Exhaustive dynamic analysis of reachability and stable states of biological regulatory networks modeled in Process Hitting using Answer Set Programming

Emna Ben Abdallah

LUNAM Université, École Centrale de Nantes, IRCCyN UMR CNRS 6597 (Institut de Recherche en Communications et Cybernétique de Nantes), 1 rue de la Noë, 44321 Nantes, France.

emna.ben-abdallah@irccyn.ec-nantes.fr

Joint work with: Olivier Roux, Morgan Magnin, Maxime Folschette

Abstract

The Process Hitting is a recently introduced framework to model concurrent processes. It is notably suitable to model biological regulatory networks with partial knowledge of co- operations by defining the most permissive dynamics. In this paper, we explain the methods we developed with ASP to find the fixed points or states states in which it is not possible any more to have evolutions of the model. We also aim at solving the problem of reachability that consists of deciding if, starting from a given initial state, it is possible to reach a given local state. Finally, we illustrate the merits of our methods by applying them to various biological examples ans comparing the results with eexisted aproches. We show that our approach succeeds in processing large models.

1 Introduction

As regulatory phenomena play a crucial role in biological systems, they need to be studied accurately. Biological Regulatory Networks (BRNs) consist in sets of either positive or negative mutual effects between the components. With the purpose of analyzing these systems, they are often modeled as graphs which make it possible to determine the possible evolutions of all the interacting components of the system. Indeed, in order to address the formal checking of dynamical properties within very large BRNs, we recently use a new formalism, named the "Process Hitting" (PH) [5], to model concurrent systems having components with a few qualitative levels. A PH describes, in an atomic manner, the possible evolutions of a "process" (representing one component at one level) triggered by the hit of at most one other "process" in the system. This particular structure makes the formal analysis of BRNs with hundreds of components tractable. PH is suitable, according to the precision of this information, to model BRNs with different levels of abstraction by capturing the most general dynamics. The objectives of the work presented in this paper are the following.

Firstly, we show that starting from one PH model, it is possible to find all possible stable states (fixed points [6]). We perform an exhaustive search of the possible states, combination processes, one process from each sort and then check if it is a fixed point.

The second phase of our work consists in computing the dynamics. It consists in determining from a known initial state the possible next states of the PH model. Finally we verify if we can reach a specific state of one or several component (gene or protein). The results are ensured to respect the PH dynamics.

Our contribution is from the results that allowed to determine the stable states, we propose to evaluate the benefits of the Answer Set Programming (ASP) [2] to compute them. ASP has been proven efficient to tackle models with a large number of components and parameters. Our aim here is to assess its potential w.r.t. the computation of some dynamical properties of the PH model. In this paper, we show that ASP turns out to be effective for these enumerative searches which justifies its use. The benefit of our approach is that it makes possible to get the minimal paths to reach our goal(s) also we can verify if it is possible after a given number of steps.

2 Preliminary definitions

In order to develop the nes methods we have used two main frameworks. The first is a logic programming language: the Answer Set Programming (ASP). Precisely it is a logic programming language on which I wrote my bibliographic research report. The second framework is the Process Hitting (PH) a new formalism for the representation of biological regulatory networks. We will see later in this section more details about these two frameworks.

2.1 Answer Set Programming

The ASP is a declarative programming paradigm with known semantics as the semantics of answer sets. This paradigm allows the programmer to specify what the problem to be solved and not how to solve it. ASP programs are written in AnsProlog* (short for "Answer Set Programming in Logic" with superscript *). These programs are composed of a set of facts and a set of rules from which other facts can be derived. A consistent set of facts that can be derived from a program using the rules is called "answer set" for the program. The sets of possible responses to an AnsProlog* program are calculated with a program called a solver.

2.1.1 Logic program

Consider an ASP logic program, as each rule is an ordered pair,[2]:

$$head \leftarrow body.$$
 (1)

with *Head* and *Body* sets of literals.

This simple language has many advantages that make it one of the most effective in terms of knowledge representation, reasoning and declarative problem solving.

2.1.2 The syntax and semantic of ASP

1. L'alphabet

According [2], the alphabet of the axiom (or just the alphabet) of the framework of the answer set is comprised of seven classes of symbols:

- Variables,
- Constants,
- Symbols of functions,
- Symbols of predicates,
- Connectors,

- Symbols of punctuation, and
- Special symbol ⊥

All these classes vary from one alphabet to another, but the sets of 5^{th} and 6^{th} classes (Connectors and symbols of punctuation) are defined as follows:

- Connectors with $\{\neg, \text{ or, } \leftarrow, \text{ not, ','}\}$
- Symbols of punctuation with { '(', ')', '.'}

The other classes remain constant as they meet some informal agreement. In general, variables start with a capital letter and contain letters and numbers (X,Y,...). The constants, symbols and predicates follow the same rule, but they begin with a lowercase letter (f,g,a,b...). Sometimes there is the addition of a supplementary agreement which covers the letters used [2]:

What seems a little fuzzy is the concept of predicate. Indeed the word predicate can be an innovation of the new grammar. Let's consider the following sentence:

Socrates was an athenian.

