COMUE L'UNAM École Doctorale STIM Sciences et Technologies de l'Information et Mathématiques



Spécialité: Informatique Laboratoire: IRCCyN Équipe: MeForBio

Exhaustive checking of dynamical properties in multi-valued Biological Regulatory Networks using Answer Set Programming

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Introduction

- Systems biology = studying and understanding of interactions inside biological systems
 - A gene produces a protein
 - Many proteins activate/inhibit other genes
- Biological systems are **very complex**, and studying them is time/CPU consuming



Analysing key properties w.r.t. Biology

• Reachability:

Initial context: $\langle a_0, b_0, c_0, z_0 \rangle$





Studying models

• Models are often **too large to be studied** exhaustively • Usual model-checkers have to compute all states



The Process Hitting framework

Process Hitting (PH)

Recent framework well adapted to large-scale models • Atomistic representation of actions

• **Fixed Points:** states where no action can be played $< a_0, b_1, c_1, d_2 >, < a_0, b_1, c_1, d_0 >, < a_1, b_0, c_0, d_2 > \dots$

Studying PH using Answer Set Programming [3]

- Translate PH to ASP: sort(A) . process(A,I). action(A,I,B,J,K).
- Dynamic behaviour: $2\{activeFromTo(B,J,K,T)\} \leftarrow playableAction(A,I,B,J,K,T),$ instate(activeProcess(A,I),T), instate(activeProcess(B,J),T), J!=K, time(T).
- Reachability verification: reached(F,T) \leftarrow goal(F), instate(F,T). getNbreGoals(X) \leftarrow X={ goal(_) }. reachedAllGoals(T) \leftarrow X={reached(F,T):goal(F)}, getNbreGoals(Y),X=Y,time(T). \leftarrow reachedAllGoals(T).
- Fixed point identification: 1 selectedProcess(A,I) : shownProcess(A,I) 1 \leftarrow sort(A).
 - \leftarrow hit(A,I,B,J), selectedProcess(A, I), selectedProcess(B, J), A != B.

Results and Benchmarks

- Compare performances with existing methods:
- Efficient results on large models (up to 50 genes)

Model specifications Fixed points Reachablity $\Lambda t(c)$

• Very efficient **reachability approximations** [1,2]



Model specifications			Tixed points		$Reachability \ \Delta t(S)$		
System	Genes	States	$\Delta t(s)$	# results	Pint[1]	GinSim[4]	ASP-PH
ttr	20	2 ¹⁹	0.004	0	0.97	2.05	1.90
erbb	42	2 ⁷⁰	0.017	3	Inconc	151.64	5.02
tcr	54	2 ⁷³	0.021	1	Inconc	-	95.08

Work in progress

 Identification of attractors • Add delays for actions : towards timed PH • Infer PH models from time series data

[1] Paulevé, Magnin, Roux in TCSB, 2012 [2] Folschette, Paulevé, Inoue, Magnin, Roux in TCS, 2015 [3] Ben Abdallah, Folschette, Roux and Magnin in *BIBM*, IEEE, 2015. [4] Gonzalez et al., *Biosystems*, 2006.

