

## I think that I shall never see a poem lovely as phylogeny...

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With the number of genome-wide experiments going on, it seems that everyone has at least a little interest in phylogenetics.

There are many tools and information pages on the Web for phylogenetics comparison. Users may be familiar already with PHYLIP's many packages, available as a downloadable [executable from University of Washington](#), or as a Web server at Pasteur Institute), or with PAUP, but interest in improving or creating new phylogenetic algorithms has definitely been on the rise.

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There are a couple of motivations behind building a phylogenetic tree: 1) for protein structural or DNA changes by species (gene trees) or 2) for purely evolutionary reasons (species trees). Genome-wide studies have led to interest in building large trees of genome disparity between individuals within species (very large gene trees).

Take a look at a site called [CIPRES](#) funded by the NSF and led by a bioinformatics specialist at the University of Texas at Austin and a number of collaborators. The tools there are collected packages previously created (Mr. Bayes and PAUP) as well as newly-created applications that are especially appropriate for very large phylogenetic tree construction using many whole-genome data sets.



Using CLUSTALW multiple sequence alignment in combination with neighbor-joining or parsimony methods is great for smaller sets of data or sequences to be compared, and is pretty common with molecular biologists. But when you start working with very large sequences and a large number of "neighbors", you may need to begin working with different tools. I learned this quite recently at a seminar on phylogenetic algorithms. Who knew? While I'm by no means an expert on phylogeny or tree-building, I've been working with a number of these tools for work and for fun, and they're worth investigating. At the CIPRES site, click on the links for the "Portal" and "Software" to see what's available to use.

Happy tree-building!

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