

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.

Keywords: Logical model, Boolean network, Trap space, Attractor computation, Petri net, Siphon, Systems biology

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`¹ demonstrated in [9] for handling medium-sized models from the literature and very large synthetic models

¹<https://github.com/bnediction/mpbn>

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

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

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

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

132 2.2. Traps spaces

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

137 A non-empty set $T \subseteq \mathcal{S}_{\mathcal{N}}$ is a *trap set* with respect to \rightarrow if for every
 138 $x \in T$ and $y \in \mathcal{S}_{\mathcal{N}}$ with $x \rightarrow y$ it holds that $y \in T$ [7]. An attractor of
 139 \mathcal{N} with respect to \rightarrow can be defined as an inclusion-wise minimal trap set
 140 of $(\mathcal{S}_{\mathcal{N}}, \rightarrow)$. An attractor can be also seen as a terminal strongly connected
 141 component of $(\mathcal{S}_{\mathcal{N}}, \rightarrow)$ [23]. An attractor of size 1 is called a fixed point,
 142 otherwise it is called a cyclic or complex attractor [7].

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

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

143 For example, $m = \star\star 1$ (for simplicity, we shall write subspaces likes states as
 144 a sequence of values) means that $D_m = \{v_3\}$, $m(v_3) = 1$, and it is equivalent
 145 to the set of states $\{001, 011, 101, 111\}$. We denote $\mathcal{S}_{\mathcal{N}}^{\star} = (\mathbb{B} \cup \{\star\})^n$ the set
 146 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].

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

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

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

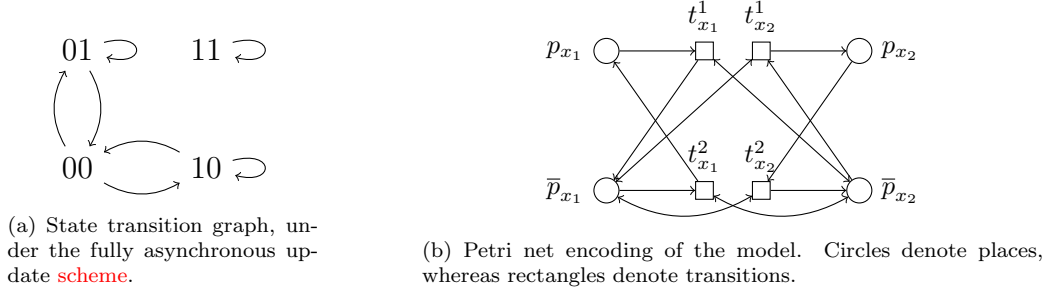


Figure 1: Dynamics and encoding of the Boolean network of Example 2.1.

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

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

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

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

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

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

²<https://www.pnml.org/>

222 using the `bioLQM`³ library. This piece of software extracted from `GINsim` [29]
 223 and part of the `CoLoMoTo`⁴ [30] software suite allows for easy conversion
 224 between standard formats. It also accepts many other common formats for
 225 Boolean networks, notably the `.bnet` files of the `BoolNet` [31, 21] tools. The
 226 conversion is executed as follows:

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

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

243 2.4. Siphons

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

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

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

³<http://www.colomoto.org/biolqm/>

⁴<http://colomoto.org/>

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

251 Note that \emptyset is trivially a siphon.

252 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
 253 conventionally $\text{pred}(S) = \text{succ}(S) = \emptyset$. We have an important property on
 254 siphons [35] as follows.

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

257 3. Trap spaces as conflict-free siphons

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

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

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

and

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

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

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

267 Intuitively, a siphon is a set of places that once unmarked remains so. If
 268 it is conflict-free it is possible to associate a subspace to it, more precisely it
 269 is the *mirror* of a subspace. Since it is a siphon, the fixed values will remain
 270 so whatever update happens, as the unmarked places remain unmarked. The
 271 subspace corresponding to that conflict-free siphon is therefore a trap space,
 272 and the maximality of the siphon is equivalent to the minimality of the trap
 273 space (as many fixed values as possible). For example, the Boolean network
 274 given in Example 2.1 has two trap spaces, $m_1 = 11$ and $m_2 = \star\star$. The
 275 Petri net encoding of this Boolean network has five generic siphons, $S_1 = \emptyset$,
 276 $S_2 = \{p_{x_1}, \bar{p}_{x_1}\}$, $S_3 = \{p_{x_2}, \bar{p}_{x_2}\}$, $S_4 = \{\bar{p}_{x_1}, \bar{p}_{x_2}\}$, and $S_5 = \{p_{x_1}, \bar{p}_{x_1}, p_{x_2}, \bar{p}_{x_2}\}$.

