

# 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-trapspaces.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 **this** 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 **current** 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.

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

$$s'(v_i) = f_i(s)$$

121 where  $s$  (resp.  $s'$ ) is the state of  $\mathcal{N}$  at time  $t$  (resp.  $t+1$ ). Note that for sim-  
122 plicity, we write  $f_i(s)$  even if  $IN(v_i) \subsetneq V$  (i.e.,  $IN(v_i)$  does not contain some  
123 nodes of  $V$ ). An update scheme of a Boolean network specifies the way that  
124 the nodes update their states through time evolution [20]. There are many  
125 different update schemes, but the two main types [20] are: *synchronous*,  
126 where all the nodes are updated simultaneously, and *fully asynchronous*,  
127 where only one node is selected non-deterministically to be updated. Follow-  
128 ing the update scheme, the Boolean network transits from a state to another  
129 state (possibly identical). This transition is called the *state transition* and  
130 denoted by  $\rightarrow \subseteq \mathcal{S}_{\mathcal{N}} \times \mathcal{S}_{\mathcal{N}}$ . For example, under the synchronous update  
131 scheme, we have  $x \rightarrow y$  if and only if  $y(v_i) = f_i(x), \forall v_i \in V$ , whereas under  
132 the fully asynchronous update scheme, we have  $x \rightarrow y$  if and only if there  
133 is a node  $v_i \in V$  such that  $y(v_i) = f_i(x)$  and  $y(v_j) = x(v_j), \forall v_j \in V, j \neq i$ .  
134 Then the dynamics of  $\mathcal{N}$  is captured by the directed graph  $(\mathcal{S}_{\mathcal{N}}, \rightarrow)$  called  
135 the State Transition Graph (STG).

## 136 2.2. Traps spaces

137 We recall here some definitions from [7] for the introduction of *trap spaces*.  
 138 Minimal trap spaces prove to be a very good approximation of the attractors  
 139 of a Boolean network under asynchronous update schemes and have become  
 140 the *de facto* standard way to analyze models of a few tens of *genes* [21, 22].

141 A non-empty set  $T \subseteq \mathcal{S}_{\mathcal{N}}$  is a *trap set* with respect to  $\rightarrow$  if for every  
 142  $x \in T$  and  $y \in \mathcal{S}_{\mathcal{N}}$  with  $x \rightarrow y$  it holds that  $y \in T$  [7]. An attractor of  
 143  $\mathcal{N}$  with respect to  $\rightarrow$  can be defined as an inclusion-wise minimal trap set  
 144 of  $(\mathcal{S}_{\mathcal{N}}, \rightarrow)$ . An attractor can be also seen as a terminal strongly connected  
 145 component of  $(\mathcal{S}_{\mathcal{N}}, \rightarrow)$  [23]. An attractor of size 1 is called a fixed point,  
 146 otherwise it is called a cyclic or complex attractor [7].

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

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

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

156 A *trap space* is defined as a subspace that is also a trap set. It is noted  
 157 that trap spaces of a Boolean network are independent of the update scheme  
 158 of this model [7], **we provide in Corollary 3.1 another proof of this**. Then, we  
 159 define a partial order  $<$  on  $\mathcal{S}_{\mathcal{N}}^{\star}$  as:  $m < m'$  if and only if  $\mathcal{S}_{\mathcal{N}}[m] \subseteq \mathcal{S}_{\mathcal{N}}[m']$   
 160 and  $\mathcal{S}_{\mathcal{N}}[m] \neq \mathcal{S}_{\mathcal{N}}[m']$ . Consequently, a trap space  $m$  is minimal if and only  
 161 if there is no trap space  $m' \in \mathcal{S}_{\mathcal{N}}^{\star}$  such that  $m' < m$ .

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

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

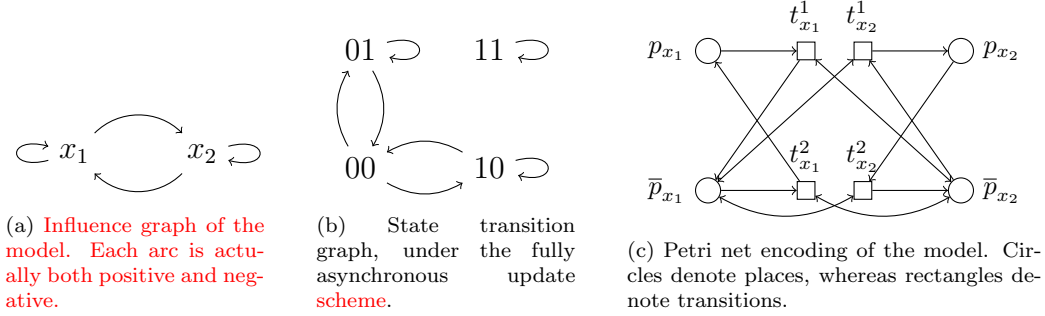


Figure 1: Dynamics and encoding of the Boolean network of Example 2.1.

### 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  $M(p) > 0$ . 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. *Note that in such nets we have  $M : P \mapsto \{0, 1\}$ , we might therefore represent a marking by the equivalent set of places containing a token and will use this notation for simplicity.* 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 [24] 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

197 two ways, either in [25] with non 1-safe Petri nets or more recently in [23]  
 198 with 1-safe nets but many more places.

199 Since our study is focused on Boolean networks, we briefly recall the orig-  
 200 inal encoding here. Its basis is that every node (*gene*)  $v$  of the original model  
 201  $\mathcal{N} = (V, F)$  is represented by two separate places ( $p_v$  and  $\bar{p}_v$ ), corresponding  
 202 to its two states, active, and inactive, respectively. Each conjunct of the  
 203 logical function that activates the *gene* will lead to a transition  $t$ , consuming  
 204 the inactive place (i.e., a directional arc from  $\bar{p}_v$  to  $t$ ), producing the active  
 205 place (i.e., a directional arc from  $t$  to  $p_v$ ), and with all other literals both  
 206 consumed and produced (i.e., a bidirectional arc). **Conversely a transition**  
 207 **is added from the active place to the inactive place for each conjunct of the**  
 208 **negation of that function.** Let  $s$  be a state of the Boolean network and  $M_s$   
 209 be its corresponding marking in the encoded Petri net. **It holds that  $\forall v \in V$ ,**  
 210  **$s(v) = 0$  if and only if  $M_s(\bar{p}_v) = 1$  and  $M_s(p_v) = 0$  and  $s(v) = 1$  if and only**  
 211 **if  $M_s(p_v) = 1$  and  $M_s(\bar{p}_v) = 0$ .** Note also that at any marking  $M$  of the Petri  
 212 **net encoding a Boolean network, it always holds that  $M(p_v) + M(\bar{p}_v) = 1$ .**

213 The main property of this encoding is that it is completely faithful with  
 214 respect to the update scheme of the original Boolean network. For each node  
 215  $v$  of  $\mathcal{N}$ , only transitions corresponding to  $v$  can change the current marking  
 216 of  $p_v$  or  $\bar{p}_v$ . **In addition, at any marking at most one of such transitions is en-**  
 217 **abled because  $M(p_v) + M(\bar{p}_v) = 1$  holds.** Hence, for any update scheme in  $\mathcal{N}$ ,  
 218 we have a corresponding firing scheme in  $\mathcal{P}$ , which preserves the equivalence  
 219 between the dynamics of  $\mathcal{N}$  and  $\mathcal{P}$  [26].

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

228 Note that given a Boolean network in the standard **SBML-Qual** format [27],  
 229 i.e., the package of SBML v3 [28] for such models, one can easily obtain its  
 230 Petri net encoding in the Petri Net Markup Language (PNML)<sup>2</sup> standard

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



231 using the `bioLQM`<sup>3</sup> library. This piece of software extracted from `GINsim` [29]  
 232 and part of the `CoLoMoTo`<sup>4</sup> [30] software suite allows for easy conversion  
 233 between standard formats. It also accepts many other common formats for  
 234 Boolean networks, notably the `.bnet` files of the `BoolNet` [31, 21] tools. The  
 235 conversion is executed as follows:

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

237 Note that transforming a Boolean network defined by its functions into its  
 238 Petri net encoding roughly relies on obtaining conditions for the activation  
 239 and inactivation of the states. In [24] this took the form of the whole truth  
 240 table of the Boolean functions, but as shown in Appendix 1 of [23] comput-  
 241 ing Disjunctive Normal Forms (DNF) of each Boolean function is enough.  
 242 Though this might appear quite computationally intensive it is important to  
 243 remark first that contrary to the **prime implicants** case, there is no need to  
 244 find *minimal* DNFs. One way to look at this is to consider that this amounts  
 245 to a similar approach as that used in [8] but with the encoding of both activa-  
 246 tion and inhibition functions as DNFs in order to take into account possible  
 247 non-local-monotonicity. This does not change the worst-case-complexity (ob-  
 248 taining a single DNF being exponential) but might matter a lot in practice.  
 249 As such, we will explore how this transformation, here using BDDs in `bioLQM`  
 250 or directly in our tool using the `pyeda`<sup>5</sup> library, and the one based on the  
 251 most-permissive semantics compare with each other in Section 6.

