shown how to adjust our approach to compute several specific types of trap spaces (e.g., maximal trap spaces, fixed points), which besides minimal trap spaces also play crucial roles in the analysis and control of Boolean networks. The proposed methods for the minimal trap space computation have been evaluated on many real-world models from the literature as well as randomly generated models. The experimental results show

857 that the new approach vastly outperforms all the state-of-the-art methods  
858 in terms of general Boolean networks and is comparable to the `mpbn` method  
859 even much better on average in terms of locally-monotonic Boolean net-  
860 works. We believe that this opens up the way to a much better analysis  
861 of large Boolean networks, which is needed with the advent of automatic  
862 model-generation pipelines [55].

863 Although the experimental results show the superiority of our approach  
864 to `mpbn` in general, we however note that there is a model in the `BBM` repos-  
865 itory (with identifier 122) where all the four proposed methods for the new  
866 approach did not manage to finish the Petri net conversion before the time-  
867 out, whereas `mpbn` can still handle this model. The model is not very large  
868 but its Boolean functions are rather complicated. This points to the fact that  
869 our current choice of using a BDD-based translation to obtain that Petri net  
870 encoding, though it provides a small/efficient ASP might be too costly to  
871 handle the complex models. In such a case, a more *naive* encoding might  
872 provide a much larger ASP program, with many redundant rules, but eas-  
873 ier/faster to obtain. The evaluation of the feasibility of such strategy, and  
874 of its impact on smaller instances, remains to be done. Recognizing that  
875 a model is locally-monotonic and applying in that specific case dedicated  
876 strategies as those of `mpbn` might also be a partial solution.

877 It is worth noting that there may be possibly other methods for comput-  
878 ing minimal/maximal conflict-free siphons in Petri nets, like the methods for  
879 generic siphon computation in the field of Petri nets (see [34] for a survey  
880 about these methods). Although these approaches do not directly support  
881 the minimal/maximal conflict-free siphon computation now, we plan to in-  
882 vestigate them in the future. They could replace our proposed methods if  
883 they give significantly better performance. However, the current methods  
884 appear to already perform very well even on the biggest models we have  
885 considered.

886 Finally, we think that the links between Petri nets and Boolean networks  
887 that we stumbled upon in this article might have deeper roots. Exploring  
888 those connections might lead both to interesting topics of research for Petri  
889 nets, like a notion of trap-spaces, and for Boolean networks. We also believe  
890 that the connection between trap spaces of Boolean networks and siphons  
891 of Petri nets can be a very useful tool for exploring and proving more new  
892 properties of trap spaces in Boolean networks, as we have used it to success-  
893 fully prove the independence of trap spaces to the update scheme and the  
894 separation of minimal trap spaces. Diving into this direction is promising

895 and one of our future work.

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