Socrate is the subject and was an athenian is the predicat. This sentence can be noted in ASP by : $athenian(Socrate) \leftarrow \top$. with \top is the symbol of True.

2. The rules Comme nous l'avons déjà mentionné, une règle est de la forme:

$$head \leftarrow body.$$
 ((1))

$$A \leftarrow B^+, \mathbf{not} \, B^-.$$
 (2)

This rule is then equivalent to:

$$L_0 \leftarrow L_1, ..., L_m, \mathbf{not} L_{m+1}, ..., \mathbf{not} L_n.$$
 (3)

And this rule states:

Si
$$L_1,...,L_m$$
 are **true** et $L_{m+1},...,L_n$ are **false** Then L_0 is **true**

with L_i literals and $k \ge 0$, $m \ge k$ and $n \ge m$.

Head is also called conclusion

Body is also called premise

Special cases rules [4, 2]:

- A rule is **constant** if all litterals are constants (noted with **ground**);
- A fact or a reality: it is a rule with an empty body. It can be written even without the arrow
 ←:

$$L_0. or L_0 \leftarrow \top.$$
 (4)

• A **constraint**: This false symbol to the head (*head*) is often eliminated and the constraint will be written generally as:

$$\leftarrow L_1,...,L_m, \text{ not } L_{m+1},..., \text{ not } L_n. \tag{5}$$

We say that a set of literals X violates the constraint (5) if $\{L_1, ..., L_m\} \subseteq X$ and $\{L_{m+1}, ..., L_n\} \nsubseteq X$. If we have a program contain this type of rule 5, then X is an answer set of the program π if and only if X is an answer set of $\pi \setminus \{r\}$, with r such a constraint 5 and X does not violate the constraint 5.

• Cardinality constraints:

It is literals extended in the following form:

$$l \{q_1, ..., q_m\} u.$$
 (6)

with $m \ge 1$, l an integer and u can be an integer or by default the infinite if it does not exist. l and u are the lower and upper limits of the cardinality of the subsets of $\{q_1, ..., q_m\}$ that satisfy the answer sets. These literals are constrained (q_i) may occur in the head and body of the rule. Cardinality constraint is satisfied in an answer set X, if the number of atoms of $\{q_1, ..., q_m\}$ belonging to X is between l and u. In other words:

$$l \leq |\{q_1,...,q_m\} \cap X| \geq u$$

with \cap symbol of intersection and |A| is the cardinality of the set A.

2.1.3 Modelisation of a problem with ASP

We can consider that the construction of models is one of the fundamental components of the scientific process. It concerns all systems we seek to control. A model has two main features [1]:

- it is a simplification of a given system
- it allows an action on the system

Models offer the possibility to provide a solution to a problem identified as such. This concept model can address another angle issues related to representation process.

- 1. **Modeling steps** The modeling process can be regarded as a special form of representation whose operations are detailed in [2]. Logical ASP programs follow the strategy of "generate and test". This strategy includes four steps:
 - Enumerate with facts;
 - Explain with the rules;
 - Generate all the possibilities with cardinalities, and finally;
 - Filter with constraints.

2. Resolving an ASP program

From [4] and [3], the couple Grounder and Solver usually work together: the grounder used to remove variables in order to achieve a constant program and the solver computes all anwser sets for stabilized programs generated by the grounder.

Example of Grounder: GRINGO, DLV, LPARSE

Example of ASP Solver: SMODELS, DLV, CMODELS, CLASP...

The combined use of the Grouder and the Solver specifies major programs in a compact, using rules with schematic variables and other abbreviations. Both systems employ grounding algorithms that work quickly and simplify the program. In developping these new methods we worked with CLINGO which is a combination of grouder GRINGO and solver clasp.

2.2 Process Hitting

3 Fixed point implementation

- 3.1 Process Hitting network presentation
- 3.2 Search of fixed points
- 4 Dynamic network evolution
- 4.1 Future states identification
- 4.2 Reachability verification
 - known steps number
 - unknown steps number: incremental approch (iclingo)

5 Experiments analysis

- 5.1 Benchmarks
- 5.2 Evaluation
- 5.3 Limitation

6 Conclusion and future directions

References

- [1] Christian Anger, Kathrin Konczak, Thomas Linke, and Torsten Schaub. A glimpse of answer set programming. *KI*, 19(1):12, 2005.
- [2] Chitta Baral. *Knowledge representation, reasoning and declarative problem solving*. Cambridge university press, 2003.
- [3] Robert Ibbotson. Extending and continuing the development of an integrated development environment for answer set programming. Master's thesis, University of Bath, 2010.
- [4] Vladimir Lifschitz. Answer set programming and plan generation. Artificial Intelligence, 138(1):39–54, 2002.
- [5] Loïc Paulevé. *Modélisation, Simulation et Vérification des Grands Réseaux de Régulation Biologique*. PhD thesis, École centrale de nantes, 2011.
- [6] Andrew Wuensche. Genomic regulation modeled as a network with basins of attraction. In R. B. Altman, A. K. Dunker, L. Hunter, and T. E. Klien, editors, *Pacific Symposium on Biocomputing*, volume 3, pages 89–102. World Scientific, 1998.