## 252 2.4. Siphons

253 Siphons are a static and classical property of Petri nets [11]. Note how-  
 254 ever that the use of siphons for the analysis of biological models, though it is  
 255 not new, has been mostly relevant to the ODE-based continuous semantics  
 256 of chemical reaction networks [32, 33, 34]. We recall here the basic definition  
 257 establishing that to produce something in a siphon you must consume some-  
 258 thing from the siphon. This corresponds to the idea that a siphon is a set of  
 259 places that once unmarked remains unmarked.

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

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

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

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

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

262 Note that  $\emptyset$  is trivially a siphon.

263 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  
 264 conventionally  $\text{pred}(S) = \text{succ}(S) = \emptyset$ . We have an important property on  
 265 siphons [35] as follows.

266 **Proposition 2.1.** *A set  $S$  of places is a siphon of a Petri net  $(P, T, W)$  if  
 267 and only if  $\text{pred}(S) \subseteq \text{succ}(S)$ .*

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

269 First let us associate subspaces and sets of places in the Petri net encod-  
 270 ing.

271 **Definition 3.1.** *Let  $m$  be a subspace of Boolean network  $\mathcal{N} = (V, F)$ . A  
 272 mirror of  $m$  is a set of places  $S$  in the Petri net encoding  $\mathcal{P}$  of  $\mathcal{N}$  such that:*

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

273 and

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

274 Now, we add a definition related to any set of places of a Petri net en-  
 275 coding a Boolean network, and notably a siphon of such a net.

276 **Definition 3.2.** *A set of places of Petri net  $\mathcal{P}$  encoding Boolean network  
 277  $\mathcal{N}$  is conflict-free if it does not contain any two places corresponding to the  
 278 active and inactive states of the same node of  $\mathcal{N}$ . Then, a conflict-free siphon  
 279  $S$  is said to be maximal if and only if there is no other conflict-free siphon  
 280  $S'$  such that  $S \subset S'$ .*

281 Intuitively, a siphon is a set of places that once unmarked remains so. If  
 282 it is conflict-free it is possible to associate a subspace to it, more precisely it  
 283 is the *mirror* of a subspace. Since it is a siphon, the fixed values will remain  
 284 so whatever update happens, as the unmarked places remain unmarked. The  
 285 subspace corresponding to that conflict-free siphon is therefore a trap space,  
 286 and the maximality of the siphon is equivalent to the minimality of the trap  
 287 space (as many fixed values as possible). For example, the Boolean network  
 288 given in Example 2.1 has two trap spaces,  $m_1 = 11$  and  $m_2 = \star\star$ . The  
 289 Petri net encoding of this Boolean network has five generic siphons,  $S_1 = \emptyset$ ,  
 290  $S_2 = \{p_{x_1}, \bar{p}_{x_1}\}$ ,  $S_3 = \{p_{x_2}, \bar{p}_{x_2}\}$ ,  $S_4 = \{\bar{p}_{x_1}, \bar{p}_{x_2}\}$ , and  $S_5 = \{p_{x_1}, \bar{p}_{x_1}, p_{x_2}, \bar{p}_{x_2}\}$ .

291 However, only  $S_1$  and  $S_4$  are conflict-free siphons and correspond to  $m_2$  and  
 292  $m_1$ , respectively. Since  $S_1 \subset S_4$ ,  $S_4$  is a maximal siphon corresponding to  
 293 the minimal trap space  $m_1$ . Hereafter, we formally prove that a (maximal)  
 294 conflict-free siphon is equivalent to a (minimal) trap space.

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

298 *Proof. First, we show that if  $m$  is a trap space of  $\mathcal{N}$ , then  $S$  is a conflict-free*  
 299 *siphon of  $\mathcal{P}$  (\*).*

300 If  $D_m = \emptyset$ , then  $S = \emptyset$  is trivially a conflict-free siphon of  $\mathcal{P}$ . Thus,  
 301 we consider the case that  $D_m \neq \emptyset$  (resp.  $S \neq \emptyset$ ). Assume that  $S$  is not a  
 302 siphon of  $\mathcal{P}$ . Then, there is a transition  $t \in T$  such that  $S \cap \text{succ}(t) \neq \emptyset$   
 303 but  $S \cap \text{pred}(t) = \emptyset$ . This implies that there is a place  $p \in S$  such that  
 304  $p \in \text{succ}(t)$  but  $p \notin \text{pred}(t)$ . Let  $v$  be the node in  $\mathcal{N}$  corresponding to  $p$ . By  
 305 the characteristics of the encoding [24], there is a directional arc from  $t$  to  $p$   
 306 and a directional arc from the complementary place of  $p$  to  $t$ . Without loss  
 307 of generality, we assume that  $p = p_v$ , then there is a directional arc from  $t$   
 308 to  $p_v$  and a directional arc from  $\bar{p}_v$  to  $t$ .

309 We follow the following procedure to find a state  $s \in \mathcal{S}_{\mathcal{N}}[m]$  such that  
 310  $M_s(p') = 1, \forall p' \in \text{pred}(t)$  where  $M_s$  is the corresponding marking in  $\mathcal{P}$  of  $s$ .  
 311 For every place  $p' \in \text{pred}(t)$ , let  $p''$  be the complementary place of  $p'$  and  $v'$   
 312 be the corresponding node in  $\mathcal{N}$  of  $p'$  and  $p''$ .

313 If  $p'' \notin S$ , then  $v' \notin D_m$  and we can always set the Boolean value to  $s(v')$   
 314 such that  $s \in \mathcal{S}_{\mathcal{N}}[m]$  and  $M_s(p') = 1$ .

315 If  $p'' \in S$ , then  $v' \in D_m$  and we set  $s(v') = m(v')$ . In this case, if  
 316  $p' = p_{v'}$  then  $s(v') = m(v') = 1$  leading to  $M_s(p') = 1$ , if  $p' = \bar{p}_{v'}$  then  
 317  $s(v') = m(v') = 0$  leading to  $M_s(p') = 0$ .

318 For the remaining nodes of  $\mathcal{N}$ , we can always set Boolean values to these  
 319 nodes to preserve that  $s \in \mathcal{S}_{\mathcal{N}}[m]$  by applying the same procedure. We also  
 320 have  $M_s(p_v) = 0$  by the characteristics of the encoding [24] (and Definition  
 321 3.1). Now,  $t$  is enabled at marking  $M_s$ . Its firing leads to a new marking  
 322  $M'_s$  such that  $M'_s(p_v) = 1$  and  $M'_s(\bar{p}_v) = 0$ . Let  $s'$  be the corresponding state  
 323 in  $\mathcal{N}$  of  $M'_s$ . We have  $s'(v) = 1$  because  $M'_s(p_v) = 1$  and  $m(v) = 0$  because  
 324  $p_v \in S$ . This implies that  $s' \notin \mathcal{S}_{\mathcal{N}}[m]$ .

325 For any firing scheme of  $\mathcal{P}$ , the firing of  $t$  always happens. Since a firing  
 326 scheme of  $\mathcal{P}$  is equivalent to an update scheme of  $\mathcal{N}$ ,  $s$  can escape from the  
 327 trap space  $m$  for any update scheme of  $\mathcal{N}$ , which contradicts to the property

of a trap space. Hence,  $S$  is a siphon of  $\mathcal{P}$ . By the definition of a mirror,  $S$  is also a conflict-free one.

*Second, we show that if  $S$  is a conflict-free siphon of  $\mathcal{P}$ , then  $m$  is a trap space of  $\mathcal{N}$  (\*\*).*

By the definition of a mirror,  $m$  is a subspace of  $\mathcal{N}$ . Let  $s$  be an arbitrary state in  $\mathcal{S}_{\mathcal{N}}[m]$  and  $M_s$  be its corresponding marking in  $\mathcal{P}$ . Assume that there is a place  $p \in S$  such that  $M_s(p) = 1$ . Let  $v$  be the corresponding node in  $\mathcal{N}$  of  $p$ . Since  $p \in S$ ,  $v \in D_m$  and  $m(v) = s(v)$ . If  $p = p_v$ , then  $M_s(p_v) = 1$  leading to  $m(v) = s(v) = 1$  by the characteristics of the encoding [24]. By the definition of a mirror,  $m(v) = 0$  because  $p_v \in S$ , meaning that  $M_s(p_v) = 0$ , which is a contradiction.