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

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

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

286 If $D_m = \emptyset$, then $S = \emptyset$ is trivially a conflict-free siphon of \mathcal{P} . Thus,
 287 we consider the case that $D_m \neq \emptyset$ (resp. $S \neq \emptyset$). Assume that S is not a
 288 siphon of \mathcal{P} . Then, there is a transition $t \in T$ such that $S \cap \text{succ}(t) \neq \emptyset$
 289 but $S \cap \text{pred}(t) = \emptyset$. This implies that there is a place $p \in S$ such that
 290 $p \in \text{succ}(t)$ but $p \notin \text{pred}(t)$. Let v be the node in \mathcal{N} corresponding to p . By
 291 the characteristics of the encoding [24], there is a directional arc from t to p
 292 and a directional arc from the complementary place of p to t . Without loss
 293 of generality, we assume that $p = p_v$, then there is a directional arc from t
 294 to p_v and a directional arc from \bar{p}_v to t .

295 We follow the following procedure to find a state $s \in \mathcal{S}_{\mathcal{N}}[m]$ such that
 296 $M_s(p') = 1, \forall p' \in \text{pred}(t)$ where M_s is the corresponding marking in \mathcal{P} of s .
 297 For every place $p' \in \text{pred}(t)$, let p'' be the complementary place of p' and v'
 298 be the corresponding node in \mathcal{N} of p' and p'' .

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

301 If $p'' \in S$, then $v' \in D_m$ and we set $s(v') = m(v')$. In this case, if
 302 $p' = p_{v'}$ then $s(v') = m(v') = 1$ leading to $M_s(p') = 1$, if $p' = \bar{p}_{v'}$ then
 303 $s(v') = m(v') = 0$ leading to $M_s(p') = 0$.

304 For the remaining nodes of \mathcal{N} , we can always set Boolean values to these
 305 nodes to preserve that $s \in \mathcal{S}_{\mathcal{N}}[m]$ by applying the same procedure. We also
 306 have $M_s(p_v) = 0$ by the characteristics of the encoding [24] (and Definition
 307 3.1). Now, t is enabled at marking M_s . Its firing leads to a new marking
 308 M'_s such that $M'_s(p_v) = 1$ and $M'_s(\bar{p}_v) = 0$. Let s' be the corresponding state
 309 in \mathcal{N} of M'_s . We have $s'(v) = 1$ because $M'_s(p_v) = 1$ and $m(v) = 0$ because
 310 $p_v \in S$. This implies that $s' \notin \mathcal{S}_{\mathcal{N}}[m]$.

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

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

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

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

325 It is symmetric for the case that $p = \bar{p}_v$. Hence, $M_s(p) = 0, \forall p \in S$. In any
 326 marking M'_s reachable from M_s regardless of the firing scheme of \mathcal{P} , we have
 327 $M'_s(p) = 0, \forall p \in S$ by the dynamical property on markings of a siphon [35].
 328 Let s' be the corresponding state in \mathcal{N} of M'_s . For every node $v \in D_m$,
 329 we have all two cases as follows. Case 1: $p_v \in S$, then $M'_s(p_v) = 0$, thus
 330 $s'(v) = 0 = m(v)$. Case 2: $\bar{p}_v \in S$, then $M'_s(\bar{p}_v) = 0$, thus $s'(v) = 1 = m(v)$.
 331 Hence, $s'(v) = m(v)$ for every $v \in D_m$. Then, $s' \in \mathcal{S}_{\mathcal{N}}[m]$. By the definition
 332 of a trap space and the arbitrariness of s , m is a trap space of \mathcal{N} .

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

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

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

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

343 Note that the original proof for this property of trap spaces (see Theorem
 344 1 of [7]) only considers the two popular update schemes (i.e., synchronous
 345 and fully asynchronous). Theorem 3.1 exhibits the very first theoretical
 346 application of the connection between trap spaces of Boolean networks and
 347 siphons of Petri nets.

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

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

359 Second, we show that if S is a maximal conflict-free siphon of \mathcal{P} , then
 360 m is a minimal trap space of \mathcal{N} (**). Since S is a conflict-free siphon of \mathcal{P} ,
 361 m is a trap space of \mathcal{N} by Theorem 3.1. Assume that m is not minimal.
 362 Then, there is another trap space m' such that $m' < m$. By the definition of
 363 the partial order $<$ on subspaces, $S_{\mathcal{N}}[m'] \subset S_{\mathcal{N}}[m]$. Let S' be the mirror of
 364 m' . S' is a conflict-free siphon by Theorem 3.1. Following the definition of
 365 a mirror, $S \subset S'$, which contradicts to the maximality of S . Hence, m is a
 366 minimal trap space of \mathcal{N} .

