A Web-Based Tree View (TV) Program for the Visualization of Phylogenetic Trees

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Abstract

We designed a web-based program, Tree View (TV), which uses a dynamic data structure algorithm to draw the phylogenetic tree for a family of homologous proteins. This program has a user-friendly interface and can be easily implemented into other programs for convenient protein sequence analysis. It is available at our web site: http://www.biology.ucsd.edu/~yzhai/biotools.html.

Introduction

Sequence alignments and phylogenetic trees can provide information about the evolutionary history of the proteins that comprise a family. In a phylogenetic tree, every terminal branch represents a specific protein, each branch intersection point defines a relationship between two sequence-related proteins, and the lengths of the two branches indicate the evolutionary distance between them. There are currently several tools for drawing phylogenetic trees, for example TREEVIEW (Page, 1996), PHYLO_WIN (Galtier et al., 1996), TREECON (Van de Peer and De Wachter, 1997), SPECTRUM (Charleston, 1998) and PhyloDraw (Choi et al., 2000). These methods allow users to easily and interactively manipulate the shapes of phylogenetic trees. All of these programs have at least one drawback: they are designed to be platform-dependent and have to be installed on a local computer before they can be used. Among these programs, TREEVIEW and SPECTRUM can only be installed on machines running MacOS or Microsoft Windows, TREECON and PhyloDraw can only be run on machines with Microsoft Windows, and PHYLO_WIN is a graphic tool only for Unix machines running X-windows.

Since completion of the sequencing of several prokaryotic and eukaryotic genomes, an abundance of biological and genomic information has become freely accessible over the internet. One outcome of this fact is the proliferation of web-based bioinformatic tools allowing annotation and organization of the data. These tools allow biologists to diagnose sequences, search databases, assign proteins to families and provide functional annotations.

Here we describe a novel Tree View (TV) program and its implementation to two other programs, Clustal W (Thompson et al., 1997) and TC-Blast (see below). The TV program allows phylogenetic trees to be drawn dynamically (on the fly). Thus, from the input data such as a multiple alignment, a phylogenetic tree can be automatically generated. This advance allows the derived trees to be viewed by any internet browser.

Description of the Program

The TV program can read tree files produced by Clustal W (Thompson et al., 1997). There are two main sections on the start page for data input. The first is for naming the tree, which has a default value of UNKNOWN; the second is for uploading the tree data. Users may upload their saved tree files using the Browse button. Currently, the program can only draw the radial tree type; more functions will be added in later versions. The output is similar to that of the TREEVIEW program. The protein sequence names are provided at the end of each branch; the unit lengths of branches are shown at the bottom of the figure.

Implementation of TV into Other Programs

Clustal W
Clustal W is a popular sequence alignment program developed by Thompson et al. (1997). It can be downloaded for local usage and can be used from the internet. For example, both the European Bioinformatics Institute (http://www2.ebi.ac.uk/clustalw/) and the Swiss Institute of Bioinformatics (http://www.ch.embnet.org/software/ClustalW.html) provide these tools, but none of them supports automatic drawing of a phylogenetic tree. By adding our newly developed TV program, users can view the sequence alignment and phylogenetic tree at the same time. The Clustal W program also has a link to the AveHAS program (Zhai and Saier, 2001), by which users can automatically generate average hydropathy, average amphipathicity and average similarity plots upon entry of a multiple alignment. The Clustal W program provides more functions and information allowing users to analyze a cluster or clusters of homologous proteins.

TC-Blast
TC-Blast is a similarity search program specifically designed for our transporter classification (TC) system (Saier, 2000; web site: www-biology.ucsd.edu/~msaier/transport/). The details of the program will be

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presented in a future paper describing the release of our transporter classification database (TC-DB). The TV program has been integrated into the TC-Blast program. Following a Blast search of TC-DB, users can automatically view the phylogenetic tree and sequence alignment of retrieved transporter family members. One can also view the position of the queried sequence in the phylogenetic tree to identify its relationship to established family members. In the latter multiple alignment, the query sequence will be presented in bold so as to facilitate comparison of the new sequence with the other established transporter sequences.

Conclusion

The TV program is a CGI (common gateway interface) program written in the C programming language. This program has been integrated into Clustal W and TC-Blast. Both the TV and Clustal W programs are available on our web site (http://www.biology.ucsd.edu/~yzhai/biotools.html). The TC-Blast program will be released in conjunction with our transporter classification database (TC-DB) in the near future.

References