evolution study: (i) designing the experiment and sampling, (ii) application of molecular techniques to gather data, and (iii) data analysis. Each chapter is written by an assemblage of authors who have expertise in its topic, and the editors provide introductory and concluding chapters that give an overview of the field, a brief historical retrospective, summaries of current controversies, and a prospective view. The book has an extensive index and bibliography and an invaluable glossary that covers the arcane lexicons of the several disciplines contributing to molecular systematics.

Section 1 comprises chapters on sampling design (Baverstock and Moritz) and on collection and storage of tissues (Dessauer *et al.*). The essential practices of molecular systematics are laid out in sections 2 and 3. Section 2 comprises six chapters concerned with the major techniques of molecular systematics: protein electrophoresis (Murphy *et al.*), immunology (Maxson and Maxson), cytogenetics (Sessions), DNA-DNA hybridization (Werman *et al.*), restriction site analysis (Dowling *et al.*), and DNA sequence analysis (Hillis *et al.*). Each of the six chapters is organized on the same ground plan, with introductory sections that present theoretical principles and assumptions, followed by a comparison of methods, a discussion of applications, and a list of laboratory equipment required, specific protocols, and recipes for stock solutions required in various protocols. The sections are extensively cross-referenced, with relevant protocols identified in the equipment lists and the applications sections providing guidance to techniques that would be useful in addressing particular problems. In the chapter on sequencing nucleic acids, for example, Hillis *et al.* provide a flow chart of alternate pathways and steps for getting from organism to sequence data, and steps in the chart are indexed to specific protocols. This enables the harried neophyte to efficiently assess the formidability of contemplated projects.

The third section of the book, concerned with data analysis, comprises chapters on the statistics of genetic differentiation within species (Weir) and on phylogeny "reconstruction" (Swofford and Olsen). These chapters are the most lucid reviews of their topics that I have read. The chapter on phylogeny is the longest in the book, reflecting the complexity of the problem as well as its central importance in systematics. To my relief, Swofford and Olsen point out early in their discussion that inferring a phylogeny is really an estimation procedure rather than determination of *the* phylogeny. This mind-set is requisite to an objective evaluation of alternative phylogenetic procedures as applied to molecular data. Having established this, the authors go on to present clear descriptions and evaluations of the major cladistic, phenetic, and maximum-likelihood methods currently used. A theoretical rationale is presented for each estimation procedure, but then the reader is taken step by step through the actual computational algorithm. This chapter makes the heretofore difficult task of understanding what these algorithms actually do relatively easy and will do much to eliminate the "black box" relationship between systematists and the computer programs they use—not to mention molecular geneticists trying to apply phylogenetic methods in their research. Swofford and Olsen conclude their chapter with a list of the major program packages available, what they do, and how to obtain them.

The 588 pages obviously cannot cover the full spectrum of theory and techniques, and there are some fairly obvious deficiencies. But it would be hard to imagine a more efficient way for biologists, whether familiar or unfamiliar with systematics, to gain an overview of molecular systematics than by reading this book—and continuing to use it as a reference and guide right down to the details of specific protocols. The book will be widely read and extensively cited.

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