It is symmetric for the case that  $p = \bar{p}_v$ . Hence,  $M_s(p) = 0, \forall p \in S$ . In any marking  $M'_s$  reachable from  $M_s$  regardless of the firing scheme of  $\mathcal{P}$ , we have  $M'_s(p) = 0, \forall p \in S$  by the dynamical property on markings of a siphon [35]. Let  $s'$  be the corresponding state in  $\mathcal{N}$  of  $M'_s$ . For every node  $v \in D_m$ , we have all two cases as follows. Case 1:  $p_v \in S$ , then  $M'_s(p_v) = 0$ , thus  $s'(v) = 0 = m(v)$ . Case 2:  $\bar{p}_v \in S$ , then  $M'_s(\bar{p}_v) = 0$ , thus  $s'(v) = 1 = m(v)$ . Hence,  $s'(v) = m(v)$  for every  $v \in D_m$ . Then,  $s' \in \mathcal{S}_{\mathcal{N}}[m]$ . By the definition of a trap space and the arbitrariness of  $s$ ,  $m$  is a trap space of  $\mathcal{N}$ .

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

Note that this proof gives us as corollary a well-known result on trap spaces.

**Corollary 3.1.** *Trap spaces of a Boolean network are independent of the update scheme.*

*Proof.* From the proof of Theorem 3.1, we can see that the theorem holds for any update scheme associated to the Boolean network. Since the Petri net encoding of a Boolean network is independent of its update scheme and siphons are a static property of a Petri net, we get that trap spaces of a Boolean network are independent of its update scheme.  $\square$

Note that the original proof for this property of trap spaces (see Theorem 1 of [7]) only considers the two popular update schemes (i.e., synchronous and fully asynchronous). Theorem 3.1 exhibits the very first theoretical application of the connection between trap spaces of Boolean networks and siphons of Petri nets.

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

365 *Proof.* First, we show that if  $m$  is a minimal trap space of  $\mathcal{N}$ , then  $S$  is  
 366 a maximal conflict-free siphon of  $\mathcal{P}$  (\*). Since  $m$  is a trap space of  $\mathcal{N}$ ,  
 367  $S$  is a conflict-free siphon of  $\mathcal{P}$  by Theorem 3.1. Assume that  $S$  is not  
 368 maximal. Then, there is another conflict-free siphon  $S'$  such that  $S \subset S'$ .  
 369 By Theorem 3.1, there is a trap space  $m'$  corresponding to  $S'$ . Following the  
 370 definition of a mirror,  $D_m \subset D_{m'}$  and  $m(v) = m'(v), \forall v \in D_m$ . It follows  
 371 that  $S_{\mathcal{N}}[m'] \subset S_{\mathcal{N}}[m]$ , thus  $m' < m$ . This contradicts to the minimality of  
 372  $m$ . Hence,  $S$  is a maximal conflict-free siphon of  $\mathcal{P}$ .

373 Second, we show that if  $S$  is a maximal conflict-free siphon of  $\mathcal{P}$ , then  
 374  $m$  is a minimal trap space of  $\mathcal{N}$  (\*\*). Since  $S$  is a conflict-free siphon of  $\mathcal{P}$ ,  
 375  $m$  is a trap space of  $\mathcal{N}$  by Theorem 3.1. Assume that  $m$  is not minimal.  
 376 Then, there is another trap space  $m'$  such that  $m' < m$ . By the definition of  
 377 the partial order  $<$  on subspaces,  $S_{\mathcal{N}}[m'] \subset S_{\mathcal{N}}[m]$ . Let  $S'$  be the mirror of  
 378  $m'$ .  $S'$  is a conflict-free siphon by Theorem 3.1. Following the definition of  
 379 a mirror,  $S \subset S'$ , which contradicts to the maximality of  $S$ . Hence,  $m$  is a  
 380 minimal trap space of  $\mathcal{N}$ .

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

382 We here showcase a theoretical application of the connection between  
 383 trap spaces in Boolean networks and conflict-free siphons in Petri nets. We  
 384 use it to prove a property of minimal trap spaces, which has surprisingly  
 385 not been formally proved. Specifically, all minimal trap spaces of a Boolean  
 386 network are mutually disjoint. **This property is important because it can**  
 387 **benefit attractor identification of Boolean networks.** Specifically, in [36], the  
 388 **authors use random walks inside each minimal trap space to obtain approx-**  
 389 **imations for attractors of a Boolean network under the fully asynchronous**  
 390 **update scheme, then they use CTL model checking to verify the quality of**  
 391 **the approximations.** In [37], the authors use the set of minimal trap spaces  
 392 **as a seed to speedup their previous attractor identification method that re-**  
 393 **lies on feedback vertex sets and reachability analysis.** The soundness of the  
 394 **two above approaches comes from the separation of minimal trap spaces.**  
 395 Note that it would be not difficult to obtain a direct proof on trap spaces  
 396 for this property, which follows the same structure as the proof on siphons.  
 397 However, we emphasize here the potential of using the connection between

398 Boolean networks and Petri nets to explore and prove properties of trap  
399 spaces in Boolean networks.

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

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

407 Consider two any distinct minimal trap spaces  $m_1$  and  $m_2$ . Assume that  
408  $\mathcal{S}_{\mathcal{N}}[m_1] \cap \mathcal{S}_{\mathcal{N}}[m_2] \neq \emptyset$ . Let  $S_1$  and  $S_2$  be the mirrors of  $m_1$  and  $m_2$ , re-  
409 spectively. By Theorem 3.2,  $S_1$  and  $S_2$  are maximal conflict-free siphons  
410 of  $\mathcal{P}$ . We have that  $S = S_1 \cup S_2$  is also a siphon because of Proposi-  
411 tion 2.1. For every node  $v \in V$ , assume that  $p_v \in S$  and  $\bar{p}_v \in S$  hold.  
412 Since  $S_1$  and  $S_2$  are conflict-free, there are all two cases. Case 1:  $p_v \in S_1$   
413 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  
414  $m_1(v) \neq m_2(v)$ ,  $m_1(v) \neq \star$ ,  $m_2(v) \neq \star$ , then  $\mathcal{S}_{\mathcal{N}}[m_1] \cap \mathcal{S}_{\mathcal{N}}[m_2] = \emptyset$ . This is a  
415 contradiction. Hence, for every node  $v \in V$ ,  $p_v \in S$  and  $\bar{p}_v \in S$  cannot hold  
416 together. Therefore,  $S$  is conflict-free. Now, we have that  $S$  is a conflict-free  
417 siphon but  $S_1 \subset S$  or  $S_2 \subset S$  holds because  $S_1 \neq S_2$ . This contradicts to the  
418 maximality of  $S_1$  and  $S_2$ . Hence,  $\mathcal{S}_{\mathcal{N}}[m_1] \cap \mathcal{S}_{\mathcal{N}}[m_2] = \emptyset$  holds.

419 □

420 A natural computational application of Theorem 3.1 is that we can effi-  
421 ciently decide whether a subspace  $m$  is a trap space. In PyBoolNet [21], this  
422 is checked by using the percolation on the **prime implicants** of the Boolean  
423 functions. As we have mentioned at the beginning of this article, the compu-  
424 tation of **prime implicants** is a demanding task for complex Boolean networks,  
425 even is sometimes intractable. Hence, the checking method in [21] shows its  
426 limitations. Instead, we can first compute the mirror  $S_m$  of  $m$  in the Petri  
427 net encoding. Then, by Proposition 2.1 and Theorem 3.1, we can check if  
428  $\text{pred}(S_m) \subseteq \text{succ}(S_m)$ . Note that the Petri net construction is less com-  
429 putationally demanding than the prime-implicant computation because it  
430 only requires computing generic (not prime) implicants of the Boolean func-  
431 tions [23]. In addition, the worst case time complexity of the above checking  
432 method is quadratic in the number of transitions of the Petri net.

