Sequence Analysis Tools on Web Server

Program	Nucleotide Sequence		Amino Acid Sequence	
	Single	Multiple	Single	Multiple
Nucleotide Contents	O	O		
Amino Acid Contents			O	O
Splice	O			
Translation	O			
Codon Usage	O			
Restriction Map	O			
Homology Search	O		O	
Motif Search			O	
Secondary Structure	O		O	
Multiple Alignment		O		O
Sequence Difference		O		O
Difference Profile		O		O
Homology Matrix		O		O
Phylogenetic Tree				O
Data Transform	O	O	O	O
Format Exchange	O	O	O	O
Data Save	O	O	O	O

The programs indicated by italicized letters are still under development.

The sequence analysis tools on our Web server also support a powerful history function which stores all user operations, input data and results. Then user can verify the previous sequence analyses and if necessary can re-execute the previous analysis.

The page for the sequence analysis tools is accessible from the home page of our center (http://www.gen-info.osaka-u.ac.jp/). To use the sequence analysis tools, user is requested to enter user name and password. In addition to the registered user in Osaka University, a guest user is also welcome to use the tools though some functions including history function are not available.

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References

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Developing Sequence Analysis Tools on Web Server

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It becomes very popular for researchers in biological field to use computer network for accessing various scientific information. For accessing various information resources on the Internet, Web browsers such as Mosaic and Netscape are commonly used. Even molecular biologists, who are not familiar with computer operation especially in command mode, are expected to manage to use such browsers. Therefore it should be very useful to use Web browser as user interface for sequence analysis tools. In this aspect, we have already developed a menu system based on NCSA Mosaic; Mosaic was modified to be able to fork programs for sequence analyses locally by clicking a mouse button[1]. Unfortunately, it is practically difficult or impossible for users to use the menu system from the computers in their laboratories such as Macintoshes and PCs, because sequence analysis tools, which are forked by Mosaic, had to be installed in their machines. Apparently it is preferable to provide sequence analysis tools which is available in Web browser on any kind of computers including personal computers like Macintosh. For the purpose, we have been developing sequence analysis tools on Web server using the Common Gateway Interface (CGI) which is a standard for interfacing external applications with Web server.

The sequence analysis tools being developed by us support various analyses for a single nucleotide sequence, multiple nucleotide sequences, a single amino acid sequence and multiple amino acid sequences. The following table shows the sequence analysis tools on our Web server.

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