

>>>About njplot

Written by M. Gouy (mgouy@biomserv.univ-lyon1.fr).

Phylogenetic trees read from Newick formatted files can be displayed, re-rooted, saved, and plotted to PostScript (or PICT for the Macintosh) files. Input trees can be with/without branch lengths, with/without bootstrap values, rooted or unrooted. Binary as well as multibranching trees are accepted.

njplot is available at

<http://pbil.univ-lyon1.fr/software/njplot.html>

for MAC, PC under Windows95/NT/XP and several unix platforms.

njplot uses the Vibrant library by J. Kans.

>>>Menu File

Open: To read a tree file in the Newick format (i.e., the file format used for trees by Clustal, PHYLIP and other programs).

Save plot: To save the tree plot in PostScript format, or in the PICT format for the Macintosh.

Save tree: To save the tree in a file with its current rooting.

>>>Menu Edit

Copy: [Mac & Windows ONLY!] Copies the current tree plot to the Clipboard so that the plot can be pasted to another application.

Paste: If the clipboard contains a parenthesized tree, this tree will be plotted.

Clear: Clears the current plot so that new tree data can be pasted.

Find: To search for a taxon in tree and display it in red. Enter a (partial) name, case is not significant.

Again: Redisplay in red names matching the string entered in a previous Find operation.

>>>Menu Font

Allows to change the font face and size used to display tree labels.

>>>Menu Paper

Allows to set the paper size used by the "Save plot" item of menu "File".

Pagecount (x): sets the number of pages used by "Save plot".

>>>Operations

Full tree: Normal tree display of entire tree

New outgroup: Allows to re-root the tree. The tree becomes displayed with added # signs. Clicking on any # will set descending taxa as an outgroup to remaining taxa.

Swap nodes: Allows to change the display order of taxa. The tree becomes displayed with added # signs. Clicking on any # will swap corresponding taxa.

Subtree: Allows to zoom on part of the tree. The tree becomes displayed with added # signs. Clicking on any # will limit display to descending taxa. Select "Show tree" to go back to full tree display.

>>>Display

Branch lengths: If the tree contains branch lengths, they will be displayed. For readability, very short lengths are not displayed.

Bootstrap values: If the tree contains bootstrap values, they will be displayed.

>>>Subtree up

When a subtree is being displayed, allows to add one more node towards the

root in the displayed tree part.