SSBD: an integrated database for Systems Science of Biological Dynamics

Yukako Tohsato[1]
yukako.tohsato@riken.jp

Kenneth Ho[1]
kenneth.ho@riken.jp

Koji Kyoda[1]
kkyoda@riken.jp

Shuichi Onami[1,2]
sonami@riken.jp

[1] Laboratory for Developmental Dynamics, RIKEN Quantitative Biology Center,
2-2-3 Minatojima-minamimachi, Chuo-ku, Kobe 650-0047, Japan
[2] National Bioscience Database Center, Japan Science and Technology Agency,
5-3 Yonbancho Chiyoda-ku, Tokyo 102-0081, Japan

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1 Introduction

It is becoming more and more important to understand animal development through analysis of quantitative data of biological dynamics. Such quantitative data are usually obtained through measurement by using experimentally obtained images/movies, or computer simulations. These quantitative data would allow us to generate more accurate mathematical models and hypotheses pertaining to biological systems. Several research groups have investigated biological dynamics using quantitative measurement and computer simulation [1-6]. However, the data formats for describing biological dynamics are different among them. Software tools for visualizing and analyzing their data have to be developed separately, making it difficult to utilize these data for further analysis. In view of this, we developed an XML-based language, Biological Dynamics Markup Language (BDML), to represent spatiotemporal quantitative data of biological dynamics. The BDML allows us to represent biological dynamics in a variety of scales, from molecules to cells to organisms. It also allows us to represent data obtained from quantitative measurement and computer simulation. We also developed a database, Systems Science of Biological Dynamics (SSBD), http://ssbd.qbic.riken.jp/, to store these BDML data together with microscopic images. BDML and SSBD provide a much-needed IT platform for Systems Science of Biological Dynamics, a new research field of systems biology with a strong focus on biological dynamics.

2 Data and Applications

SSBD is a relational database system. It manages microscopic images as well as quantitative data of biological dynamics. The quantitative data are usually produced from either quantitative measurement by using experimentally obtained images/movies or computer simulation (Fig. 1).

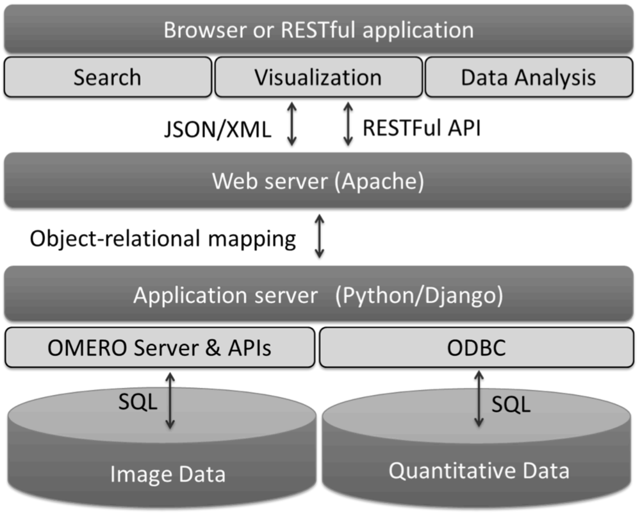

Figure 1: Overview of our SSBD database

Image data as well as experimental conditions of obtaining them are managed through OMERO system [7]. OMERO is a global standard of client-server application for microscope images. It is integrated within the SSBD database system. OMERO supports 127 different image file formats, including those of all major microscope makers.

BDML ver.0.15 was developed to represent quantitative data of biological dynamics. Materials and methods used to acquire the data are also represented in BDML. BDML schema is available online at http://ssbd.qbic.riken.jp/bdml/.

SSBD provides a wide variety of quantitative data of biological dynamics, e.g. measurements of nuclear dynamics in zebrafish [1], *Drosophila melanogaster* [2], and *Caenorhabditis elegans* [3,4] embryos; computer simulation results of microtubule-dependent nuclear dynamics in *C. elegans* embryos [5] and single-molecule dynamics in *Escherichia coli* [6]. See Table 1 for more details.

Table 1: List of available resources.

Organism	Dynamics	Source	Paper	#BDML	#Image
Zebrafish	Nuclear	Measurement	Keller et al. 2008 [1]	7	
D. melanogaster	Nuclear	Measurement	Keller et al. 2010 [2]	2	
C. elegans	Nuclear	Measurement	Bao et al. 2005 [3]	2	
C. elegans	Nuclear	Measurement	Kyoda et al. 2013 [4]	186	33480
C. elegans	Nuclear	Simulation	Kimura & Onami 2005 [5]	100	
E. coli	Single-molecule	Simulation	Arjunan & Tomita 2010 [6]	1	

We provide a set of RESTful API for accessing the SSBD database system. It is a simple WEB-based services interface allowing third party users to access quantitative data in SSBD. Users can utilize this API to interact with SSBD using any programming language and platform through the HTTP protocol. We implemented a browser-based application to visualize the quantitative data in the SSBD database through this API (Fig. 2).

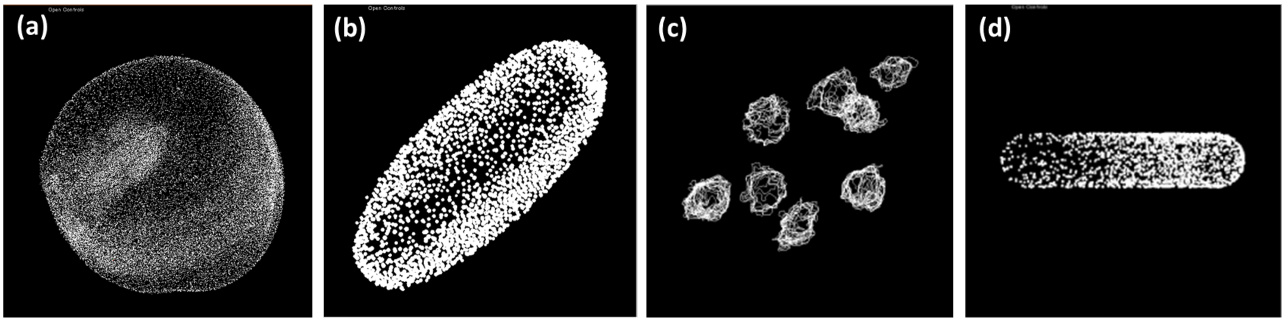

Figure 2: Visualizations of quantitative data of biological dynamics in a web browser: experimental results of (a) nuclear dynamics of zebrafish, (b) nuclear dynamics of *D. melanogaster*, (c) nuclear dynamics of *C. elegans* and (d) simulation results of single-molecule dynamics in *E. coli*.

3 Conclusion and Future Works

We developed a new database that collects quantitative information of a wide variety of biological dynamics. We are developing image-processing tools to generate BDML data from microscopic images in SSBD database. We are also planning to develop software applications to work with BDML content, e.g. programming libraries to read/write/translate BDML files; editing applications based on ImageJ, etc.

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