



Phylogenetic Trees Made Easy: A How-to Manual, Third Edition

Barry G. Hall

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Phylogenetic Trees Made Easy helps the reader get started in creating phylogenetic trees from protein or nucleic acid sequence data. Although aimed at molecular and cell biologists, who may not be familiar with phylogenetic or evolutionary theory, it also serves students who may be familiar with phylogenetic theory but are unfamiliar with the tools used to apply that theory. The reader is led, step by step, through identifying sequences that are homologous to a sequence of interest, downloading these sequences from databases, creating multiple alignments, and using several different methods to construct trees. Learn More boxes present background on the various concepts and methods, and a website provides files needed for working through the tutorials in the text as well as additional software that facilitates some of the methods discussed. Key Changes to the Third Edition * Over 90% of the text and screenshots are new. * A new program, MEGA, that has dramatically simplified and sped up the most tedious parts of making trees searching for and downloading sequences, aligning those sequences, and getting them into suitable formats is introduced as the primary tool for constructing trees. * PHYML, another new program that has sped up the Maximum Likelihood method by more than 100-fold, making it a practical alternative to other methods, is introduced. * Chapter 9 is devoted to a detailed method for reconstructing very ancient ancestral sequences, and software to facilitate that method is made available on the website. * Chapter 10 speaks to detecting adaptive evolution. * The final chapter comprises detailed instructions for working with programs on Macintosh, Windows, and Unix platforms.

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