

Java Applets for Handling Genome Maps in KEGG

Kazushige Sato¹ Toyoko Katsurada Tomomi Kamiya
kazs@scl.kyoto-u.ac.jp toyoko@scl.kyoto-u.ac.jp tomomi@scl.kyoto-u.ac.jp
Mayuko Egoshi Minoru Kanehisa
mayu@scl.kyoto-u.ac.jp kanehisa@kuicr.kyoto-u.ac.jp

Institute for Chemical Research, Kyoto University
Uji, Kyoto 611, Japan

Abstract

Java has a potential of transforming the World Wide Web (WWW) from a static information resource to be retrieved to a more dynamic resource to be computed. We are developing a suite of Java applets for KEGG which is a deductive database in the sense that additional information is logically deduced from the stored information. Different types of computations are required in KEGG, and Java has enabled us to implement computation and graphics handling capabilities to be performed locally on the user's machine. We report here Java applets for handling genome maps and gene catalogs.

1 Introduction

KEGG (Kyoto Encyclopedia of Genes and Genomes)[1] is an attempt to provide a systematic view of the functional aspects of genes and genomes. To accomplish this task, first, the current knowledge of biological functions in molecular and cellular biology is being computerized in terms of the information pathways that consist of interacting genes and molecules. This may be considered the process of making a functional catalog of living organisms. Second, gene catalogs being obtained by genome sequencing projects of different organisms are linked to individual components of the functional catalog. This may be considered the processing of mapping a gene catalog to the functional catalog.

The functional catalog is represented in KEGG by graphical pathway maps and by hierarchically organized texts describing classifications of molecules. The gene catalog is represented by graphical genome maps and by hierarchical texts of gene classifications. For the WWW version of KEGG, we previously wrote cgi-bin scripts for browsing pathway map graphics and hierarchical texts. However, it was not possible to implement genome map graphics by the server program alone, for they need be utilized not only for just browsing but also for local manipulations. In order to include such capabilities we developed a Java package for KEGG.

¹Permanent address: Cray Research Japan LTD., Ichibancho, Chiyoda-ku, Tokyo 102, Japan

2 Results and Discussion

The two versions of genome map handling Java applets were developed: ZoomDial for circular genome maps and ZoomLine for linear genome maps. ZoomDial is currently used in KEGG for the genomes of *H. influenzae*, *M. genitalium*, *M. jannaschii*, and *Synechocystis* sp., while ZoomLine is used for *S. cerevisiae*. Either of the genome maps contains a zoom-up window and an overall view. The gene identifiers in the zoom-up window are clickable to retrieve the definition of the gene stored in the hierarchical gene catalog, and then additional information from the existing databases through the DBGET retrieval system. An example of local handling of the genome map is the following. Suppose one wish to see if tryptophan operon is conserved in *E. coli* and *H. influenzae*. Starting from the *E. coli* gene catalog of operons, the genes are mapped on the functional catalog of the metabolic pathway, and then the corresponding *H. influenzae* genes are identified. All these queries are done on the server. The last step of examining if the *H. influenzae* genes are localized in the genome to possibly form an operon is done locally by searching and marking the genes on the genome map.

In the past, genome map handling tools, such as Genomatica[2] and HyperGenome[3], were developed under the client-server mechanism. From the user's point of view this mechanism requires the downloading and installation of specialized client software, which often inhibits the wide usage in the international genome research community. From the developer's point of view, the necessity of developing different software for different platforms has been a nightmare. Java is supposed to solve these problems. The Java applets reported in this paper are designed to handle the genomes whose genomic sequences are known, which is somewhat similar to Genomatica, while we also developed an applet named MarkupChrom for browsing human chromosomes, which is similar to HyperGenome. In addition, we are in the process of developing applets for the pathway maps and hierarchical texts as well, for use in the CD version of KEGG.

Acknowledgement

The program to handle hierarchical texts was originally developed by Dr. Yutaka Akiyama. This work was supported in part by a Grant-in-Aid for Scientific Research on Priority Areas, 'Genome Science', from the Ministry of Education, Science, Sports and Culture of Japan. The computation time was provided by the Supercomputer Laboratory, Institute for Chemical Research, Kyoto University.

References

- [1] Goto, S., Bono, H., Ogata, H., Fujibuchi, W., Nishioka, T., Sato, K., Kanehisa, M., "Organizing and computing metabolic pathway data in terms of binary relations," *Pacific Symposium on Biocomputing '97, in press* (1997).
- [2] Akiyama, Y., Yakoh, T., Mori, H. and Ogasawara, N., "A server-client version of Genomatica integrated genome information browser." *Proc. Genome Informatics Workshop 1994*, pp. 202-203 (1994).
- [3] Goto, S., Kuhara, S., Takagi, T. and Kanehisa, M., "Extension of the integrated database HyperGenome for genome maps and sequence information." *Proc. Genome Informatics Workshop 1994*, pp. 204-205 (1994).