

The background of the entire cover is a repeating pattern of small, teal-colored, eight-pointed stars or snowflakes arranged in a grid-like fashion.

The phylogenetic handbook
a practical approach
to DNA and protein phylogeny

edited by Marco Salemi
and Anne-Mieke Vandamme.

The Phylogenetic Handbook

A Practical Approach to DNA and Protein Phylogeny

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Foreword

Theodosius Dobzhansky (1973) wisely said, "Nothing in biology makes sense except in the light of Evolution." This truism is so often repeated that it is nearly a mantra and, with the complete genomes of many organisms being completed nearly daily, all kinds of people, but especially molecular biologists and informaticists, are rediscovering that truth. And with that discovery they are coming to need to know the tools of the trade that have been under development for nearly forty years. This book is for them in particular but it has much that, except for polymaths, may be useful even to the cognoscenti.

The book has grown out of Drs. Vandamme's and Salemi's annual course in these methods at the Katholieke Universiteit in Leuven, Belgium, where they have produced an exceptional workshop for eight years that does for Europe what a similar outstanding and long-running workshop at Woods Hole did for the United States and Canada. But the latter has not created a book like this.

The coverage is comprehensive. Topics touched upon include databases, multiple alignments, nucleotide substitution models, phylogeny inference methods (such as distance, maximum likelihood, and maximum parsimony), post-phylogenetic information (such as molecular clocks and selection), and useful subsidiary statistical techniques (such as bootstrapping and likelihood ratio tests).

Each of the major sections is written by an expert in the field, and each such section is divided into two major subsections, theory and practice. This permits the novice to proceed with his analysis without having to master the theory. That is, of course, very dangerous in this field where so many methods have different assumptions and the failure of any one of those assumptions (clocklike behavior, all sites equally mutable, all substitutions neutral) can reduce your analysis to rubbish, if untrue, which they frequently are. Still, there are people like that and we may hope that a good text such as this, with its many caveats and generally simple prose, will reduce the published trash.

The material is enhanced by the use of specific examples from which you can see what to expect, and see if you can get the same answer, and then try your own data

to see if anything strange has happened. The examples also aid in locating what you need to find in the text.

Another aspect of the book that enhances its utility for the reader is the repeated use of the same three data sets, even by different authors, to illustrate the methods. This increases immensely the value of the exercises. This is especially true when the results from different methods are ostensibly for the same desired end, and one gets to see how they differ and why (or at least to worry about it).

The example data sets used in the book can be downloaded from the book's website [<http://www.kuleuven.ac.be/aidslab/phylogenybook.htm>]. On the website the reader can also find useful links to the major phylogeny resources on the internet, as well as the results of all the analyses discussed in the text, including phylogenetic trees, unaligned and aligned sequences, and so forth.

It is appropriate to compare this work with others in the general area. The first two are by Weir (1990) and by Waterman (1995). They are both highly theoretical and quite capable of turning off many biologists quickly (although Waterman's book can be highly engaging as in his recounting of the efforts of George Gamow to predict that the genetic code was a commaless code). At the other extreme, Hall (2001) is really simple-minded enough (intentionally so) that a bright senior could easily master the methods. However, the Hall book lacks the comprehensiveness of the Salemi and Vandamme work. Two other good books, Li (1998), and Page and Holmes (1998), are largely theoretical although they make a great effort to make the subject palatable to the biologist who is mathematically challenged. In sum, there is no other book even trying to occupy the niche of this one.

In conclusion, this is a relatively easy-to-use workbook for phylogenetics, especially if the index is properly looked to (I haven't seen it). However, I have to present a strongly worded negative comment. Although tables and figures in the book have titles, many have no legends and many of the remainder have poor legends. For example, numbers normally have dimensions, (such as nucleotide differences per hundred nucleotide positions), that should have been given. Figures and tables should be as self-sufficient as is reasonable. This is not true here. Let us hope this is corrected in the next printing, which I am sure this book will achieve.

Walter M. Fitch

December 27, 2002

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Note: During the writing of this book the alpha release of the new version of PHYLIP, PHYLIP 3.6 has been made available on the PHYLIP web page. All the exercises with PHYLIP refer to version 3.5, but additional exercises covering PHYLIP v3.6 can be found on the book website.

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