# Genomic Object Net: Petri Net Enhancement for Multi-Cellular Processes

${f Yuichi}$ Hirata $^1$	${f Hiroshi}$ Matsuno $^2$
hirata@ims.u-tokyo.ac.jp	matsuno@sci.yamaguchi-u.ac.jp
$Makiko Sasaki^1$	Satoru Miyano $^1$
maki-s@ims.u-tokyo.ac.jp	miyano@ims.u-tokyo.ac.jp

<sup>1</sup> Human Genome Center, Institute of Medical Science, University of Tokyo, 4-6-1 Shirokanedai, Minato-ku, Tokyo 108-8639, Japan

<sup>2</sup> Faculty of Science, Yamaguchi University, 1677-1 Yoshida, Yamaguchi 753-8512, Japan

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#### 1 Introduction

Recent study of cell lineage of multi-cellular organism such as C. elegans shows us that cell-cell interaction and localization of gene products take very important role in the development of early embryo [3]. In order to describe such multi-cellular processes, we extend the software tool Genomic Object Net [2, 4] in which we enhanced the hybrid parametrized functional Petri net (HPFPN) model to extend the parameter space of elements of Petri net and carry out the dynamical change of Petri net.

#### 2 Hybrid Parametrized Functional Petri Net

A place P of a hybrid parameterized functional Petri net (HPFPN) holds a vector  $(d_1, \ldots, d_{r_P}, c_1, \ldots, c_{s_T})$  of nonnegative integers  $d_1, \cdots, d_{r_P}$  called the discrete components and nonnegative real numbers  $c_1, \ldots, c_{s_T}$  called the continuous components as its contents. A transition T of a HPFPN is specified with input arcs  $a_1, \ldots, a_p$  coming from places  $P_1, \ldots, P_r$  and output arcs  $b_1, \ldots, b_q$ going to places  $Q_1, \ldots, Q_q$  (Fig. 1). Each input arc  $a_i$  specifies how the contents of  $P_i$  is consumed through the arc  $a_i$  with a function  $A_i([P_1], \ldots, [P_p], [Q_1], \ldots, [Q_q])$ , where  $[P_i]$  and  $[Q_j]$  denote the contents of  $P_i$  and  $Q_i$ , respectively. For a discrete component  $d_k, A_i$  defines the amount which is removed from  $d_k$  through  $a_i$  by firing. For a continuous component  $c_l$  of  $P_i, A_i$  defines the speed of consumption from  $c_l$  through  $a_i$ . Each output arc  $b_j$  specifies how the contents of  $Q_j$  is increased through the arc  $b_j$  with a function  $B_i([P_1], \ldots, [P_p], [Q_1], \ldots, [Q_q])$ .



Figure 1: Transition of hybrid parametrized functional Petri net.

With the components of a place in HPFPN, we can represent, for example, the concentration, localization, phosphorylation, etc. of some protein.

In order to describe dynamical changes of Petri net, we employ the following rules (R1-R12) (Table 1) of synthesis and reduction which have been introduced for Petri net [1]. A rewriting procedure is defined as a program which specifies how these rules are applied by using the parameter values of a HPFPN which is being rewritten (e.g. Fig. 2-5).



### 3 Discussions and Future Works

By using HPFPN, place can hold both continuous and discrete parameters. This gives us much flexibility for describing biological objects and their networks. This enables us to simulate the dynamical changes of Petri net as shown in Fig. 2-5. In Fig. 2 the Petri net has only one place and START operation is executed. In Fig. 3, after R2 rule is executed, then the place is divided into series places as shown in Fig. 4. Finally, R12 rule is executed for the place and self-loop transition is created. R8 rule is also executed for the transition and it is divided into parallel transitions in Fig. 5. Here, END operation stops the evolution of element. With this method of rewriting, we can describe the developmental process of Petri net deductively. We are planning to simulate a realistic multi-cellular process such as the development of *C. elegans* embryo with this framework of HPFPN.

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## References

- [1] Jensen, K., Coloured Petri Nets: Basic Concepts, Analysis Methods and Practical Use, Vol. 1, EATCS Monographs on Theoretical Compute Science, Springer-Verlag, 1992.
- [2] Matsuno, H., Doi, A., Hirata, Y., Tanaka, Y., Aoshima, H., and Miyano, S., Genomic Object Net: basic architecture for representing and simulating biopathways, *submitted*, 2001.
- [3] Schnabel, R. and Priess, J.R., Specification of cell fates in the early embryo, *C.elegans* II, Cold Spring Harbor Laboratory Press, 361–382, 1997.
- [4] http://www.genomicobject.net/