

WebPHYLIP: a web interface to PHYLIP

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Abstract

Summary: A web interface to PHYLIP (version 3.57 C) is implemented using CGI/Perl programming. It enables users to do phylogenetic analysis through the Internet.

Availability: WebPHYLIP is available at <http://sdmc.krdl.org.sg:8080/~lxzhang/phylip>.

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With the advances of the Internet and World Wide Web technology, web browsers provide powerful interfaces for both on-site and off-site applications. For this reason, WebPHYLIP is created to facilitate the use of the free package PHYLIP (version 3.57 c) for phylogenetic analysis (Felsenstein, 1995; Swofford *et al.*, 1996).

WebPHYLIP is a user-friendly web interface to PHYLIP which is created with a set of Common Gateway Interface (CGI) programs in Perl and C. In comparison to other available web interfaces to PHYLIP, WebPHYLIP has the following advantages: (1) users can conduct phylogenetic analysis step by step easily since WebPHYLIP keeps intermediate results automatically; (2) users can set all the parameters of each program; and (3) context-related help is available since WebPHYLIP contains on-line documents for both programs and parameters.

To implement the features mentioned above, the interface window is divided into three frames (see Figure 1). The *left frame* displays the program menus. All programs are organized in a hierarchical structure as illustrated in Figure 2.

The *right-bottom frame* is an INPUT Frame that is used to run the program. When the user clicks a program link appearing in the left frame, the parameters and data input area will appear in the right-bottom frame.

The *right-top frame* has two purposes. First, it displays the results, as an OUTPUT Frame, after a program is run. Secondly, the right-top frame displays the program documentation. More importantly, explanations of various input parameters can also be displayed (after the user clicks parameter links in the right-bottom frame).

This 'three-frame' arrangement has a couple of advantages. Since parameters and their explanations appear in

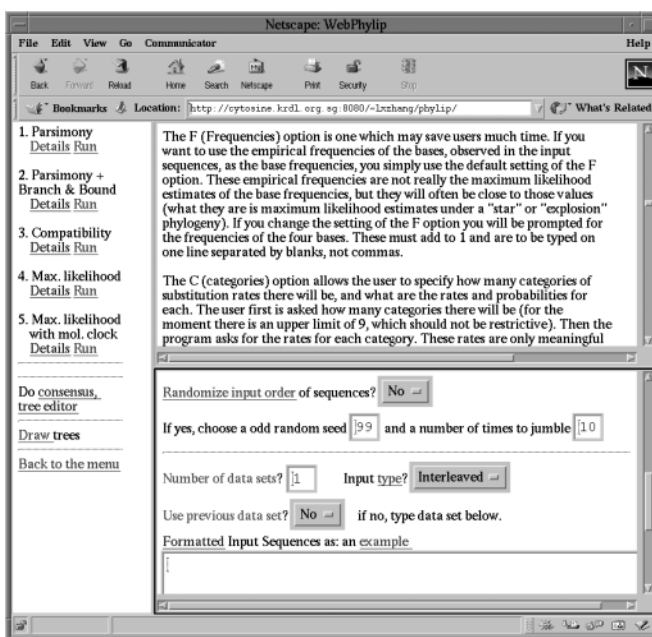


Fig. 1. Maximum likelihood in WebPHYLIP.

different frames, it becomes easier for the user to set the appropriate parameter values when running a complicated program such as Maximum Likelihood that has as many as 17 parameters. Since input and output appear in different frames, the user can view the results which allow one to modify parameter values until one is satisfied with the analysis. Moreover, since WebPHYLIP saves the previous data such as input data and tree files, the user can finish the analysis by choosing to do phylogenetic analysis and tree drawing programs consecutively. Also, the user can save any of the intermediate results to his local computer.

WebPHYLIP includes all programs in PHYLIP except for the following. All the interactive programs in PHYLIP become unnecessary and hence are not included because the web interface provides interactive capability. These programs are Interactive DNA parsimony (DNAMOVE), Interactive Wagner, Camin-Sokal,

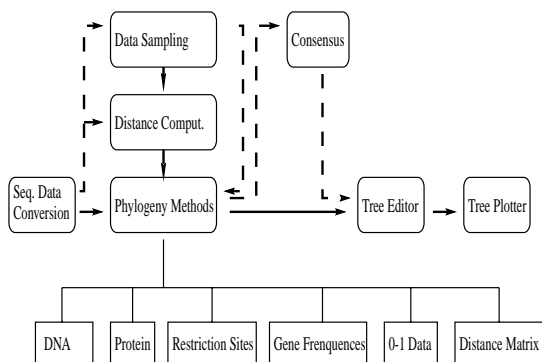


Fig. 2. The hierarchical structure in WebPHYLIP.

mixed parsimony program (MOVE), and Interactive Dollo method (DOLMOVE).

Two other missing programs are DNAINVAR, a phylogenetic invariants method for DNA sequences, and CON-

TRAST, a program which computes contrasts and correlations for comparative method studies on gene frequency data. We decide not to include these two programs because of their narrow applications. In addition, two 'un-supported' programs, MAKEINF and PROTML, are not included.

Finally, WebPHYLIP includes a new program, Clustal-Converter, which converts the multi-alignment of molecular sequences done in Clustal to the PHYLIP input format. In the future, more sequence format convertors will be added.

References

- Felsenstein, J. (1995) PHYLIP (Phylogeny Inference Package), version 3.57c., Department of Genetics, University of Washington, Seattle.
- Swofford, D., Olsen, G., Waddell, P. and Hillis, D.M. (1996) Phylogenetic inference. In Hillis, D.M., Moritz, C. and Mable, B.K. (eds), *Molecular Systematics* 2nd Edition, Sinauer Associates, Mass.