Phylogenetic Tree Viewing Software

Determining the relatedness of species is fundamental to understanding biology. Unfortunately, software packages for representing this relatedness in phylogenies do not have the features that an evolutionary biologist needs to easily visualize species relationships. Outdated visualization techniques with limited support for current phylogenetic formats limits the usefulness of current phylogenetic tree viewing software and makes creating a publication-ready tree difficult and time-consuming. Using a web-based programming language such as JavaScript, phylogenetic tree viewing software should have the following features:

1. Fully editable so that users can correct misspelled taxa on the tree
2. Easily color specific clades with one or more colors, including an optional legend
3. Able to add arrows (to point to regions) or other clip art to any part of the phylogeny
4. Easily add clade pictures from http://phylopic.org/
5. Variable and editable font sizes/ font type/ branch lengths
6. Collapsible clades so that large trees can be condensed
7. Support horizontal gene transfer with dashed lines
8. 3D drag (for web/app) for viewing horizontal gene transfer relationships better
9. Be able to copy the phylogeny without saving it
10. Save phylogeny as a JPEG, PNG, and SVG
11. Auto-format the smallest clades to the top of the phylogeny
12. Support JSON format for reading and exporting. Also support legacy formats
13. Option to manually add/remove taxa
14. Option to align taxa to the far right
15. Option to make all edges equal sizes
16. Option to make edges square or rounded
17. Add bootstrap/ custom labels
18. Format phylogeny to fit on a single page.
    a. Support tall and skinny phylogenies
    b. Support short and fat phylogenies
19. Option for circular phylogeny
20. Option for phylogeny/ clade titles
21. Option for a watermark

This software package will significantly impact the scientific community and facilitate publishing high quality phylogenetic trees.