GeneWeb II: Sequence Analysis Tools on Web Server Using Java API

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1 Introduction

In recent years, the computer network, including Internet, came into wide use and researchers in many fields came to utilize it routinely. World Wide Web (WWW) and its browser software such as Netscape or Internet Explorer are probably the most powerful and useful tools for researchers who search documents or retrieve information from remote computers distributed over Internet. Especially in molecular and genome biology, researchers need to access to the various extremely large biological database on the network and to retrieve them. Therefore, the researchers are expected to be accustomed to use Web browser, even if they are not familiar with the computer operation other than Web browser. In this aspect, we had been developing sequence analysis tools on Web server named GeneWeb I in 1995 [1]. This system provided sequence analysis tools which was available on Web browser in any kind of computers.

For improving graphical user interface (GUI), we have been developing new software named GeneWeb II (Fig. 1) which is developed by using Java Application Programming Interface (Java API) for GUI and for interfacing external applications with Web server.

2 GeneWeb II

GeneWeb II programmed by Java API was compiled to architecture neutral byte code format. So, it can be executed on many different kinds of computers such as a IBM PC, a Macintosh and etc. with 'Java Virtual Machine'. GeneWeb II supports various analysis tools, most of which are established free software such as fasta, blast, clustalw and so on, for a single and multiple nucleotide or amino acid sequences; including format conversion, sequence data acquisition from databases, nucleotide or amino acids contents, restriction enzyme map, codon usage, translation, open reading frame, homology searches, multiple sequence alignment, phylogenetic tree reconstruction and so on. In addition, GeneWebII is designed for that it is feasible to update the tools and import new sequence analysis tools in GeneWeb II. Furthermore, the figure of the result for, for example, phylogenetic tree or the secondary structure of sequence, is also provided in PostScript file with high quality suitable for publication.

There are several advantages of GeneWeb II compared with GeneWeb I which used Common Gateway Interface (CGI) as the interface between Web server and applications. First of all, using

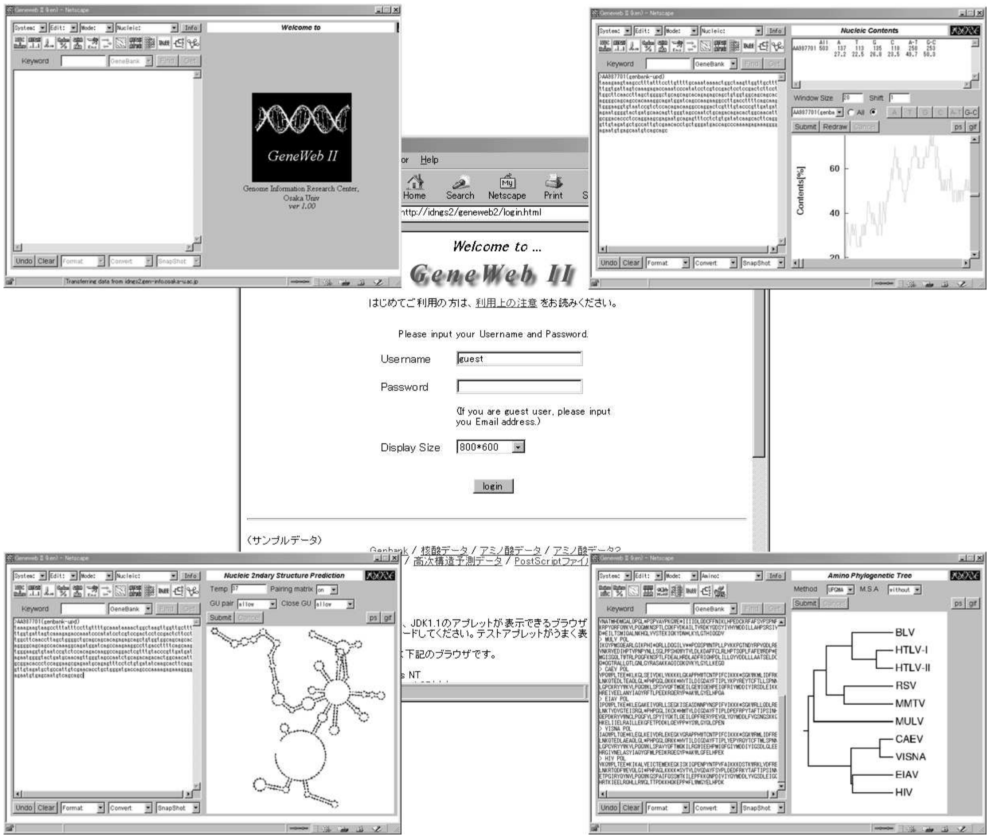

Figure 1: Examples of sequence analyses on GeneWeb II.

Application Windowing Toolkit (java.awt), the user interface is improved by its excellent GUI components. Because the processes, such as checking input parameter, displaying arrows , and etc., are executed on the client computers, the load of server computer is reduced. Moreover, the load of the network communication is also reduced in GeneWeb II.

However, as Java system is also still under development, it has some bugs. There is no guarantee about the workings of the application on every platform. Indeed, in a Macintosh, GeneWeb II can not be executed on even the latest version of Netscape Communicator (version 4.5b2). We expect that this problem will be resolved in near future.

GeneWeb II is accessible from the WWW page of our center(http://www.gen-info.osaka-u.ac.jp/), and the on-line manual are also available on our WWW page in Portable Document Format (PDF) file. To use GeneWeb II, user is requested to enter user name and password. A guest user is also welcome to use it with entering the e-mail address as password, although some functions such as batch processing and history function are unavailable.

References

[1] Yasunaga, T., Takagi, T., Takeuchi, A. and Niiyama, T., Developing Sequence Analysis Tools on Web Server, *Proc. Genome Informatics Workshop 1995*, Universal Academy Press, 164–165, 1995.