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

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

384 Boolean networks and Petri nets to explore and prove properties of trap
385 spaces in Boolean networks.

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

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

393 Consider two any distinct minimal trap spaces m_1 and m_2 . Assume that
394 $\mathcal{S}_{\mathcal{N}}[m_1] \cap \mathcal{S}_{\mathcal{N}}[m_2] \neq \emptyset$. Let S_1 and S_2 be the mirrors of m_1 and m_2 , re-
395 spectively. By Theorem 3.2, S_1 and S_2 are maximal conflict-free siphons
396 of \mathcal{P} . We have that $S = S_1 \cup S_2$ is also a siphon because of Proposi-
397 tion 2.1. For every node $v \in V$, assume that $p_v \in S$ and $\bar{p}_v \in S$ hold.
398 Since S_1 and S_2 are conflict-free, there are all two cases. Case 1: $p_v \in S_1$
399 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
400 $m_1(v) \neq m_2(v)$, $m_1(v) \neq \star$, $m_2(v) \neq \star$, then $\mathcal{S}_{\mathcal{N}}[m_1] \cap \mathcal{S}_{\mathcal{N}}[m_2] = \emptyset$. This is a
401 contradiction. Hence, for every node $v \in V$, $p_v \in S$ and $\bar{p}_v \in S$ cannot hold
402 together. Therefore, S is conflict-free. Now, we have that S is a conflict-free
403 siphon but $S_1 \subset S$ or $S_2 \subset S$ holds because $S_1 \neq S_2$. This contradicts to the
404 maximality of S_1 and S_2 . Hence, $\mathcal{S}_{\mathcal{N}}[m_1] \cap \mathcal{S}_{\mathcal{N}}[m_2] = \emptyset$ holds.

405 □

406 A natural computational application of Theorem 3.1 is that we can effi-
407 ciently decide whether a subspace m is a trap space. In PyBoolNet [21], this
408 is checked by using the percolation on the **prime implicants** of the Boolean
409 functions. As we have mentioned at the beginning of this article, the compu-
410 tation of **prime implicants** is a demanding task for complex Boolean networks,
411 even is sometimes intractable. Hence, the checking method in [21] shows its
412 limitations. Instead, we can first compute the mirror S_m of m in the Petri
413 net encoding. Then, by Proposition 2.1 and Theorem 3.1, we can check if
414 $\text{pred}(S_m) \subseteq \text{succ}(S_m)$. Note that the Petri net construction is less com-
415 putationally demanding than the prime-implicant computation because it
416 only requires computing generic (not prime) implicants of the Boolean func-
417 tions [23]. In addition, the worst case time complexity of the above checking
418 method is quadratic in the number of transitions of the Petri net.

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

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

440 4. Computation methods

441 First, we discuss the complexity of siphon computation in Petri nets.
 442 Siphons are a prominent concept in the field of Petri nets, but unfortunately
 443 there are very few studies focusing on the complexity aspect. In this field,
 444 researchers mainly focus on practical methods for computing minimal generic
 445 siphons (also many related types) in general or special Petri nets and the
 446 applications of such types to the control of real-world systems modeled by
 447 Petri nets [35]. The problem of finding a minimal siphon of a 1-safe Petri
 448 net is solvable in polynomial time [38]. Clearly, the problem of finding a
 449 siphon of a 1-safe Petri net is also solvable in polynomial time. However, the
 450 problem of computing all (minimal) siphons is not easier than the problem
 451 of computing a (minimal) siphon but its complexity still not clear. Note
 452 that the number of siphons (even minimal siphons) can be exponential in
 453 the number of places of the Petri net [35]. Moreover, there is no complexity
 454 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} ,

- 473 • $D(p) = \mathbb{B}$ for all $p \in R$, i.e., the variables are Boolean,
- 474 • $C = \{\neg p_v \vee \neg \bar{p}_v = 1 \mid \forall v \in V\} \wedge \{(p = 1 \rightarrow \bigvee_{p' \in \text{pred}(t)} p' = 1) \mid p \in$
- 475 $P, t \in \text{pred}(p)\}$.

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

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

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

477 *Proof.* By the former part $\neg p_v \vee \neg \bar{p}_v = 1$ of C , the conflict-freeness is imposed
 478 because for any satisfiable valuation r , $r(p_v) = r(\bar{p}_v) = 1$ is impossible for all
 479 $v \in V$. As shown in [17], the latter part of C can characterize the set of all
 480 generic siphons of \mathcal{P} . Hence, we can conclude the proof.

