

# Genomic Object Net 1.6: A Platform for Biopathway Modeling and Simulation

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**Keywords:** biopathways, simulation, database, Petri net, Genomic Object Net, pathway modeling

## 1 Introduction.

In the post-genome era, biopathway information processing is one of the most important issues in bioinformatics. Development of Genomic Object Net [5] is our approach to this issue. This software aims at describing and simulating structurally complex dynamic causal interactions and processes such as metabolic pathways, signal transduction cascades, gene regulations. In Dec/2002, we have released Java based software Genomic Object Net 1.0 [2]. The software was based on Hybrid Functional Petri net (HFPN) [1]. With HFPN, we can model rule based biological processes in biopathways, *e.g.* gene regulation and also ODEs-based kinetics, *e.g.* chemical processes in biopathways. In fact, with HFPN, we have modeled and simulated: the glycolytic pathway of *Escherichia coli*, gene regulation of circadian rhythms in *Drosophila*, boundary formation by notch signaling in *Drosophila*, and apoptosis induced by *Fas* ligand [4].

## 2 Architecture.

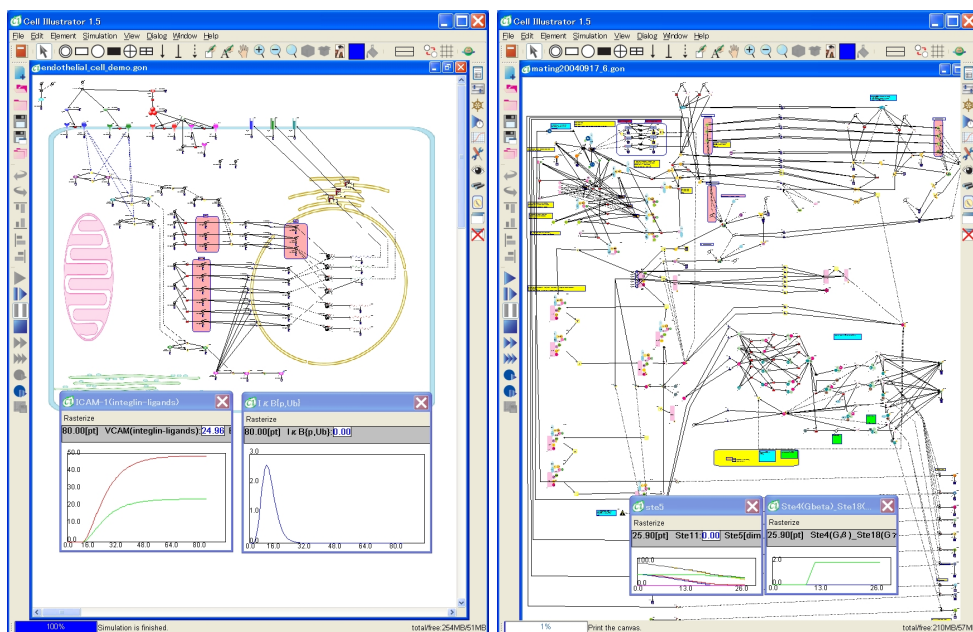
However, when modeling biopathways with HFPN, we have realized that three extensions will be useful for modeling and simulating more complicated biopathway processes (*e.g.* activities of enzymes for a multi-modification protein) and other biological processes that are not normally treated in biopathways (*e.g.* alternative splicings, frameshiftings). The first is, an entity should be extended to contain more than one value, such as **list** and **pair**, because, (i) every part in a cell should contain 3D information, *e.g.* position and speed, (ii) proteins often have many modified states, *e.g.* *p53* has known sixteen phosphorylation positions and two acetylation positions and modified states of *p53* can be  $2^{18}$ . In HFPN, an entity can contain only one value. The second is, HFPN should be extended to handle other primitive types, *e.g.* **boolean**, **string**, because major parts in a cell contain information similar to strings such as DNA sequences, mRNA sequences and protein sequences. In HFPN, an entity has only two types, **discrete** (non-negative integers) and **continuous** (non-negative real numbers). The third is, HFPN should be extended to handle more advanced type, **object** that consists of variables and methods. Many parts in a cell, *e.g.* DNA, mRNA, protein, have known functions, *e.g.* translation, transcription, degradation, and modification. Thus, if an entity takes the type **object** that has the methods with these known functions, each process that connects to the entity only needs to call a method of the **object** in the

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(a) A Signaling pathway in endothelial cell.

(b) A MAPK signaling pathway in budding yeast.

entity. To realize these three extensions, we have defined two special components; entity and process, called *generic entity* and *generic process*, respectively. We name this extension of Petri net *hybrid functional Petri net with extension* (HFPNe) [3]. With these extended architecture HFPNe, we have developed Genomic Object Net 1.6 while extensively updating GUI features, e.g. Biological Elements Dialog and Biological Libraries [5]. On the new version, we are modeling large scale biopathways, e.g. signaling pathways in endothelial cell (see Fig.1 (a)) and MAPK signaling pathways for various kind of stress response in budding yeast (see Fig.1 (b)).

## References

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