Furthermore, by Theorem 3.2, we can reduce the problem of computing all minimal trap spaces of a Boolean network to the problem of computing all maximal conflict-free siphons of its Petri net encoding. Note that in the case of special types of trap spaces (e.g., fixed points), this can be put in regard to special types of siphons in Petri nets. See Subsection 4.5 for more discussions about many special types of trap spaces. It might actually be possible to generalize our result to any 1-safe place-complementary (i.e., places are defined by pairs such that the markings are complementary) Petri net to define a notion of trap spaces that might be useful for the analysis of Petri nets, but this is out of the scope of the present article. Note also that conversely, investigating static analyses on such 1-safe place-complementary nets might allow for a more efficient computation of their siphons and hence of trap spaces.

Note that there are no existing methods specifically designed for computing maximal conflict-free siphons (even maximal generic siphons) of a Petri net. The reason might be that researchers mainly focus on minimal generic siphons [35] in the field of Petri nets. While adapting those methods to obtain minimal conflict-free siphons would sometimes be possible, the switch from minimality to maximality is quite a leap. Hence, we here propose several methods for computing maximal conflict-free siphons of a Petri net. The details of the proposed methods shall be given in the next section.

## 4. Computation methods

First, we discuss the complexity of siphon computation in Petri nets. Siphons are a prominent concept in the field of Petri nets, but unfortunately there are very few studies focusing on the complexity aspect. In this field, researchers mainly focus on practical methods for computing minimal generic siphons (also many related types) in general or special Petri nets and the applications of such types to the control of real-world systems modeled by Petri nets [35]. The problem of finding a minimal siphon of a 1-safe Petri net is solvable in polynomial time [38]. Clearly, the problem of finding a siphon of a 1-safe Petri net is also solvable in polynomial time. However, the problem of computing all (minimal) siphons is not easier than the problem of computing a (minimal) siphon but its complexity still not clear. Note that the number of siphons (even minimal siphons) can be exponential in the number of places of the Petri net [35]. Moreover, there is no complexity result for the case of maximal siphons. Regarding the conflict-free siphons,

we believe that the polynomial algorithm for computing a minimal generic siphon presented in [38] can be adapted to find a (minimal) conflict-free siphon. This is not in contrast to the NP-hardness of some problems on trap spaces in Boolean networks [39] because in general the number of transitions of the Petri net encoding of a Boolean network can be exponential in the number of nodes of this Boolean network. However, again the complexity of the problem of computing all (minimal/maximal) conflict-free siphons is still open.

#### 4.1. Characterization

We here show the characterization of all conflict-free siphons of the encoded 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

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

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

#### 4.2. Constraint satisfaction problem

A Constraint Satisfaction Problem (CSP) is defined by a triple giving its variables, their domains, and the constraints on those variables. The following Boolean CSP directly derives from the above characterization:

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

- $R = P$ , i.e., a variable is introduced for each place of  $\mathcal{P}$ ,



- 497 •  $D(p) = \mathbb{B}$  for all  $p \in R$ , i.e., the variables are Boolean,
- 498 •  $C = \{\neg p_v \vee \neg \bar{p}_v = 1 \mid \forall v \in V\} \wedge \{(p = 1 \rightarrow \bigvee_{p' \in \text{pred}(t)} p' = 1) \mid p \in$
- 499  $P, t \in \text{pred}(p)\}$ .

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

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

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

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

506  $\square$

507 In [17], the set of all siphons of a given Petri net is characterized by a sim-  
 508 ilar Boolean CSP except the conflict-freeness constraint. From the encoded  
 509 CSP, the set of all *minimal* siphons of the Petri net can be enumerated in the  
 510 set inclusion order. For enumerating siphons in the set inclusion order, the  
 511 **method proposed in** [17] uses the technique that labels directly the Boolean  
 512 variables with increasing value selection (i.e., to test first the absence, then  
 513 the presence of a place in the candidate solution). The method has two  
 514 implementations, one uses an iterated SAT procedure and the other uses  
 515 Constraint Programming (CP) with backtracking.

516 One natural question is that how to use the CSP-based method for enu-  
 517 merating all the maximal conflict-free siphons of a Petri net encoding a  
 518 Boolean network? Of course, the set of all conflict-free siphons of the Petri  
 519 net can easily be characterized by the CSP model presented in [17] along with  
 520 the additional constraint  $\neg p_v \vee \neg \bar{p}_v = 1$ , for each  $v \in V$ , which represents  
 521 the conflict-freeness. However, the main concern is to enumerate all the  
 522 *maximal* ones, which is not trivial to adapt from the CSP-based method.  
 523 By Proposition 4.1, the set of all maximal conflict-free siphons of  $\mathcal{P}$  can be  
 524 enumerated in the (maximality) set inclusion order, by restarting the search  
 525 each time a conflict-free siphon  $S$  is found, with the following additional con-  
 526 straint for disallowing any subset of that conflict-free siphon:  $\bigvee_{p \notin S} p = 1$ .  
 527 For enumerating conflict-free siphons in the set inclusion order, we can use  
 528 the same technique as used in [17] but with the opposite setting, i.e., labeling

529 directly the Boolean variables with decreasing value selection. The correct-  
 530 ness of this technique comes from the fact that once  $S$  is found, it is the  
 531 conflict-free siphon of maximum cardinality among all the remaining feasible  
 532 conflict-free siphons. Similar to [17], the newly CSP-based method can also  
 533 be implemented with SAT and CP solvers.

534 This method was implemented using the state-of-the-art CP solver Chuffed<sup>6</sup>  
 535 [40] via its MiniZinc [41] interface. Because it is a high-level interface, the  
 536 backtrack-and-replay method of [17] was not used but rather the alterna-  
 537 tive implementation with two global constraints for lexicographic ordering  
 538 (ensuring enumeration of solutions) and iterated non-subset of each already  
 539 found solution (for maximality).

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

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

543 and

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

544 We set a soft clause for each variable of the CSP and then use a “minimal cor-  
 545 rection subset” blocking strategy, which will ensure set-inclusion maximality  
 546 of the solutions. We implement this approach by using the RC2 MaxSAT  
 547 solver [42] available through the `python-sat` package<sup>7</sup>.

#### 548 4.3. Answer set programming-based method

549 Another possible method is to translate the characterization shown in  
 550 Subsection 4.1 into the ASP  $\mathcal{L}$  as follows. We introduce atom `p-v` (resp.  
 551 `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  
 552 as  $\mathcal{A} = \bigcup_{v \in V} \{\text{p-v}, \text{n-v}\}$ . For each pair  $(p, t)$  where  $p \in P, t \in T, t \in \text{pred}(p)$ ,  
 553 we translate the rule (1) into the ASP rule

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

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

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

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

556 the ASP rule

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

557 for each  $v \in V$ . This ASP rule guarantees that two places representing  
 558 the same node in  $\mathcal{N}$  never belong to the same siphon of  $\mathcal{P}$ , representing  
 559 the conflict-freeness. Naturally, a Herbrand model (see, e.g., [43]) of  $\mathcal{L}$  is  
 560 equivalent to a conflict-free siphon of  $\mathcal{P}$ . To guarantee that a Herbrand  
 561 model is also a stable model (an answer set), we need to add to  $\mathcal{L}$  the two  
 562 choice rules

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

563 for each  $v \in V$ . Note that the number of atoms of  $\mathcal{L}$  is only  $2n$ , whereas  
 564 the ASP encoding shown in [7] has as many atoms as the number of **prime**  
 565 **implicants** of the Boolean network and that number might be exponential in  
 566  $n$ . In [8], there is an ASP characterization of trap spaces that does not rely  
 567 on minimal DNFs either and thus seems very similar to our ASP encoding.  
 568 Remarkably it only requires the DNF for the *activation* part, using the in-  
 569 formation that it will only be used for locally-monotonic Boolean networks.  
 570 We would therefore expect that, when available, it will have comparable per-  
 571 formance on the ASP part (the ASP program would be approximately twice  
 572 smaller, though redundancy is not always bad in that field), but can also  
 573 avoid combinatorial explosion of the Petri net encoding for some formula  
 574 where the activation DNF is simple but the inhibition is not. Since **mpbn** is  
 575 included in our benchmark this will be evaluated in our experiments.