481

□

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

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

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

509 This method was implemented using the state-of-the-art CP solver Chuffed⁶
 510 [40] via its MiniZinc [41] interface. Because it is a high-level interface, the
 511 backtrack-and-replay method of [17] was not used but rather the alterna-
 512 tive implementation with two global constraints for lexicographic ordering
 513 (ensuring enumeration of solutions) and iterated non-subset of each already
 514 found solution (for maximality).

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

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

and

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

515 We set a soft clause for each variable of the CSP and then use a “minimal cor-
 516 rection subset” blocking strategy, which will ensure set-inclusion maximality
 517 of the solutions. We implement this approach by using the RC2 MaxSAT
 518 solver [42] available through the `python-sat` package⁷.

519 4.3. Answer set programming-based method

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

$$\text{a_1}; \dots ; \text{a_k} :- \text{a}.$$

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
 set of atoms representing places in $\text{pred}(t)$. The rule (2) is translated into

⁶<https://github.com/chuffed/chuffed>

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

the ASP rule

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

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

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

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

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

544 4.4. Integer linear programming-based method

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

binary variable $\mathbf{p-v}$ (resp. $\mathbf{n-v}$) to denote place p_v (resp. \bar{p}_v), $\forall v \in V$. The set of all binary variables in \mathcal{I} is $\bigcup_{v \in V} \{\mathbf{p-v}, \mathbf{n-v}\}$. For each pair (p, t) where $p \in P, t \in T, t \in \text{pred}(p)$, we translate the rule (1) into the ILP inequality

$$\mathbf{a} \leq \mathbf{a_1} + \dots + \mathbf{a_k}$$

where \mathbf{a} is the binary variable representing place p and $\{\mathbf{a_1}, \dots, \mathbf{a_k}\}$ is the set of binary variables representing places in $\text{pred}(t)$. The rule (2) is translated into the ILP inequality

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

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

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

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

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

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

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

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

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

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

552 conflict-free siphon. Indeed, abide by the newly added inequality, we have
553 $S' \cap (P \setminus S^*) \neq \emptyset$ because there is some $\mathbf{a-p}$ with $p \in P \setminus S^*$ such that
554 $I'(\mathbf{a-p}) = 1$. This implies that it is impossible that $S' = S^*$ or $S' \subset S^*$.
555 By the objective function, it means that S' is the conflict-free siphon of
556 maximum cardinality among the conflict-free siphons that are not contained
557 in S^* . Hence, S' is also a maximal conflict-free siphon. Again, we add to \mathcal{I}
558 a new inequality with respect to the newly found siphon. The above process
559 is iterated until \mathcal{I} becomes unfeasible, this means that there is no further
560 maximal conflict-free siphon. Thus, all the maximal conflict-free siphons of
561 the Petri net have been found.

562 Since we used the MiniZinc framework to interface with the CP solver, it
563 was simple to make the slight modifications described above and to use that
564 same interface to call the Coin-OR CBC solver⁸ [44].

565 4.5. Computation of special types of trap spaces

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

574 First, the work presented in [19] uses the concept of *stable motifs* to build
575 the succession diagram of a Boolean network, a summary of the decisions in
576 the network dynamics that lead to successively more restrictive nested stable
577 motifs. The succession diagram is useful for control and decision making
578 on this Boolean network. In particular, the proposed control methods are
579 independent to the update scheme. Note that, in [19], the succession dia-
580 gram is also used to identify all attractors of a Boolean network under the
581 fully asynchronous update scheme. It has been shown that a stable motif
582 of a Boolean network is equivalent to a *maximal trap space* of this Boolean
583 network [19]. Indeed, the computation of stable motifs is a bottleneck of
584 the methods proposed in [19]. Hence, it is necessary to develop an efficient
585 method for computing maximal trap spaces of a Boolean network. We shall

⁸<https://github.com/coin-or/Cbc>

586 show how to adjust the ASP-method presented in Subsection 4.3 to compute
 587 maximal trap spaces.

We first provide the definition of maximal trap spaces. Let ε be the special trap space of \mathcal{N} where all the nodes are free. Of course, ε 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 ε from the set of trap spaces). To do this, we add to \mathcal{L} the ASP rule

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

588 that ensures that every answer set of \mathcal{L} cannot be empty. Then a set-inclusion
 589 minimal answer set of \mathcal{L} is equivalent to a minimal conflict-free siphon of \mathcal{P} ,
 590 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

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

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

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

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

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

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

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

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

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

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

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

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

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

rule

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

602 where $\{v_{i1}, \dots, v_{ik}\}$ is the set of free nodes of m^* . This rule ensures that
603 $m \neq m^*$. In the case that $m^* = \varepsilon$, we have all maximal trap spaces of the
604 original Boolean network.

