

A Macintosh Hypercard compilation of small subunit ribosomal RNA sequences

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Molecular biologists, particularly those working with unicellular organisms, are becoming increasingly aware of the importance of understanding the phylogenetic (evolutionary) relationships between their model systems and other organisms. Currently, the best method for determining quantitatively the phylogenetic relationships in a group of organisms is the analysis of small subunit ribosomal RNA (ssu rRNA) sequences (Woese, 1984). To assist in this type of analysis, the Ribosomal RNA Database Project (RDP) collects and distributes ssu rRNA sequences and software for phylogenetic analysis (Olsen *et al.*, 1991). The *ssu rRNA sequence stack* is collection of almost 500 aligned ssu rRNA sequences taken from the first public release of the RDP sequence collection.

The *ssu rRNA sequence stack* consists of a series of 'cards' each containing the ssu rRNA sequence of a single organism (Figure 1), from which the sequence can be copied (either with or without alignment information) or saved as a text file in GenBank format. Navigation in the stack is via a series of linked phylogenetic trees. Starting with a 'universal tree', clicking on the branch of interest takes the user to increasingly more specific and detailed trees. In the most specific trees, clicking on a branch either takes the user directly to the sequence card (if only one sequence is available representing that group) or presents the user with a pop-up menu of available sequences. Alternatively, the user can choose the desired sequence from a list containing the names of all of the available sequences, or choose to search the sequence names for a specific character string.

The *ssu rRNA sequence stack* is written in Hypertalk v. 2.1, and requires v. 2.0 (or greater) of Hypercard, which in turn requires at least a Macintosh Plus, 1 Mbyte of RAM, the Macintosh operating system v 6.0.5 (or greater), and preferably a hard disk drive. The *ssu rRNA sequence stack* is available by anonymous FTP from ftp.bio.indiana.edu, by E-mail from the author at jwbrown@bio.indiana.edu or brownjw@iu-bacs.bitnet, or on floppy disk (enclose a single formatted high-density disk) free of charge on written request to the author.

References

- Olsen, G.J., Larsen, N. and Woese, C.R. (1991) The ribosomal RNA database project. *Nucleic Acids Res.*, **19**, 2017-2018.
Woese, C.R. (1984) Bacterial evolution. *Microbiol. Rev.*, **51**, 221-271.

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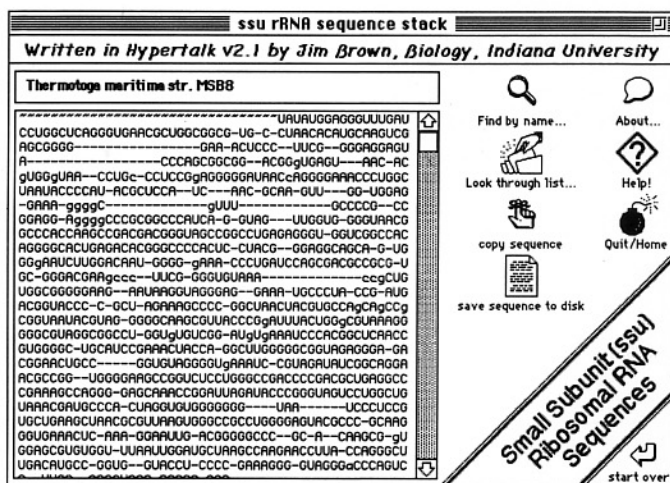
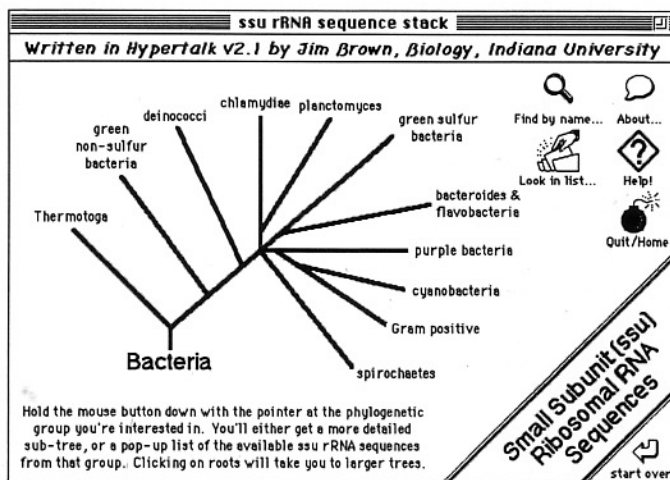


Fig. 1. The *ssu rRNA sequence stack* user interface. Example navigation and sequence cards are shown. The navigation card (top) contains a phylogenetic tree of the bacteria, which is accessible from a 'universal tree' card, and contains links to several other, more detailed, sub-trees. After choosing a sequence from a tree, the user is taken to a sequence card (bottom) which contains the sequence and set of tools for copying (aligned or not aligned) or saving the sequence as a disk file.

Circle No. 16 on Reader Enquiry Card