576 Now, a solution (simply an answer set)  $A \subseteq \mathcal{A}$  of  $\mathcal{L}$  is equivalent to a  
 577 conflict-free siphon  $S$  of  $\mathcal{P}$ , thus a trap space  $m$  of  $\mathcal{N}$ . The conversion from  $A$   
 578 to  $m$  is straightforward. If  $\text{p-v} \in A$  then  $v \in D_m$  and  $m(v) = 0$ . Conversely,  
 579 if  $\text{n-v} \in A$  then  $v \in D_m$  and  $m(v) = 1$ . Otherwise,  $v \notin D_m$ . Comput-  
 580 ing multiple answer sets is built into ASP solvers and the solving collection  
 581 **POTASSCO** [43] also features the option to find set-inclusion maximal answer  
 582 sets with respect to the set of atoms. Naturally, a set-inclusion maximal  
 583 answer set of  $\mathcal{L}$  is equivalent to a maximal conflict-free siphon of  $\mathcal{P}$ , thus a  
 584 minimal trap space of  $\mathcal{N}$ . By using this built-in option, we can compute all  
 585 the set-inclusion maximal answer sets of  $\mathcal{L}$  (resp. all the minimal trap spaces  
 586 of  $\mathcal{N}$ ) in one execution.

#### 587 4.4. Integer linear programming-based method

588 We first show how an Integer Linear Programming (ILP)  $\mathcal{I}$  can define  
 589 a set of all conflict-free siphons of the encoded Petri net  $\mathcal{P}$ . We introduce

590 *binary* variable  $\mathbf{p-v}$  (resp.  $\mathbf{n-v}$ ) to denote place  $p_v$  (resp.  $\bar{p}_v$ ),  $\forall v \in V$ . The  
 591 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  
 592  $p \in P, t \in T, t \in \text{pred}(p)$ , we translate the rule (1) into the ILP inequality

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

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

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

596 for each  $v \in V$ . This inequality forbids both  $\mathbf{p-v}$  and  $\mathbf{n-p}$  receive the value  
 597 1, thus representing the conflict-freeness. Since we only consider feasible  
 598 solutions, the objective function is set to  $\max \mathbf{p-v}$  for some  $v \in V$ . Naturally,  
 599 a solution  $I$  of  $\mathcal{I}$  is equivalent to a conflict-free siphon  $S$  of  $\mathcal{P}$ . The conversion  
 600 is that

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

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

602 We can see the similarity between  $\mathcal{I}$  and the encoded ASP shown in the  
 603 previous subsection. However, due to the nature of solutions of an ILP, it is  
 604 hard to compute all the set-inclusion maximal solutions of  $\mathcal{I}$  in one execution  
 605 of an ILP solver. Hence, we propose an iterative approach as follows.

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

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

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

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

613 where  $\mathbf{a-p}$  is the binary variable presenting place  $p$ . Now, we solve  $\mathcal{I}$  again to  
 614 find a new solution. If a new solution  $I'$  exists, then let  $S'$  be its corresponding

615 conflict-free siphon. Indeed, abide by the newly added inequality, we have  
616  $S' \cap (P \setminus S^*) \neq \emptyset$  because there is some  $\mathbf{a-p}$  with  $p \in P \setminus S^*$  such that  
617  $I'(\mathbf{a-p}) = 1$ . This implies that it is impossible that  $S' = S^*$  or  $S' \subset S^*$ .  
618 By the objective function, it means that  $S'$  is the conflict-free siphon of  
619 maximum cardinality among the conflict-free siphons that are not contained  
620 in  $S^*$ . Hence,  $S'$  is also a maximal conflict-free siphon. Again, we add to  $\mathcal{I}$   
621 a new inequality with respect to the newly found siphon. The above process  
622 is iterated until  $\mathcal{I}$  becomes unfeasible, this means that there is no further  
623 maximal conflict-free siphon. Thus, all the maximal conflict-free siphons of  
624 the Petri net have been found.

625 Since we used the MiniZinc framework to interface with the CP solver, it  
626 was simple to make the slight modifications described above and to use that  
627 same interface to call the Coin-OR CBC solver<sup>8</sup> [44].

#### 628 4.5. Computation of special types of trap spaces

629 In the field of systems biology, biologists may want to compute more  
630 special types of trap spaces beyond minimal trap spaces [21], which also play  
631 crucial roles in analysis and control of Boolean networks [22, 19]. We shall  
632 show that our proposed methods can be easily adjusted to compute such  
633 popular types of trap spaces. We illustrate the adjustments via the ASP-  
634 based method (see Subsection 4.3) because ASP is declarative by nature,  
635 but these adjustments are completely applicable for other approaches such  
636 as MaxSAT, CP, and ILP.

637 First, the work presented in [19] uses the concept of *stable motifs* to build  
638 the succession diagram of a Boolean network, a summary of the decisions in  
639 the network dynamics that lead to successively more restrictive nested stable  
640 motifs. The succession diagram is useful for control and decision making  
641 on this Boolean network. In particular, the proposed control methods are  
642 independent to the update scheme. Note that, in [19], the succession dia-  
643 gram is also used to identify all attractors of a Boolean network under the  
644 fully asynchronous update scheme. It has been shown that a stable motif  
645 of a Boolean network is equivalent to a *maximal trap space* of this Boolean  
646 network [19]. Indeed, the computation of stable motifs is a bottleneck of  
647 the methods proposed in [19]. Hence, it is necessary to develop an efficient  
648 method for computing maximal trap spaces of a Boolean network. We shall

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

show how to adjust the 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

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

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

Second, we consider *fixed points* in Boolean networks. To date, the analysis 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 [45]. 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 [37]. 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

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

that ensures that for every conflict-free siphon  $S$ , it contains either  $\text{p-v}$  or  $\text{n-v}$  for every  $v \in V$ . Equivalently, the trap space corresponding to  $S$  is always

683 a fixed point. Now, the set of answer sets of the encoded ASP is equivalent  
 684 to the set of fixed points of  $\mathcal{N}$ . In particular, when solving the encoded ASP  
 685 using an ASP solver, we do not need to use the built-in option for computing  
 686 set-inclusion maximal answer sets. Note that we can also build another ASP  
 687 characterizing all fixed points of  $\mathcal{N}$  based on the equivalence between a fixed  
 688 point of  $\mathcal{N}$  and a deadlock of its Petri net encoding [23]. This approach may  
 689 give a more compact ASP.

690 Third, we consider the trap spaces *intersecting* a given subspace  $m^*$  of  
 691 a Boolean network. Such trap spaces (along with minimal trap spaces) are  
 692 used in the phenotype control method [22]. This method uses the prime  
 693 implicant-based method [7, 21] to compute trap spaces, which has been shown  
 694 inefficient. Hence, having a more efficient method for computing such trap  
 695 spaces can push the barrier previously existing in this control method. A  
 696 trap space  $m$  intersects  $m^*$  if and only if  $S_{\mathcal{N}}[m] \cap S_{\mathcal{N}}[m^*] \neq \emptyset$ . It follows  
 697 that for every  $v$ , if  $m^*(v) = 0$  then  $m(v) = 0$  or  $m(v) = \star$ , if  $m^*(v) = 1$  then  
 698  $m(v) = 1$  or  $m(v) = \star$ . For the former case, we add to  $\mathcal{L}$  the ASP rule

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

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

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

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

703 Finally, we consider the trap spaces that are *inside* a given subspace  $m^*$   
 704 of a Boolean network. Such trap spaces are used in the iterative procedure  
 705 of building the succession diagram of a Boolean network [19], which is hier-  
 706 archical. We first adjust  $\mathcal{L}$  to characterize all such trap spaces. A trap space  
 707  $m$  is inside  $m^*$  if and only if  $m(v) = m^*(v)$  for every  $v \in D_{m^*}$ . If  $m^*(v) = 0$ ,  
 708 we add to  $\mathcal{L}$  the ASP rule

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

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

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

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

713 rule

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

714 where  $\{v_{i1}, \dots, v_{ik}\}$  is the set of free nodes of  $m^*$ . This rule ensures that  
715  $m \neq m^*$ . In the case that  $m^* = \varepsilon$ , we have all maximal trap spaces of the  
716 original Boolean network.

