

## ***TreeView: An application to display phylogenetic trees on personal computers***

Roderic D.M. Page

### **Introduction**

TreeView is a simple, easy to use phylogenetic tree viewing utility that runs under both MacOS (on Apple Macintosh computers) and under Microsoft Windows on Intel based computers, the two most common personal computers used by biologists. Some phylogeny programs, such as PAUP (Swofford, 1993) and MacClade (Maddison and Maddison, 1992) already provide excellent tree drawing and printing facilities, however at present these programs are restricted to Apple Macintosh computers. Furthermore, they require the user to load a data set before any trees can be displayed which is inconvenient if the user simply wants to view the trees. More portable programs, such as DRAWGRAM and DRAWTREE in the PHYLIP package (Felsenstein, 1993) can run on both MacOS and Windows computers, but make little, if any use of the graphical interface features available under those operating systems. TreeView runs as a native application on either MacOS or Windows computers, enables the user to use the standard fonts installed on their machine, their printer, and supports the relevant native graphics format (PICT and Windows metafile) for either creating graphics files or pasting pictures to other applications via the clipboard. The program also supports standard file operations, such as 'drag and drop' whereby dragging a file's icon onto the program opens that file. TreeView can read a range of tree file formats (see below) and can display trees in a range of styles (Fig. 1). Additional information, such as edge lengths and internal node labels can also be displayed. The order of the terminal taxa in the tree can be altered, and the tree can be rerooted. If the tree file contains more than one tree the user can view each tree in turn. The program can also save

trees in a variety of file formats, so that it can be used to move trees between programs that use different file formats.

### **Tree file formats**

TreeView can read tree files produced by the CLUSTAL W (Thompson *et al.*, 1994), COMPONENT (Page, 1993), fastDNAm1 (Olsen *et al.*, 1994), Hennig86 (Farris, 1988), MacClade (Maddison and Maddison, 1992), PAUP (Swofford, 1993), PHYLIP (Felsenstein, 1993), the Ribosomal Database Project (Maidak *et al.*, 1994), among others. These programs use a variant of the nested parentheses format for describing trees, variously referred to as the 'Newick' or 'New Hampshire' format. This format has yet to be formally described and so is subject to slightly varying interpretations. Details of how TreeView interprets files produced by these different programs is available in the program's documentation.

### **Availability**

TreeView can be obtained from the World Wide Web site <http://taxonomy.zoology.gla.ac.uk/rod/treeview.html>. The program is available in versions for both Motorola 68000 and PowerPC based Macintosh computers, and in 16 and 32 bit versions for MS Windows 3.1 and Windows 95/NT, respectively. The interface to the Macintosh and Windows versions is essentially identical.

### **Acknowledgements**

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*Division of Environmental and Evolutionary Biology, Institute of Biomedical and Life Sciences, University of Glasgow, Glasgow G12 8QQ, UK. E-mail: r.page@bio.gla.ac.uk*

