Corrigenda

The Ribosomal Database Project: updated description

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Nucleic Acids Research, **19**, pp. 2017−2021 (1991)

The RDP (Ribosomal Database Project) was recently announced. An updated version is provided below.

The initial RDP release includes 473 complete (or nearly so) aligned prokaryotic small subunit rRNA sequences and a corresponding phylogenetic tree. Also included are rRNA secondary structure diagrams, created by R. R. Gutell, M. W. Gray and M. N. Schnare (2), and some programs for editing and analysis of aligned sequences. The latter include G.J.O.'s VAX/VMS-based 'sequence editor and analysis program' and least-squares distance tree inference program; T.J.Macke's Unix-based alignment editor and analysis program (ae2); and the Genetic Data Environment (GDE), a UNIX/X-windows-based package designed in collaboration with S. Smith. By the time of publication, we anticipate adding an alignment of about 100 eukaryotic small subunit rRNA sequences (provided by M. L. Sogin) and an alignment of large subunit rRNA sequences.

Other alignments soon to be added to the RDP offerings include 5S rRNA sequences (3) as well as organellar and various partial rRNA sequences. We will support alternative alignments and alternative phylogenetic relationships for those persons willing to supply them in machine readable form. The RDP will also offer a 'sequence assessment' system that aligns a new sequence within an existing alignment, and reports by electronic mail salient characteristics of that sequence (idiosyncrasies, group diagnostic features, possible sequencing errors, etc). The sequence alignment (with indication of regions of alignment uncertainty), phylogenetic analyses and secondary structural representation will be available for investigators who do not themselves have such capacities. Future software will include a program for interacting with phylogenetic trees and an electronic mail facility for finding those subsequences that can be used to identify specific species or groups (i.e., possible probe sequences).

The current data and tools are available via anonymous ftp to info.mcs.anl.gov. Once you are logged into that machine via ftp (using the user-id 'anonymous' and an arbitrary password), the top level RDP directory can be accessed with the command: cd pub/RDP. You should 'get' and examine the README file and then access whatever other files are appropriate.

The data are also available by electronic mail. Send the message HELP to the RDP electronic mail server (RDP@mcs.anl.gov), and you should receive a reply with further instructions and a summary of available data.

For other questions, or for requests to be placed on our 'mailing list,' please send electronic mail to RDP@scotty.life.uiuc.edu. Written contact is also possible for researchers not having access to electronic mail. Telephone contact is through Terry Davis at 217−333−1142. As the needs of the community become defined by user feedback, RDP's user interface will become more automated and the modes of access broadened and standardized.

REFERENCES

1. Olsen,G.J., Larsen,N. and Woese,C.R. (1991) *Nucleic Acids Res.*, **19**, 2017−2021.
2. Gutell,R.R., Schnare,M.N. and Gray,M.W. (1990) *Nucleic Acids Res.*, **18**, 2319−2330.
3. Specht,T., Wolters,J. and Erdmann,V.A. (1990) *Nucleic Acids Res.*, **18**, 2215−2235.