## 717 5. Motivating example

718 For a few years now we have been collaborating with biologists who build  
719 very large detailed and annotated maps and now wish to analyze the dy-  
720 namics of the corresponding models. One of the main maps studied this way  
721 represents knowledge about the Rheumatoid Arthritis [46], and was the main  
722 motivation for the development of a tool to automatically transform it into  
723 an executable Boolean network [6]. In the supplementary material of the pa-  
724 per, an excerpt of the map, focused around the apoptosis (cell death) module  
725 is transformed into a model of *reasonable* size, namely 180 Boolean variables  
726 (model `F5_RA_apoptosis_executable_module.sbml` of supplementary ma-  
727 terial S3, and model “RA\_apoptosis” of Subsection 6.3). The study of such  
728 model, though, is a big hurdle. Indeed, as stated in the article about another  
729 model of the same size: “*The size of the CaSQ-inferred MAPK model (181*  
730 *nodes) made the calculation of stable states a non-realistic endeavour.*”

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

738 However, using a state-of-the-art tool like `PyBoolNet` [7] on that model  
739 **unfortunately** fails at the phase of prime-implicant generation. `mpbn` [9] can  
740 return the first 1000 solutions within 1.43s, but indeed, it limits the model-  
741 ing range of the modelers as it does not permit using non-locally-monotonic  
742 Boolean functions. This is also true for the Alzheimer model also mentioned  
743 in that same article and originally from [47] (F4 file in the original supple-  
744 mentary material, and “Alzheimer” in Table 2), where `PyBoolNet` also fails  
745 at the prime-implicant computation and `mpbn` does not give any answer be-  
746 cause this model is actually non-locally-monotonic. The current practice



usually revolves then around fixing some source nodes to plausible values and reducing the model accordingly. While this approach makes sense, it relies on potentially arbitrary decisions, and *hides away* critical modelling choices that were **clearly** not part of the original Boolean network or even of the starting map.

For the “RA\_apoptosis” model, using the ASP-based method presented in Subsection 4.3, it is **now** possible to obtain the first 1000 minimal trap spaces (including ones that contain more than one state) within 0.19s, which is much quicker than `mpbn`. The needed time for the “Alzheimer” model is 0.79s.

## 6. Evaluation

To evaluate the performance of the newly proposed methods (implemented as a Python package named `Trappist` and available on the Python package index<sup>9</sup>) and the state-of-the-art methods (`bioLQM`<sup>10</sup>, `PyBoolNet` [7, 21], and `mpbn` [9]), we compared them on both `PyBoolNet`’s own model repository and many real-world models from various sources in the literature. To our knowledge, these models are a highly representative sample of Boolean models currently available. It is worth noting that `mpbn` [9] only handles locally-monotonic models, whereas the other methods can handle general models. To obtain a more comprehensive comparison, we also used random models generated by a third-party software `BoolNet R` package [31]. As explained in Section 5, in our benchmarks, we only searched for the first 1000 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` [43] and the same configuration as that used in `PyBoolNet` [7, 21] 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 × 16, 16 GB DDR4 RAM, Ubuntu 20.04.5 LTS. Finally, we set a time limit of three minutes for each model.

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

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

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

#### 784 6.1. *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+	N/A	<b>0.85</b>	<b>0.45</b>	<b>0.56</b>	<b>NF</b>	<b>NF</b>	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	<b>NM</b>	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	<b>NM</b>	0.01	<b>0.77</b>	<b>0.67</b>	0.01
22 randomnet_n7k3	7	10	<b>0.10</b>	0.01	<b>NM</b>	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+	N/A	<b>0.48</b>	<b>0.28</b>	<b>0.28</b>	<b>NF</b>	<b>NF</b>	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>	<b>NF</b>	0.04
29 zhang_tlgl.v2	60	258	<b>0.64</b>	0.04	0.08	0.11	<b>69.95</b>	<b>NF</b>	0.04

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. “NF” 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 record 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 models, but Trappist-ASP is much faster for the jaoude\_thdiff and selvaggio\_empt 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 [43]. 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

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

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 **non**-locally-monotonic but all the other methods did, which confirms the limit of **mpbn** on the applicable class of models.

## 6.2. *BBM repository*

The research group behind the **BBM** repository has recently undertaken considerable effort for building a collection 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 out of them are non-locally-monotonic), peaking at 321 nodes, 1100 regulations among the nodes, and 133 source nodes, respectively. It is released and maintained at <https://github.com/sybila/biodivine-boolean-models>. We here tested all the compared methods on this model repository.

Figure 2 (upper panel) shows cumulative numbers of the **BBM** models that 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

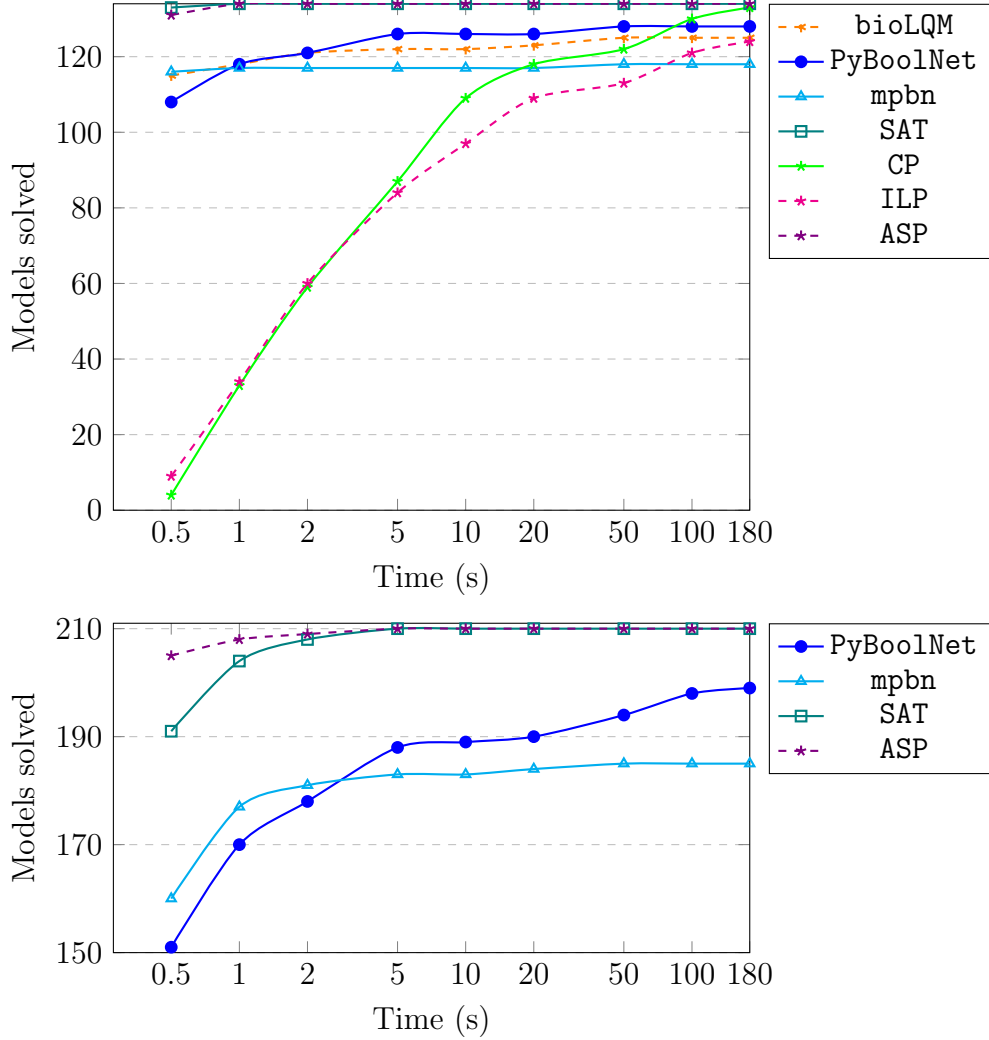


Figure 2: Cumulative numbers of the BBM models that have less than 1000 minimal trap spaces (upper panel) and BBM models solved by the compared methods with respect to enumerating the first 1000 minimal trap spaces (lower panel).

857 first see that **Trappist-ASP** and **Trappist-MaxSAT** are still the two best  
858 methods as they can handle every model within 1s and always can handle  
859 more models than all the remaining methods on every time limit. Second,  
860 **Trappist-CP** is better than **Trappist-ILP**, which is consistent with their  
861 comparison shown in the previous subsection. Third, one notable remark is  
862 that for the time limit of 100s or 180s, **Trappist-CP** can handle more models

863 than all `bioLQM`, `PyBoolNet`, and `mpbn`. This remark shows that even **without**  
864 **focusing on the optimization of our implementation**, our alternative approach  
865 is still better than the state-of-the-art methods on a certain set of real-world  
866 models. This is supported by the fact that our alternative approach avoids  
867 the need for computing prime implicants (as opposed to `PyBoolNet`) and can  
868 handle non-locally-monotonic Boolean networks (as opposed to `mpbn`).

