



Molecular Systematics.

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MOLECULAR SYSTEMATICS.

Edited by David M. Hillis and Craig Moritz. Sinauer Associates, Sunderland (Massachusetts). \$65.00 (hardcover); \$37.95 (paper). xvi + 588 p.; ill.; index. ISBN: 0-87893-279-8 (hc); 0-87893-280-1 (pb). 1990.

The study of molecular systematics is currently undergoing its second revolution. The first revolution took place more than 20 years ago with the use of isozyme electrophoresis; now the development of the polymerase chain reaction (PCR) is having a profound impact on systematic biology. Almost 50 percent of all proposals that are reviewed by the systematic biology panel at the National Science Foundation are based on PCR, up from 0 percent two years ago. This technique not only speeds up the collection of DNA sequence data by orders of magnitude (and it is technically less involved than cloning), but also addresses completely new questions. Therefore, it is going to permit many researchers to study genetic variation at its most fundamental level, the actual DNA sequence. Although PCR has obvious advantages over more traditional techniques in molecular systematics, it is not and should not be the only technique used in the field.

This timely book is concerned with the practical aspects of all stages of conducting a study in molecular systematics, from the design of the experiment, collection and storage of samples, and techniques of data collection, to the analysis of molecular data. It guides the apprentice through explanations of experimental design and explains which method might suit particular problems. Since it is only 588 pages long, this book is not long enough to go into every detail and aspect of molecular systematics. Some of the chapters could and should be expanded into a separate book, e.g., Swofford and Olsen's chapter (see below). In spite of the book's length, however, the contributors and editors have managed to adequately address a great portion of the field.

The first two chapters give useful hints for specimen collection in the field and storage in the laboratory. The book should mention, more explicitly than it does, that samples to be used in PCR-based studies do not need to be frozen, but can be stored in ethanol for seemingly indefinite periods of time without affecting the quality of DNA. This characteristic will make the lives of many field workers much easier.

The next six chapters comprise the most useful part of the book. They cover isozyme electrophoresis, immunological techniques, molecular cytogenetics, DNA-DNA hybridization, restriction fragment analysis, and DNA sequencing. They include detailed protocols that will guide the novice through the first study in molecular systematics.

The editors did an excellent job in directing the contributors to write their chapters in the same format, which makes for a very readable, cohesive book.

The third part contains two excellent chapters: one on statistical analysis of intraspecific data (Weir), and the other on phylogenetic reconstruction (Swofford and Olsen). The latter, in particular, gives the most comprehensive treatment on the subject since Felsenstein's review papers. The last chapter of the book, authored by the editors, puts the virtues and limitations of molecular data in systematic biology into perspective.

The ease with which DNA sequences can be determined is not matched with the ease of phylogenetic analysis of these data, since not all nucleotide positions contain the same amount of phylogenetic information at particular phylogenetic levels. Factors such as gene- or domain-specific rates of nucleotide substitution and level of phylogenetic analysis further complicate the choice of which characters to use in the systematic analysis. The book would have benefitted from an additional chapter outlining general aspects of the molecular rather than systematic aspects of DNA sequences. Nonetheless, the editors did an admirable job. This book deserves a wide readership, including beginners and experts alike.

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REPRODUCTION & DEVELOPMENT

PATTERN FORMATION: CILIATE STUDIES AND MODELS.

By Joseph Frankel; illustrated by Jane A. Otto. Oxford University Press, New York. \$65.00. xvii + 314 p.; ill.; index. ISBN: 0-19-504890-3. 1989.

Frankel likes models. Models of pattern formation, and critical assessment of the ability of models to explain and predict the data, are the pervasive themes of this excellent book. Frankel finds problems even with his own current model (the cylindrical-coordinate model), and he suggests possible approaches for future improvements.

In addition to modeling, Frankel reminds the reader that the Ciliophora have been extremely useful organisms in the study of intracellular patterning. But ciliate protozoa have also provided concepts of considerable value in the development of positional information models of pattern formation, such as the ideas that: (1) all of the heritable information in a cell does not reside in the form of nucleic acid sequences, (2) various regions of the cell are nonequivalent in regard to their potential