BOOK REVIEW

Inferring phylogenies: an instant classic

Inferring Phylogenies

Reviewed by AJ Drummond

Joe Felsenstein has had more positive influence on the statistical revolution of phylogenetics than any other researcher in the field. For that reason, many biologists view him as the father of statistical phylogenetics. It was with this in mind that I finally got my hands on his long-awaited book, *Inferring Phylogenies*. The short answer is: it delivers. In a narrow sense, Felsenstein's book could be viewed as old-fashioned, with a number of chapters devoted to 'old' methods such as parsimony and distance-based approaches. This view misses the point. No other book gives as clear and comprehensive a picture of the major problems, solved or otherwise, in phylogenetic inference. In fact, it is perhaps precisely because Felsenstein follows the progress of statistical phylogenetics from its early beginnings that the book will be so enduring. It is enjoyable to read and is written in an uncluttered way that invites the reader to understand the details, and to work them out with pen and paper when the answer is not explicitly given. Scientists should know their tools, and Felsenstein does his best to explain to tree-builders what in fact they are actually doing when they run an analysis using popular phylogeny programs like PAUP* or PHYLIP. But this book is not just about building trees. There are also chapters devoted to modeling changes in gene frequencies, genealogy-based population genetics (the coalescent) and quantitative genetics, to mention just a few. Not only is this an unrivalled reference book for users of phylogenetic methods, but it also serves as a foundation stone on which developers of phylogenetic methods can build. The nature of the material demands that the difficulty level is a bit uneven from chapter to chapter, but an effort is always made to convey the essential features of the discipline discussed. The book is well balanced, containing enough detail to suit most readers, and providing ample references for those that require more.

If you were to read *Inferring Phylogenies* from cover to cover, you would be rewarded with a charming digression on the history of phylogenetics in Chapter 10, not to mention an explanation of diverse topics such as Hadamard methods, 'stratolikelihood' and host–parasite tree reconciliation. A comprehensive treatment of phylogenetic methods is a very challenging undertaking that Felsenstein succeeds in admirably. Despite the enjoyable educational journey that reading this book was, it seems to me that *Inferring Phylogenies* could be treated just as well as a quality reference text or teaching aid. It is clear from reading the book that Felsenstein is still not short of ideas, and the book contains plenty of nuggets of wisdom and suggestions for improvements. Of necessity, large fields of research have sometimes been reduced to a very short treatment, but as often as not this condensation distills out the fundamental ideas. The essential topics of bootstrapping, the coalescent, the comparative method, maximum likelihood, models of sequence evolution and parsimony are all described in a clear and instructive style.

If pressed on my grievances with this book, I would say that it might be a tad sterile for the average biologist. There are few interesting data sets used as examples and, although abundant intuition on the methods is provided, less intuition on the nature of biological reality is offered. The amount of genetic data now available is astounding and some direct account of what this ocean of information actually tells us about the process of molecular evolution would have been well received. Another possible point of contention is Felsenstein's description of Bayesian MCMC methods in phylogenetics. His chapter on Bayesian methods focuses primarily on the negative aspects and it might be argued that he ignores the sagacious reasons for their growing use. Like Felsenstein, Bayesian phylogeneticists choose to use detailed probabilistic models of the data. Furthermore, the large amount of genetic data now available has clearly demonstrated that the early probabilistic models of sequence evolution are not adequate. The need for robust probabilistic treatment of complex models on large amounts of data leads naturally to a sampling method like MCMC and the subsequent introduction of priors. This point of view has been made more eloquently elsewhere, but I feel that for all the good he does Felsenstein does a mild disservice to the continued development of statistical phylogenetics by downplaying one of the primary vehicles of recent progress. This is particularly clear in the very last section of the book where the list of widely used phylogeny programs does not include Mr Bayes – one of the most widely used phylogeny programs currently available.

Gripes aside, the value of Felsenstein's book cannot be overestimated and I would whole-heartedly recommend it to readers of Heredity, especially those interested in a comprehensive understanding of phylogenetics and related methodologies used in the wider field of evolutionary biology. *Inferring Phylogenies* is quite simply an instant classic.

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