869 Figure 2 (lower panel) shows cumulative numbers of the `BBM` models solved  
870 by the compared methods (except `bioLQM`, `Trappist-CP`, and `Trappist-ILP`)  
871 with respect to enumerating the first 1000 minimal trap spaces. We omit  
872 the results of `Trappist-CP` and `Trappist-ILP` because they can handle  
873 no model with more than 1000 minimal trap spaces. Again, we can see  
874 that `Trappist-ASP` and `Trappist-MaxSAT` are the two best methods as they  
875 can handle every but one model within 5s. They also always handle many  
876 more models than both `PyBoolNet` and `mpbn` on every time limit. Note that  
877 with the time limit of 0.5s, `Trappist-ASP` can handle 14 more models than  
878 `Trappist-MaxSAT`, which is opposed to the case of models with less than  
879 1000 minimal trap spaces (see Figure 2 (upper panel)). This observation  
880 confirms the disadvantage of `Trappist-MaxSAT` compared to `Trappist-ASP`  
881 for the case of many minimal trap spaces.

### 882 6.3. Selected models

883 We used a set of real-world Boolean networks lying in various scales col-  
884 lected from numerous bibliographic sources in the literature. Most of these  
885 models are quite big (in size), complex (i.e., having high average in-degree,  
886 which is related to the number of **prime implicants**), and have never been  
887 fully analyzed. Note that these models are not included in the `PyBoolNet`  
888 and `BBM` repositories. We then applied `bioLQM`, `PyBoolNet`, `mpbn`, and the  
889 four variants of `Trappist` to computing minimal trap spaces of these real-  
890 world models. Table 2 shows the obtained experimental results. A number  
891 in bold indicates a ratio greater than or equal to 10 compared to the best  
892 result. The remaining notations are similar to those in Table 1. Hereafter, we  
893 analyze in detail the results with respect to minimal trap space computation.

894 First, we obtained some observations on the four variants of `Trappist`  
895 consistent with the observations obtained in the previous subsections. More  
896 specifically, `Trappist-ASP` is still the best variant with a running time below  
897 one second for every model, and followed by `Trappist-MaxSAT`. In particular,  
898 the difference in running time between `Trappist-ASP` and `Trappist-MaxSAT`  
899 is bigger for larger models or models with more than 1000 minimal trap

Table 2: Timing comparisons (in seconds) between bioLQM (LQM), PyBoolNet (PBN), mpbn and the four variants of Trappist on selected models from the literature. **The models are sorted by size with a horizontal rule inserted to split at 100 and 200 nodes, as in [18]**

model	$n$	$ M $	LQM	PBN	mpbn	Trappist			
						SAT	CP	ILP	ASP
1 metastatic [48]	10	4	<b>0.10</b>	0.04	NM	0.01	<b>1.15</b>	<b>0.89</b>	0.02
2 Arabidopsis_thaliana [48]	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 [48]	16	1	0.38	<b>1.76</b>	NM	0.08	0.53	0.43	0.14
4 p53_low_dna [48]	16	1	0.41	<b>1.76</b>	NM	0.07	0.58	0.48	0.14
5 FT-GRN [49]	23	32	<b>NF</b>	<b>NF</b>	NM	0.03	<b>8.41</b>	<b>12.38</b>	0.19
6 DNA_damage [48]	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 [48]	33	2	0.17	0.57	<b>40.39</b>	0.07	<b>0.74</b>	0.56	0.11
8 Pluripotency [50]	36	440	<b>NF</b>	<b>NF</b>	NM	0.16	<b>138.92</b>	<b>NF</b>	0.28
9 Pluripotent [48]	36	276	0.37	0.43	NM	0.07	<b>72.40</b>	<b>NF</b>	0.06
10 Pancreatic.Cancer [48]	43	1000+	N/A	0.11	0.36	0.17	<b>NF</b>	<b>NF</b>	0.06
11 Drosophila [51]	52	128	0.33	0.05	0.07	0.06	<b>32.66</b>	<b>126.22</b>	0.05
12 Cacace_TdevModel [52]	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 [48]	65	1000+	N/A	<b>NF</b>	0.50	0.34	<b>NF</b>	<b>NF</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>NF</b>	0.05
15 Bcell [53]	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>NF</b>	<b>NF</b>	0.15
17 Corral_ThIL17diff [45]	92	1000+	N/A	<b>107.57</b>	0.76	0.56	<b>NF</b>	<b>NF</b>	0.16
18 Adhesion_CIP [54]	121	78	<b>56.81</b>	<b>4.25</b>	0.23	0.17	<b>25.20</b>	<b>NF</b>	0.19
19 EMT_Mech [55]	136	82	<b>NF</b>	<b>14.01</b>	0.27	0.20	<b>27.55</b>	<b>NF</b>	0.25
20 macrophage [48]	136	1000+	N/A	0.54	1.09	0.84	<b>NF</b>	<b>NF</b>	0.27
21 angiogenesis [48]	141	1000+	N/A	0.16	1.07	1.06	<b>NF</b>	<b>NF</b>	0.16
22 angiofull [56]	142	1000+	N/A	0.17	1.06	0.88	<b>NF</b>	<b>NF</b>	0.23
23 EMT_Mech_TGFBeta [55]	150	492	<b>NF</b>	<b>11.28</b>	0.78	0.69	<b>NF</b>	<b>NF</b>	0.35
24 RA_apoptosis [6]	180	1000+	N/A	<b>NF</b>	1.43	1.55	<b>NF</b>	<b>NF</b>	0.19
25 MAPK [6]	181	1000+	N/A	<b>13.58</b>	1.76	1.51	<b>NF</b>	<b>NF</b>	0.27
26 Snf1-pathway [57]	202	1000+	N/A	1.13	1.47	1.43	<b>NF</b>	<b>NF</b>	0.31
27 T-cell-co-receptor [48]	206	1000+	N/A	<b>NF</b>	1.52	2.26	<b>NF</b>	<b>NF</b>	0.35
28 TcellCheckPoint [58]	218	1000+	N/A	<b>4.99</b>	NM	1.96	<b>NF</b>	<b>NF</b>	0.28
29 Mycobacterium [48]	317	1000+	N/A	0.42	2.36	<b>4.91</b>	<b>NF</b>	<b>NF</b>	0.44
30 Leishmania [48]	342	1000+	N/A	<b>NF</b>	2.56	<b>5.62</b>	<b>NF</b>	<b>NF</b>	0.46
31 Cholecystokinin [6]	383	1000+	N/A	0.36	2.99	<b>4.81</b>	<b>NF</b>	<b>NF</b>	0.37
32 Alzheimer [6]	762	1000+	N/A	<b>NF</b>	NM	<b>18.21</b>	<b>NF</b>	<b>NF</b>	0.79

spaces. Trappist-CP and Trappist-ILP still have a much worse performance, with Trappist-CP better than Trappist-ILP. They still can handle no model with more than 1000 minimal trap spaces. However, Trappist-CP or Trappist-ILP can handle the FT-GRN and Pluripotency models, whereas all bioLQM, PyBoolNet, and mpbn cannot.

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

911 Third, for 11 of the 32 models (more than 34%), **mpbn** did not give any an-  
 912 swer because these models are non-locally-monotonic. For 21 of the 32 mod-  
 913 els where **mpbn** returned the answers, **mpbn** and **Trappist-ASP** are roughly  
 914 comparable in computation time, but **mpbn** appears quite slower on aver-  
 915 age. In particular, for the Rho-GTPases model, **mpbn** is  $577\times$  slower than  
 916 **Trappist-ASP**. This observation along with the comparisons between **mpbn**  
 917 and **Trappist-ASP** in the previous subsections are quite surprising because  
 918 the ASP encoding of **mpbn** only requires the DNF for the activation part of a  
 919 Boolean function, whereas that of **Trappist-ASP** requires both the activation  
 920 and inhibition parts (see Subsection 4.3). However, the reason may lie on the  
 921 differences in the ASP encoding characteristics of the two methods and the  
 922 fact that **mpbn** needs to spend time checking the local-monotonicity of each  
 923 Boolean function in a Boolean network. We expect that **mpbn** may outper-  
 924 form **Trappist** for a certain set of models, but not for the set of real-world  
 925 models considered in this article.

926 Fourth, regarding the comparison of the ASP-based methods (i.e.,  
 927 **PyBoolNet**, **mpbn**, and **Trappist-ASP**), we note that for all the models where  
 928 **PyBoolNet** did not finish before the time limit, the timeout occurred during  
 929 the computation of the **prime implicants**. Hence, not even a single minimal  
 930 trap space was output by that method. For all the remaining models, once  
 931 **PyBoolNet** went through the prime-implicant phase, its ASP solving phase  
 932 quickly returned the first 1000 minimal trap spaces, all under one second.  
 933 Hence, with the experimental results shown in this subsection as well as the  
 934 two previous subsections, the practical differences between the ASP encod-  
 935 ing of **Trappist-ASP** and that of **PyBoolNet** are not distinctly exposed. The  
 936 fact that our new ASP encoding is guaranteed to be linear in the number of  
 937 nodes of the original model (see Subsection 4.3) does not seem to be crucial  
 938 here, however a much deeper analysis of those cases shall be shown in the  
 939 next subsection.