605 5. Motivating example

606 For a few years now we have been collaborating with biologists who build
607 very large detailed and annotated maps and now wish to analyze the dy-
608 namics of the corresponding models. One of the main maps studied this way
609 represents knowledge about the Rheumatoid Arthritis [46], and was the main
610 motivation for the development of a tool to automatically transform it into
611 an executable Boolean network [6]. In the supplementary material of the pa-
612 per, an excerpt of the map, focused around the apoptosis (cell death) module
613 is transformed into a model of *reasonable* size, namely 180 Boolean variables
614 (model `F5_RA_apoptosis_executable_module.sbml` of supplementary ma-
615 terial S3, and model “RA_apoptosis” of Subsection 6.3). The study of such
616 model, though, is a big hurdle. Indeed, as stated in the article about another
617 model of the same size: “*The size of the CaSQ-inferred MAPK model (181*
618 *nodes) made the calculation of stable states a non-realistic endeavour.*”

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

626 However, using a state-of-the-art tool like `PyBoolNet` [7] on that model
627 **unfortunately** fails at the phase of prime-implicant generation. `mpbn` [9] can
628 return the first 1000 solutions within 1.43s, but indeed, it limits the model-
629 ing range of the modelers as it does not permit using non-locally-monotonic
630 Boolean functions. This is also true for the Alzheimer model also mentioned
631 in that same article and originally from [47] (`F4` file in the original supple-
632 mentary material, and “Alzheimer” in Table 2), where `PyBoolNet` also fails
633 at the prime-implicant computation and `mpbn` does not give any answer be-
634 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 index⁹) and the state-of-the-art methods (`bioLQM`¹⁰, `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.

⁹<https://pypi.org/project/trappist/>

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

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

672 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	0.13	0.01	0.00	0.00	0.97	0.96	0.01
2 calzone_cellfate	28	27	0.12	0.02	0.01	0.01	5.59	6.03	0.01
3 dahlhaus_neuroplastoma	23	32	0.11	0.03	0.01	0.01	6.56	6.99	0.01
4 davidich_yeast	10	12	0.11	0.02	0.01	0.01	2.56	2.21	0.01
5 dinwoodie.life	15	7	0.11	0.01	0.00	0.01	1.68	1.39	0.01
6 dinwoodie.stomatal	13	1	0.10	0.01	0.00	0.00	0.39	0.29	0.01
7 faure_cellcycle	10	2	0.11	0.02	0.01	0.01	0.58	0.46	0.01
8 grieco_mapk	53	18	0.19	0.03	0.02	0.03	3.93	10.46	0.02
9 irons_yeast	18	1	0.12	0.03	0.01	0.01	0.37	0.39	0.02
10 jaoude_thdiff	103	1000+	N/A	0.85	0.45	0.56	NF	NF	0.09
11 klamt_tcr	40	8	0.11	0.01	0.01	0.01	1.98	1.22	0.02
12 krumsiek_myeloid	11	6	0.10	0.01	0.00	0.00	1.48	1.26	0.01
13 multivalued	13	4	0.10	0.01	0.00	0.00	0.93	0.86	0.01
14 n12c5	11	5	0.11	17.83	0.01	0.01	1.21	1.10	0.01
15 n3s1c1a	2	2	0.10	0.01	0.00	0.00	0.63	0.49	0.01
16 n3s1c1b	2	2	0.09	0.02	0.00	0.00	0.56	0.49	0.01
17 n5s3	4	3	0.10	0.02	NM	0.00	0.74	0.69	0.01
18 n6s1c2	5	3	0.10	0.02	0.00	0.00	0.91	0.59	0.01
19 n7s3	6	3	0.11	0.02	0.00	0.00	0.79	0.68	0.01
20 raf	3	2	0.10	0.01	0.00	0.00	0.55	0.39	0.01
21 randomnet_n15k3	15	3	0.10	0.02	NM	0.01	0.77	0.67	0.01
22 randomnet_n7k3	7	10	0.10	0.01	NM	0.00	2.07	1.46	0.01
23 remy_tumorigenesis	34	25	0.15	0.94	0.02	0.02	5.98	7.98	0.02
24 saadatpour_guardcell	13	1	0.10	0.06	0.00	0.00	0.53	0.45	0.02
25 selvaggio.emt	56	1000+	N/A	0.48	0.28	0.28	NF	NF	0.09
26 tournier_apoptosis	12	3	0.10	0.01	0.00	0.00	0.74	0.75	0.01
27 xiao_wnt5a	7	4	0.10	0.01	0.00	0.00	1.00	0.89	0.01
28 zhang_tlgl	60	156	0.60	0.09	0.09	0.07	37.26	NF	0.04
29 zhang_tlgl.v2	60	258	0.64	0.04	0.08	0.11	69.95	NF	0.04