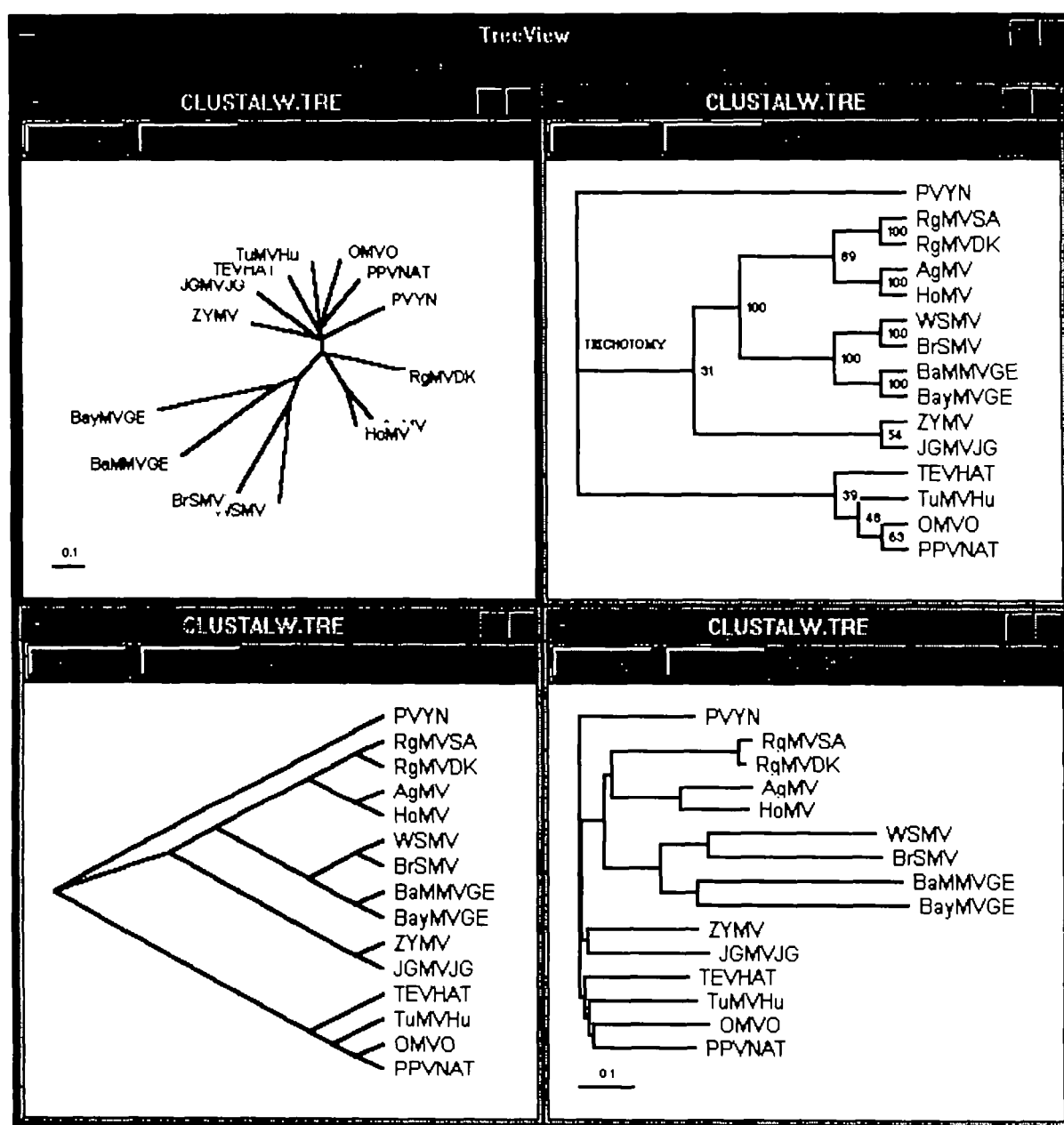


Fig. 1. A screen shot of TreeView running under Windows 3.1 showing four different ways of displaying the same tree.

## References

- Farris, J.S. (1988) *Hennig86, version 1.5 Computer program and documentation*. Port Jefferson Station, New York.
- Felsenstein, J. (1993) *PHYLIP (Phylogeny Inference Package) version 3.5c*. Distributed by the author. Dept. of Genetics, University of Washington, Seattle, USA.
- Maddison, W.P. and Maddison, D.R. (1992) *MacClade. analysis of phylogeny and character evolution. Version 3.0* Sinauer Associates, Sunderland, Massachusetts.
- Maidak, B.L., Larsen, N., McCaughy, M.J., Overbeek, R., Olsen, G.J., Fogel, K., Blandy, J. and Woese, C.R. (1994) The Ribosomal Database Project. *Nucleic Acids Res.*, **22**, 3485–3487.
- Olsen, G.J., Matsuda, H., Hagstrom, R. and Overbeek, R. (1994) FastDNAm1: a tool for construction of phylogenetic trees of DNA sequences using maximum likelihood. *Comput. Applic. Biosci.*, **10**, 41–48.
- Page, R.D.M. (1993) *COMPONENT: tree comparison software for Microsoft Windows, version 2.0*. The Natural History Museum, London.
- Swofford, D.L. (1993) *PAUP: Phylogenetic Analysis Using Parsimony, version 3.1.1*. Laboratory of Molecular Systematics, Smithsonian Institution, Washington D.C.
- Thompson, J.D., Higgins, D.G. and Gibson, T.J. (1994) CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. *Nucleic Acids Res.*, **22**, 4673–4680.

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