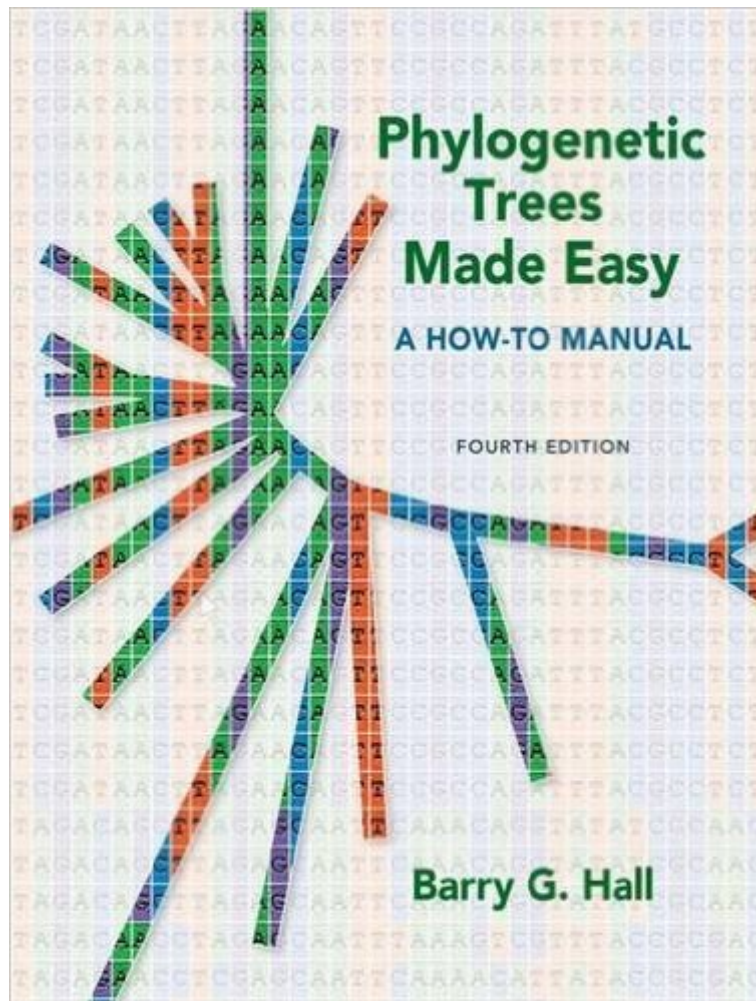


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# Phylogenetic Trees Made Easy: A How To Manual, Fourth Edition



## Synopsis

Reflecting new software updates, and with more advanced topics, the Fourth Edition helps the student create phylogenetic trees from protein or nucleic acid sequence data. The reader is taken step-by-step from identifying the sequences required, to drawing the tree for presentation to an intended audience.

## Book Information

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Average Customer Review: 4.3 out of 5 stars [See all reviews](#) (23 customer reviews)

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## Customer Reviews

Buy this if you must but there is a third edition. They complement each other to some extent but the third edition is more useful as it is more up to date and even slimmer and yet more powerful in that it totally obviates the need to pour over Paup. Here is a good treatment of Paup. Wonderful for beginners. Review for the 3rd Edition (as only allow one review per set) - I now give it 5 stars and a title would be: Buy it, Do it ... or something similar. Shortly after I got the second edition, I got the third. Within the covers of this slim volume is all the information you will need to generate the most elaborate hypotheses you may dare to venture on the basis of all the hard work you may have put into obtaining a data set of protein or DNA sequences. The chapters are clearly laid out and this is a cook book - you can follow the instructions chapter by chapter using freely available software that it recommends. All the way from organizing your data, making an alignment and turning this into a simple tree, to computing genetic distances and finally producing trees by Bayesian Inference or Maximum Likelihood. Within certain relevant chapters are essays explaining the mathematical bases of tree building, models employed and the various kinds of trees and how they are built up -

chapters on Trees, Neighbour Joining, Maximum Parsimony, Maximum Likelihood, Bayesian Inference and there are downloadable programs that work fine as per the instructions like Fas2PhyNex which instantly transforms your Fasta file format into a Phylip and Nexus format.

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