Software Platform for Systems Biology

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1 Introduction

In this paper, we introduce our work to develop a software platform for performing research in the field of "systems biology". Systems biology is a new methodology in biological field to understand biological phenomena from systematical viewpoint. So far, there have been many attempts to develop simulation for analyzing biological phenomena [2, 4, 3, 1]. On the other hand, computer simulation is certainly necessary in the field of engineering, physics, and so forth. In particular, developing semiconductor chip or robots cannot be done without the verification process of the simulation. It should be noted that the significance of the simulation has arise recently. Furthermore, systematical analysis (e.g., dynamical control analysis, bifurcation analysis) is also a very important issue in the field of biology, allowing us to understand the biological mechanisms from system viewpoint. Above all, we believe that it is significant to deal with above issues all together in a unified manner. Thus we try to develop and integrate software technologies all together specifically aimed at molecular biology. We established a taskforce for the development of the unified software platform, involving further members (e.g., computer scientists, biologists, mathematicians) to be de facto standard in the field of systems biology. The establishment of it shall be a driving force of the research in the whole field of biology.

2 Software Technologies

Here we summarize the least technologies and tools to be required for the platform:

Symbolic schematic capture Intuitive point & click windows environment so that our tool can be used directly by experimental molecular biologists without the need for extensive training.

Simulator Independent User Interface Common data-exchange format, common script language, and common user environment, by which any simulator, tools, databases can be accessed uniformally.

Data storage and characterization Pre-process the data collected from large-scale assays, and to translate the data into forms amenable to further modeling.

Intelligent database interface Direct data input from genome and proteome databases, and data mining, data translation, for related experimental data, and analogous models.

Computer algebra interface Interface between model and analysis so that direct convert to algebraic formulation can be possible.

Data filtering Image processing, or statics analysis for image data stored in biological database.

Visualization Visualization of biological model from various viewpoints to understand it intuitively.

Analytical engine Tools by which various modeling (e.g.,stochastic modeling, deterministic modeling, or even hybrid modeling) can be handled.

Reverse engineering Unravel causal correlations between genes from large–scale gene expression profiles.

Parameter optimization Optimization for parameters of models to avoid false data fits.

3 Future Works

Since we have just started this work, there are still little results to be addressed. We open to the public the activities of our taskforce via web at `http://www.systems-biology.org`. There will appear the first draft and protocol proposal of the platform shortly. Moreover, we hold a workshop regarding the software platform at California Institute of Technology in spring, and hold a conference called "The first Conference on Systems Biology" at Tokyo in fall. After establishing the protocol of the platform, even brief, we will apply some test suites (e.g, Xenopus cell cycle) to evaluate if it works sufficiently and effectively.

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