Table 1 shows the experimental results on the models from the official PyBoolNet repository¹¹. 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

¹¹<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

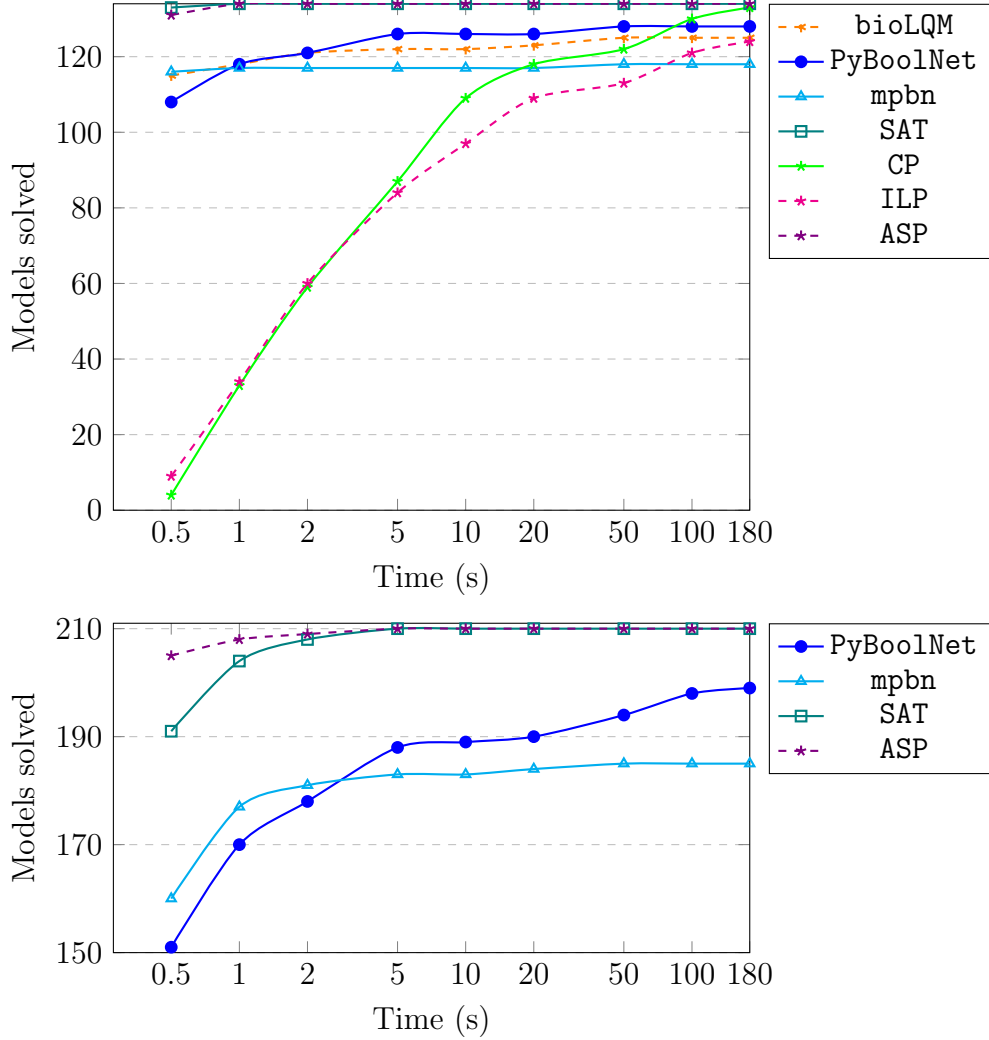


Figure 2: Cumulative numbers of the BBM models that have less than 1000 minimal trap spaces (upper panel) and BBM models solved by the compared methods with respect to enumerating the first 1000 minimal trap spaces (lower panel).

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

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

757 Figure 2 (lower panel) shows cumulative numbers of the `BBM` models solved
758 by the compared methods (except `bioLQM`, `Trappist-CP`, and `Trappist-ILP`)
759 with respect to enumerating the first 1000 minimal trap spaces. We omit
760 the results of `Trappist-CP` and `Trappist-ILP` because they can handle
761 no model with more than 1000 minimal trap spaces. Again, we can see
762 that `Trappist-ASP` and `Trappist-MaxSAT` are the two best methods as they
763 can handle every but one model within 5s. They also always handle many
764 more models than both `PyBoolNet` and `mpbn` on every time limit. Note that
765 with the time limit of 0.5s, `Trappist-ASP` can handle 14 more models than
766 `Trappist-MaxSAT`, which is opposed to the case of models with less than
767 1000 minimal trap spaces (see Figure 2 (upper panel)). This observation
768 confirms the disadvantage of `Trappist-MaxSAT` compared to `Trappist-ASP`
769 for the case of many minimal trap spaces.

