

Protein Synthesis

AVACS S3
Phase 2

July 28, 2011

1 Description of the Benchmark

We analyze in this test case a stochastic Petri net (SPN) model of protein synthesis [1] as depicted in Figure 1. In biological cells, each protein is encoded by a certain gene.

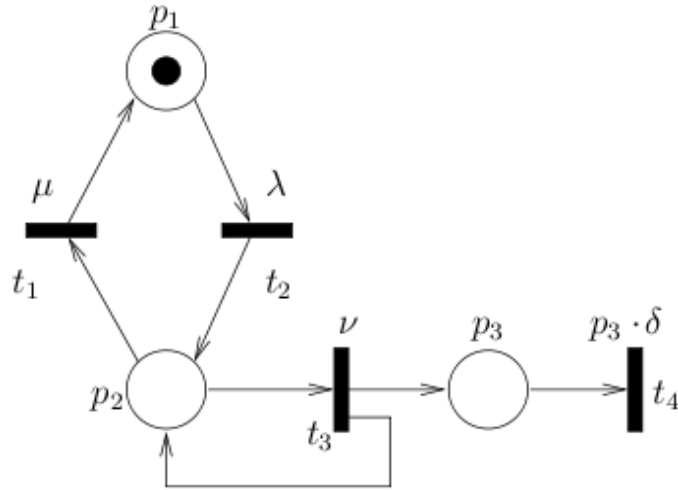


Figure 1: SPN of the synthesis model

If the gene is active, the corresponding protein will be synthesized. Also, proteins may degenerate and thus disappear after a time. Activation and deactivation of genes, protein synthesis (in case of active gene) as well as protein degeneration are modeled by stochastic rates. In the model, place p_1 corresponds to an inactive gene encoding the protein, p_2 corresponds to an active gene and p_3 gives the numbers of existing proteins. The transition t_1 deactivates the gene with rate μ , while t_2 activates it with rate λ . If the gene is active, t_3 can produce new proteins with rate ν . Each individual protein degenerates with rate δ , which is modeled by the transition t_4 . We consider the property that, within time t but later than 10 time units, a state is reached in which 20 or more proteins exist and the gene is inactive. The following formula formalizes this property: $P_{=?}(F^{[10,t]} p_3 \geq 20 \wedge inactive)$ where *inactive* is an atomic proposition representing inactive genes.

t	Uniform			Layered			FSP					
	depth	time (s)		n	depth	time (s)		n	depth	time (s)		n
300	2300	0.9/	2.0	4659	2047	0.9/	1.7	4093	34	1.0/0.0		67
500	3636	0.9/	7.8	7271	3308	1.0/	6.4	6615	35	1.0/0.0		69
1000	6830	0.9/	74.5	13659	6420	1.4/	68.0	12839	36	1.2/0.0		71
2000	13103	1.0/	567.0	26205	12577	2.7/	502.2	25153	37	1.4/0.0		73

Table 1: Comparison of Uniform-, Layered- and FSP-configuration

2 Results

We implemented this model in a *PRISM* [3]-like language and applied *INFAMY* [2]. Our implementation was tested with three different configurations and fixed parameters $\lambda = 1$, $\mu = 5$, $\nu = 1$ and $\delta = 0.02$. Here, for the computation of the truncation point we used a precision of 10^{-6} . A comparison of all configurations for this test case is given in Table 1. The probability of our property for various t is given in Table 2. All results were obtained on a Linux machine with an AMD Athlon XP 2600+ processor at 2 GHz equipped with 2 GB of RAM.

In this case study, the sum of the outgoing rates of a state mainly depends on $p_3 \cdot \delta$. Thus the model is rate-unbounded. On newly explored states where p_3 is higher, the uniformization rate could also be increased. Thus, only time bounds $t \leq 45$ can be handled of the initial approach [4]. Since in the Uniform and Layered chain configurations only forward exit rates are considered, very large time bounds can now be handled. Remarkably, the depth grows very slowly with respect to time if FSP is used. Even though global rates are unbounded, this is of no consequence since most of the rates lead back to states at lower depth. This also means that the probability of going out is very small. Both Uniform and Layered chain configuration do not exploit this. Thus, the resulting truncation depth is significantly higher.

t	prob.
300	2.07E-02
500	4.39E-02
1000	9.99E-02
2000	2.02E-01

Table 2: Computed probabilities for $P_{=?}(F^{[10,t]}p_3 \geq 20 \wedge inactive)$

References

- [1] Peter J. E. Gross and Jean Peccoud. Quantitative modeling of stochastic systems in molecular biology by using stochastic Petri nets. *Proc. Natl. Acad. Sci.*, 95:6750–6755, 1998.
- [2] H. Hermanns, E. M. Hahn, B. Wachter, and L. Zhang. Time-Bounded Model Checking of Infinite-State Continuous-Time Markov Chains. *Fundamenta Informaticae*, 95:129–155, 2009.
- [3] M. Kwiatkowska, G. Norman, and D. Parker. PRISM: Probabilistic Model Checking for Performance and Reliability Analysis. *ACM SIGMETRICS Performance Evaluation Review*, 36(4):40–45, 2009.
- [4] Lijun Zhang, Holger Hermanns, E. Moritz Hahn, and Björn Wachter. Time-bounded model checking of infinite-state continuous-time Markov chains. In *ACSD*, pages 98–107. IEEE, 2008.