Menu System Based on NCSA Mosaic and Programs Forked from the Menu

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We have developed a mouse-selected menu system based on NCSA Mosaic which is one of the most famous clients of World Wide Web (WWW) server. Mosaic was modified to be able to fork programs locally by clicking mouse button.

We use the modified Mosaic as menu system for researchers in biological field who are unfamiliar with computer operation. When a user logs in our workstation, the menu system is automatically executed and the menu window appears on the display screen of the workstation. The information displayed in the menu window includes hyper phrase of 'program execution' in addition to usual hyper text information of Mosaic/WWW. Clicking 'program execution', the next menu window including hyper phrases of programs appears. By clicking one of the hyper phrases of programs, the corresponding program begins to run.

The programs forked through the menu system are shown in the below. Asterisks indicate the programs developed by us which are explained later.

1. ghom* : Homology search system based on client-server model.
2. gnome : A sequence data management tool to access e-mail servers for molecular biological analysis[1].
3. editalign : Multiple sequence alignment and editor[2].
4. GCG : Sequence analysis software package by Genetics Computer Groupe, Inc.
5. BioResearch : Sequence analysis software package by Fujitsu Ltd.
6. pfasta* : Parallel processing using multiple workstations for fasta.

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GHOM: Ghom is a homology search system based on a client-server model. In the server workstation, the fasta[3] and blast[4] programs are used as homology search engines. The engines remain intact. That is, we never modified the programs of fasta and blast in the server system. This means that we can easily add a new program as the engine if necessary. The server program was designed to provide interface between the client and the engines and was developed using perl interpreter language.

Ghom client has a user friendly graphical user interface like the gnome. The window of the client has the three sub-windows. The first sub-window provides menus for homology search engines and sequence databases. User can easily select both a program and database for homology search by mouse operation. The second sub-window is a mini sequence editor for a query sequence. A query sequence data can be entered from a keyboard or a file. The result of the search performed in the server is displayed on the third sub-window.

Ghom client was developed by C language with the vibrant library. The vibrant library was developed at NCBI to support three window systems, X-window, Macintosh window and Microsoft Windows. In fact, at present we have readily developed the clients for both X-window and Mac window.

PFASTA: Pfasta performs parallel processing of homology search, fasta using multiple workstations which are connected to each other through computer network. A database to be searched is divided into parts, each one is stored in each workstation as a local file. When pfasta is requested to do search, it instructs each workstation to execute the fasta program for the assigned part of the database. Pfasta is waiting for finishing all jobs in the workstations and then gather their results and reports the result which is the same one as fasta is executed on a single machine. The present implementaion of pfasta using fifteen workstations (Iris Challenge L, 2*Sun4/1000, 2*Sun4/10 and 10*Sun4/LX) performs homology search against pir protein database about seven times shorter in turn around time compared with the search performed on the fastest machine in our center, Iris Challenge L.

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