# Gnome: Recent Developments

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We have developed an e-mail based sequence analysis tool "Gnome(GenomeNet Open Mail-service Environment)" since 1993 [1, 2]. With the Gnome system, users can conduct homology searches (BLAST and FASTA), motif searches, and keyword searches against the latest databases maintained at the Human Genome Center (University of Tokyo, Japan) or the National Center for Biotechnology Information (NIH, USA). Since Gnome is designed for biologists who might be unfamiliar with computers, its interface is user-friendly: most commands can be issued by mouse-clicking. The whole system is distributed at the Human Genome Center, free of charge (ftp.genome.ad.jp /pub/hgc/gnome). The number of sites where the Gnome server was installed has already exceeded ten and a mailing-list is maintained, where both Gnome users and developers are exchanging information and discussing the future of the system. In this year, the following points were improved:

- Users can now specify multiple sequence-data files as input and send them to a search server simultaneously. This function is especially useful for large-scale sequencing experiments.
- The server process of Gnome is now forked from the 'inetd' process so that the server process is invoked only when needed, rather than always existing as a daemon process. This reduces the usual load of the server machine.

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- The sequence editor supports various data formats, such as FASTA, Stanford (IG), and Staden.
- The Gnome client newly works on platforms based on OSF1 (for DECstations) and Microsoft WINDOWS. Thus, the client now supports 6 systems in total.

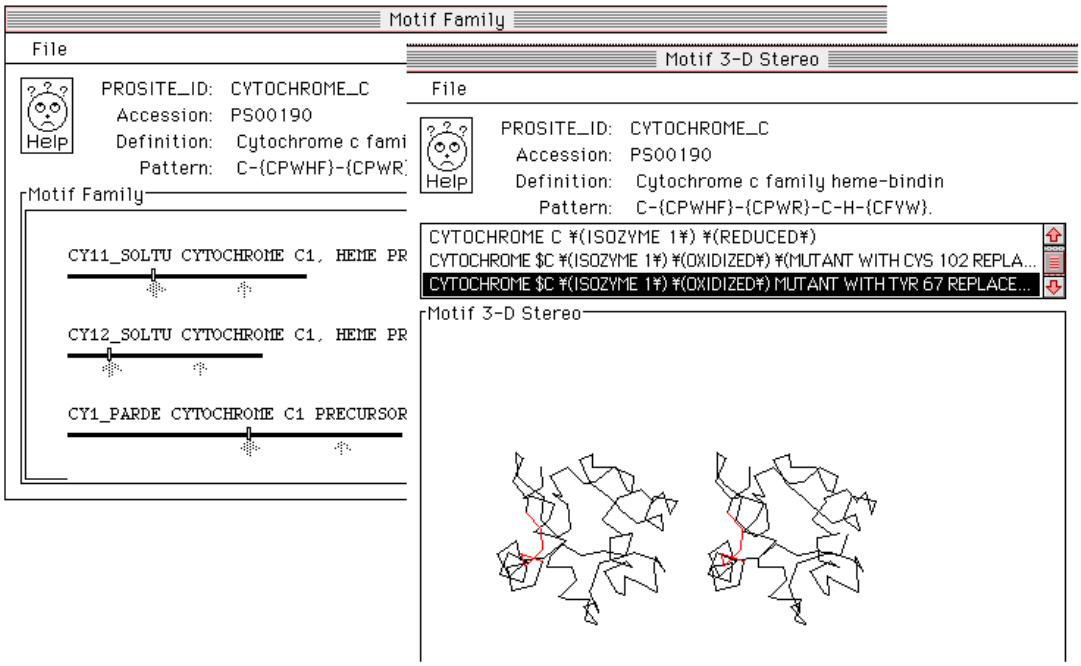


Figure 1: The Motif Search Window (Macintosh Version)

# References


[1] T.Niiyama, T.Tokimori,A.Ogiwara, I.Uchiyama and K.Nakai, "GNOME: a sequence data management tool to access homology, motif, and other data analysis servers" *Proc. Genome Informatics Workshop IV*, pp. 385-393, 1993.

[2] K.Nakai, T.Tokimori,A.Ogiwara, I.Uchiyama and T.Niiyama, "GNOME – an Internet-based sequence analysis tool" *Comp. Appl. Biol. Sci.*, in press, 1994.