

Distributed Client-Server System Architecture for High Performance Simulations on Genomic Object Net

Tomokazu Kono¹

i9097@oshima-k.ac.jp

Masao Nagasaki³

masao@ims.u-tokyo.ac.jp

Ryuhei Noda¹

i9114@oshima-k.ac.jp

Atsushi Doi²

atsushi@ib.sci.yamaguchi-u.ac.jp

Hironori Kitakaze¹

kitakaze@oshima-k.ac.jp

Hiroshi Matsuno²

matsuno@sci.yamaguchi-u.ac.jp

Satoru Miyano³

miyano@ims.u-tokyo.ac.jp

¹ Oshima National College of Maritime Technology, 1091-1 Komatsu, Oshima-cho, Oshima-gun, Yamaguchi 742-2193, Japan

² Faculty of Science, Yamaguchi University, 1677-1 Yoshida, Yamaguchi 753-8512, Japan

³ Human Genome Center, Institute of Medical Science, University of Tokyo, 4-6-1 Shirokane-dai, Minato-ku, Tokyo 108-8639, Japan

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1 Introduction

As studies of genome analysis proceed, information processing of biopathway in vivo becomes one of the most important topics in bioinformatics. By processing biopathway information, medical development and/or appropriate treatments would be possible in the future; that is, it could be a great help for us. We have developed Genomic Object Net (GON), with which we simulated biopathway models such as metabolic pathways, signal transduction, and gene control mechanisms, based on hybrid functional Petri net with extension (HFPNe) [2, 3]. In GON, places and transitions, are converted to biological/medical terms. It also provides colorful viewpoints to simulations by GON with “Visualizer [1]”, the presentation tool for XML documents into visible state. However, GON is not good for simulation with super computers at remote locations despite growing needs of high-speed work to process complex pathways. Besides, users have to download the latest version, each time they want to use it.

Thus, the purpose of the paper is to set a goal to build a client-server system that utilizes distributed objects, and that make it possible to control simulations at the central server and to share information.

2 Client-Server Distributed System for GON

The GON is written in Java. With Java, it is possible to develop flexible client-server systems for distributed computation. Figure 1 shows an architecture of client-server system which allows GON to have more high-performance computational power. In this architecture, the components for simulation engine and the components for user editor are separated. Communications between these two components are coordinated by JavaRMI, which is a techniques for realizing distributed computational environments.

In the following, the flow of processes in this architecture is shown.

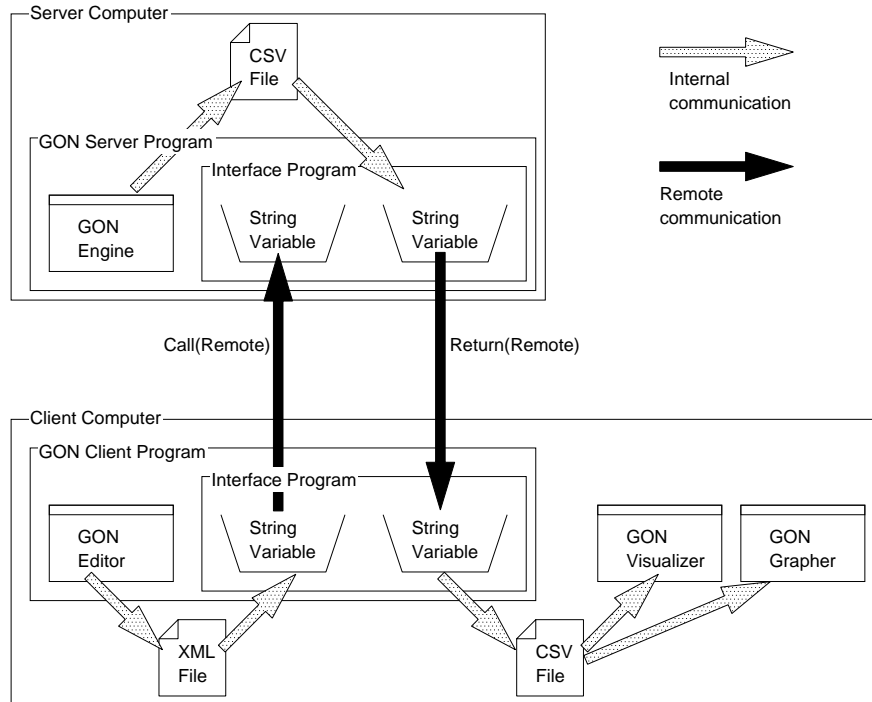


Figure 1: Distributed Client-Server System for GON.

1. Pathways are created by GON Editor and saved in a client as XML files.
2. The saved XML files is processed by Interface Program as an object in the type of string variable.
3. Simulation is performed in the GON Engine of the server. Results of the simulation are exported in the server file system as CSV files.
4. These CSV files are processed by the Interface of the server in the type of string variable, and transported to the Interface of client. These files are saved in the client as CSV files.
5. The saved CSV files are loaded in the GON Grapher and GON Visualizer components of the client for presenting the simulation results in the views of graphs and animation.

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References

- [1] Matsuno, H., Doi, A., Hirata, Y., and Miyano, S., XML documentation of biopathways and their simulations in Genomic Object Net, *Genome Informatics*, 12:54–62, 2001.
- [2] Nagasaki, M., Doi, A., Matsuno, H., and Miyano, S., Genomic Object Net: a platform for modeling and simulating biopathway, *Applied Bioinformatics*, in press.
- [3] <http://www.GenomicObject.Net/>