#### 940 6.4. Randomly generated models

941 We randomly generated a set of N-K models [1] with network size  $n$  in the  
 942 set  $\{100, 150, 200, 250, 300, 350, 400\}$  and in-degree  $K = 3$  (i.e., each node  
 943 has exactly three input nodes). We chose N-K models because they are a  
 944 useful tool for studying the dynamics of Boolean networks [1, 7, 19]. For each  
 945 network size, 50 instances were generated using the `generateRandomNKNetwork`  
 946 function. In total, we have 350 random models. We then applied the com-  
 947 pared methods to these models and recorded the running time of each method  
 948 for each model. It is worth noting that N-K models usually have small num-  
 949 bers of minimal trap spaces [7]. Hence, we searched for all solutions in each  
 950 model, which makes the comparison to `bioLQM` more comprehensive. In addi-  
 951 tion, each node has only three input nodes, **leading to a small number of prime**  
 952 **implicants of the associated Boolean function**. Hence, `PyBoolNet` always  
 953 passed the phase of computing **prime implicants** in every model even within  
 954 one second, which enables us to compare the ASP encoding of `PyBoolNet`  
 955 and that of `Trappist-ASP`.

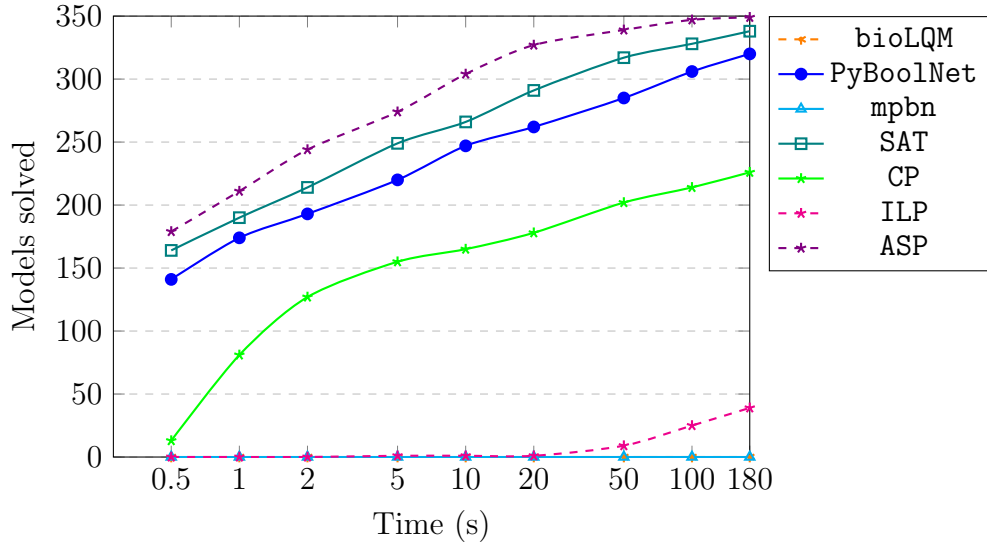


Figure 3: Cumulative numbers of random models solved by the compared methods with respect to enumerating all the minimal trap spaces.

956 Figure 3 shows cumulative numbers of random models solved by the com-  
 957 pared methods with respect to enumerating all the minimal trap spaces. The  
 958 number of succeeded models within three minutes for each method is: `bioLQM`

(0), PyBoolNet (320), mpbn (0), Trappist-maxSAT (338), Trappist-CP (226), Trappist-ILP (39), Trappist-ASP (349). We can see that Trappist-ASP is the only method that can handle every model, but one. Note that none of the other methods can handle that only model failed by Trappist-ASP. We also obtained some observations consistent with those obtained for real-world models. More specifically, Trappist-MaxSAT is still the second best method and Trappist-CP is better than Trappist-ILP. Upon closer inspection, we obtained several notable observations as follows.

First, mpbn was not able to handle any model because all the models are non-locally-monotonic. Recall that a Boolean network is non-locally-monotonic if only one of its Boolean functions is non-locally-monotonic. Hence, it is apparent that all **these types** 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 **generic** 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,

996 PyBoolNet, and mpbn). This is evidence for the advantages of an alternative  
997 approach compared to what preexisted.

998     Regarding general Boolean networks, Trappist-ASP (even Trappist-  
999 MaxSAT) is far more efficient than both bioLQM and PyBoolNet. The speedups  
1000 of Trappist-ASP or Trappist-MaxSAT are large, even between one and three  
1001 orders of magnitude for most models. In addition, the experimental results  
1002 also confirm that the ASP encoding of Trappist-ASP is much more efficient  
1003 than that of PyBoolNet.

1004     Regarding locally-monotonic Boolean networks, the performance of mpbn  
1005 is roughly comparable to that of Trappist-ASP or Trappist-MaxSAT. How-  
1006 ever, mpbn is quite slower than Trappist-ASP on average. This shows the  
1007 practical advantage of Trappist-ASP compared to mpbn, though its ASP  
1008 encoding may be more complex than that of mpbn in theory.

## 1009 7. Conclusion

1010     In this article we have explored and proved for the first time the equiva-  
1011 lence between (minimal) trap spaces of a general Boolean network and (max-  
1012 imal) conflict-free siphons of its Petri net encoding. We have shown sev-  
1013 eral useful applications of this finding to studying properties of trap spaces  
1014 in Boolean networks. As an important practical application of the equiva-  
1015 lence, we have proposed a new approach for the computation of minimal trap  
1016 spaces in Boolean networks, based on the enumeration of maximal conflict-  
1017 free siphons of Petri nets. We have also proposed four possible methods  
1018 using MaxSAT, CP, ILP, and ASP for implementing the new approach. In  
1019 particular, we have shown how to adjust our approach to compute several  
1020 specific types of trap spaces (e.g., maximal trap spaces, fixed points), which  
1021 besides minimal trap spaces also play crucial roles in the analysis and con-  
1022 trol of Boolean networks. The proposed methods for the minimal trap space  
1023 computation have been evaluated on many real-world models from the liter-  
1024 ature as well as randomly generated models. The experimental results show  
1025 that the new approach vastly outperforms all the state-of-the-art methods  
1026 in terms of general Boolean networks and is comparable to the mpbn method  
1027 even much better on average in terms of locally-monotonic Boolean net-  
1028 works. We believe that this opens up the way to a much better analysis  
1029 of large Boolean networks, which is needed with the advent of automatic  
1030 model-generation pipelines [59].

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

Another direction to speed up our approach in the side of Boolean networks is to apply reduction techniques to the original Boolean network. Many reduction techniques on Boolean networks [60, 61] have been proposed and some of them fully preserve attractors of a Boolean network under the fully asynchronous update scheme. In particular, a reduction technique on elimination of negatively auto-regulated nodes with respect to asynchronous attractors has recently been proposed [61]. However, there are two major issues needed to be considered. First, the question of whether these reduction techniques fully preserve minimal trap spaces of a Boolean network is still open. Second, although these reduction techniques can reduce the number of nodes, they can also increase the complexity of Boolean update functions [60], which is also an important factor for the performance of computation methods. It raises the question of whether they really simplify the computational burden of trap space computation. We will deeply investigate the two issues. Furthermore, we believe that the connection between trap spaces and siphons can be a very useful tool for addressing the first issue.

It is worth noting that there may be possibly other methods for computing minimal/maximal conflict-free siphons in Petri nets, like the methods for generic siphon computation in the field of Petri nets (see [35] for a survey about these methods). Although these approaches do not directly support the minimal/maximal conflict-free siphon computation now, we plan to investigate them in the future. In particular, several approaches based on the network structure at the Petri net level (e.g., the decomposition approaches [62, 63] for identifying minimal generic siphons) can be adapted

to help the identification of minimal conflict-free siphons. Making use of the specific structure (1-safe, place-complementary) might also reveal new techniques to be considered. It is potentially possible because in the field of Petri nets, most of the methods for identifying minimal generic siphons focus on various net classes with special structures [35]. The above potential approaches could replace our proposed methods if they give significantly better performance. However, the current methods appear to already perform very well even on the biggest models we have considered.

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

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