770 6.3. Selected models

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

782 First, we obtained some observations on the four variants of `Trappist`
783 consistent with the observations obtained in the previous subsections. More
784 specifically, `Trappist-ASP` is still the best variant with a running time below
785 one second for every model, and followed by `Trappist-MaxSAT`. In particular,
786 the difference in running time between `Trappist-ASP` and `Trappist-MaxSAT`
787 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	0.10	0.04	NM	0.01	1.15	0.89	0.02
2 Arabidopsis_thaliana [48]	15	8	0.10	0.06	NM	0.01	2.06	1.83	0.02
3 p53_high_dna [48]	16	1	0.38	1.76	NM	0.08	0.53	0.43	0.14
4 p53_low_dna [48]	16	1	0.41	1.76	NM	0.07	0.58	0.48	0.14
5 FT-GRN [49]	23	32	NF	NF	NM	0.03	8.41	12.38	0.19
6 DNA_damage [48]	26	16	0.24	0.33	NM	0.02	3.91	5.33	0.05
7 Rho-GTPases [48]	33	2	0.17	0.57	40.39	0.07	0.74	0.56	0.11
8 Pluripotency [50]	36	440	NF	NF	NM	0.16	138.92	NF	0.28
9 Pluripotent [48]	36	276	0.37	0.43	NM	0.07	72.40	NF	0.06
10 Pancreatic.Cancer [48]	43	1000+	N/A	0.11	0.36	0.17	NF	NF	0.06
11 Drosophila [51]	52	128	0.33	0.05	0.07	0.06	32.66	126.22	0.05
12 Cacace_TdevModel [52]	61	28	1.29	5.67	NM	0.06	7.51	23.15	0.08
13 hedgehog [48]	65	1000+	N/A	NF	0.50	0.34	NF	NF	0.33
14 EMT [19]	69	268	39.22	1.01	0.20	0.12	75.81	NF	0.05
15 Bcell [53]	73	72	0.23	0.04	0.08	0.06	18.95	81.85	0.05
16 mast_cell [6]	73	1000+	N/A	0.09	0.55	0.37	NF	NF	0.15
17 Corral_ThIL17diff [45]	92	1000+	N/A	107.57	0.76	0.56	NF	NF	0.16
18 Adhesion_CIP [54]	121	78	56.81	4.25	0.23	0.17	25.20	NF	0.19
19 EMT_Mech [55]	136	82	NF	14.01	0.27	0.20	27.55	NF	0.25
20 macrophage [48]	136	1000+	N/A	0.54	1.09	0.84	NF	NF	0.27
21 angiogenesis [48]	141	1000+	N/A	0.16	1.07	1.06	NF	NF	0.16
22 angiofull [56]	142	1000+	N/A	0.17	1.06	0.88	NF	NF	0.23
23 EMT_Mech_TGFBeta [55]	150	492	NF	11.28	0.78	0.69	NF	NF	0.35
24 RA_apoptosis [6]	180	1000+	N/A	NF	1.43	1.55	NF	NF	0.19
25 MAPK [6]	181	1000+	N/A	13.58	1.76	1.51	NF	NF	0.27
26 Snf1-pathway [57]	202	1000+	N/A	1.13	1.47	1.43	NF	NF	0.31
27 T-cell-co-receptor [48]	206	1000+	N/A	NF	1.52	2.26	NF	NF	0.35
28 TcellCheckPoint [58]	218	1000+	N/A	4.99	NM	1.96	NF	NF	0.28
29 Mycobacterium [48]	317	1000+	N/A	0.42	2.36	4.91	NF	NF	0.44
30 Leishmania [48]	342	1000+	N/A	NF	2.56	5.62	NF	NF	0.46
31 Cholecystokinin [6]	383	1000+	N/A	0.36	2.99	4.81	NF	NF	0.37
32 Alzheimer [6]	762	1000+	N/A	NF	NM	18.21	NF	NF	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.

