

## Book Review

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*Inferring Phylogenies*. By Joseph Felsenstein. Sunderland, MA: Sinauer Associates, 2003. Pp. 664. \$60.

The contributions of Joseph Felsenstein to the theory and practice of phylogenetic inference are well known. Felsenstein advanced the use of likelihood methods in phylogenetic inference and wrote one of the most widely used software tools for inferring phylogenies, PHYLIP. More recently, Felsenstein has been involved in the use of coalescence theory to make inferences about population history. Felsenstein addresses both of these problems at length in *Inferring Phylogenies*, and he is well qualified to do so. The clear goal of *Inferring Phylogenies* is to provide readers with a comprehensive discussion of the theory and algorithms behind the inference of phylogenetic trees. The book achieves this goal.

Beginning with fundamental issues, such as the counting of evolutionary changes (chapter 2), the book goes on to cover various categories of inference algorithms (parsimony methods in chapters 1 and 7, distance methods in chapter 11, and likelihood methods in chapter 16), as well as their specific implementations. Felsenstein is a good writer, and these discussions are clear enough to give a basic idea of how each method works with just a quick reading. Closer reading reveals that plenty of detail is provided, and numerous references are included where detail is absent. These descriptions of inference algorithms are potentially useful for writing software and the like, but their real value is in Felsenstein's enumeration of the strengths, weaknesses, and idiosyncrasies of each of the various methods. For instance, on page 168 we learn that "when neighbor-joining is used together with bootstrap resampling, an arbitrary resolution of ties can produce the appearance of strong support for a grouping when there is none." The ubiquity of bootstrapped neighbor-joining trees in the human genetics literature suggests that more than one study might have this problem. The latter part of the book is concerned with the

statistical analysis of phylogenies: comparisons of trees (chapter 19), evaluation of statistical support for tree topologies (chapter 20), and other tests.

Human geneticists will be most interested in the sections of this book that deal with the generation and analysis of phylogenetic trees. Chapters of particular interest will likely be those describing the various methods of inference (chapters 1, 2, 11, and 16), which are useful for choosing and evaluating methods for use with one's own data. Chapter 29 will also be of considerable interest to many human geneticists, since it covers (albeit briefly) several common problems in human genetics: sequence alignment, the analysis of gene families, and other genomic issues. A potential complaint of human geneticists will be the lack of interesting examples. Although many simple examples are provided to illustrate particular theoretical points, few analyses of real data are discussed. Felsenstein must have opinions and suggestions about common practices in the actual usage of phylogenetic inference. I, for one, would like to hear them.

*Inferring Phylogenies* is not an instruction book and is not intended to be one. Felsenstein has succeeded in his goal of providing an informative and useful guide to the techniques employed to develop and analyze phylogenetic trees. Although the book does not offer much help in the logistics of data analysis, it does constitute a well-organized resource that will inform study design and allow the critical interpretation of studies that have already been done. At \$60, the book is a steal and is recommended for any laboratory exploring phylogenetic inference.

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