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

799 Third, for 11 of the 32 models (more than 34%), **mpbn** did not give any an-
 800 swer because these models are non-locally-monotonic. For 21 of the 32 mod-
 801 els where **mpbn** returned the answers, **mpbn** and **Trappist-ASP** are roughly
 802 comparable in computation time, but **mpbn** appears quite slower on aver-
 803 age. In particular, for the **Rho-GTPases** model, **mpbn** is $577\times$ slower than
 804 **Trappist-ASP**. This observation along with the comparisons between **mpbn**
 805 and **Trappist-ASP** in the previous subsections are quite surprising because
 806 the ASP encoding of **mpbn** only requires the DNF for the activation part of a
 807 Boolean function, whereas that of **Trappist-ASP** requires both the activation
 808 and inhibition parts (see Subsection 4.3). However, the reason may lie on the
 809 differences in the ASP encoding characteristics of the two methods and the
 810 fact that **mpbn** needs to spend time checking the local-monotonicity of each
 811 Boolean function in a Boolean network. We expect that **mpbn** may outper-
 812 form **Trappist** for a certain set of models, but not for the set of real-world
 813 models considered in this article.

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

6.4. Randomly generated models

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

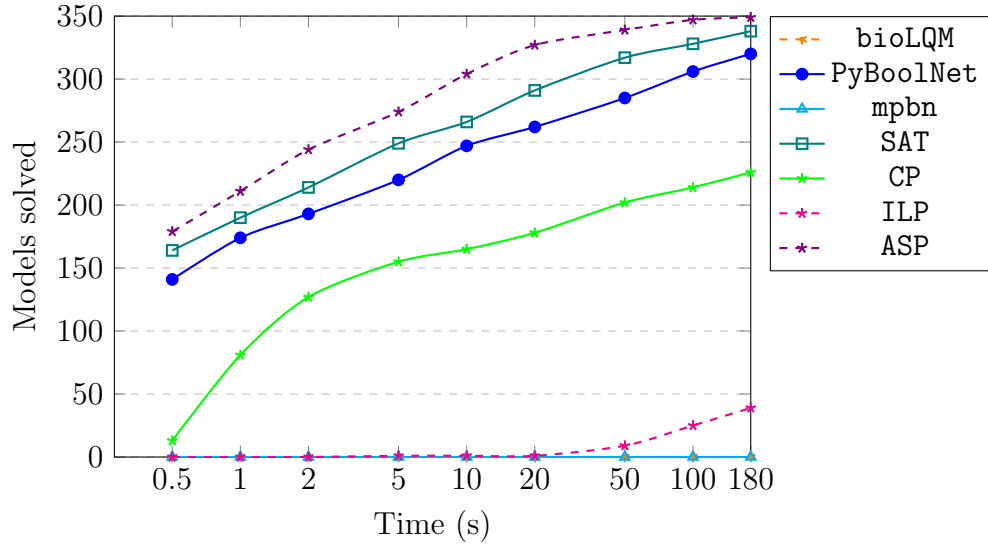


Figure 3: Cumulative numbers of random models solved by the compared methods with respect to enumerating all the minimal trap spaces.

Figure 3 shows cumulative numbers of random models solved by the compared methods with respect to enumerating all the minimal trap spaces. The 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,

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

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

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

897 7. Conclusion

898 In this article we have explored and proved for the first time the equiva-
899 lence between (minimal) trap spaces of a general Boolean network and (max-
900 imal) conflict-free siphons of its Petri net encoding. We have shown sev-
901 eral useful applications of this finding to studying properties of trap spaces
902 in Boolean networks. As an important practical application of the equiva-
903 lence, we have proposed a new approach for the computation of minimal trap
904 spaces in Boolean networks, based on the enumeration of maximal conflict-
905 free siphons of Petri nets. We have also proposed four possible methods
906 using MaxSAT, CP, ILP, and ASP for implementing the new approach. In
907 particular, we have shown how to adjust our approach to compute several
908 specific types of trap spaces (e.g., maximal trap spaces, fixed points), which
909 besides minimal trap spaces also play crucial roles in the analysis and con-
910 trol of Boolean networks. The proposed methods for the minimal trap space
911 computation have been evaluated on many real-world models from the liter-
912 ature as well as randomly generated models. The experimental results show
913 that the new approach vastly outperforms all the state-of-the-art methods
914 in terms of general Boolean networks and is comparable to the mpbn method
915 even much better on average in terms of locally-monotonic Boolean net-
916 works. We believe that this opens up the way to a much better analysis
917 of large Boolean networks, which is needed with the advent of automatic
918 model-generation pipelines [59].

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

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

949 It is worth noting that there may be possibly other methods for comput-
 950 ing minimal/maximal conflict-free siphons in Petri nets, like the methods for
 951 generic siphon computation in the field of Petri nets (see [35] for a survey
 952 about these methods). Although these approaches do not directly support
 953 the minimal/maximal conflict-free siphon computation now, we plan to in-
 954 vestigate them in the future. In particular, several approaches based on
 955 the network structure at the Petri net level (e.g., the decomposition ap-
 956 proaches [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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