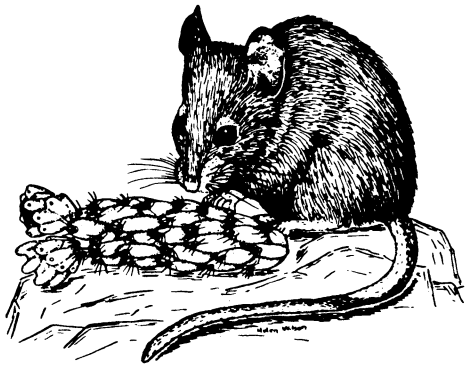

White-throated packrat. This species "was responsible for building most of the fossil packrat middens in the Chihauhuan Desert. It apparently has lived in the Hueco mountains of Texas for the last 42 ka, adapting to *in situ* vegetation changes from Wisconsin woodlands to Chihuahuan desert-scrub." [From *Packrat Middens*; drawing by Helen A. Wilson]

American Southwest. The biotic history offered by these diversified data provides a unique perspective on semiarid ecosystems and their sensitivity to climatic change. For that reason, the volume will be of interest to ecologists, biogeographers, and Quaternarists alike.

The history of semiarid regions has long eluded the paleoecologist, who in temperate and boreal latitudes relies upon fossil pollen preserved in wetlands for a continuous record of vegetation and climatic change. Playa-lake sediments and spring deposits provided pollen records for some semiarid regions, but the paleozonation of vegetation remained unresolved. It was first reported in 1964 that packrat middens found in caves and rock ledges preserved a fossil record of wood, seeds, leaves, bones, and insects. Midden materials were identifiable to species (unlike most pollen grains) and had their provenance in the immediate area, enabling a detailed reconstruction of local vegetation. The organic remains were dated to as early as 50,000 years ago and thus could provide a record of biotic change from the present back through the last glaciation. In the last 26 years, the analysis of packrat middens from the American Southwest has proceeded at a rapid rate, thanks largely to Paul Martin and former students at the University of Arizona and to Philip Wells at the University of Kansas. Today the paleoecologic database assembled in this and other publications rivals that from any temperate region of the world.

The book is divided into four parts. In the first section, important questions are addressed concerning the behavior and ecology of modern *Neotoma* and the taphonomic limitations that might be imposed on the fossil record. Might dietary preferences bias a midden assemblage? (Depends on the species.) What is the collecting radius of a wood rat? (Usually less than 30 meters.) Do midden assemblages provide a good representation of local vegetation today? (They contain the dominant plants, but a complete picture of vegetation requires sampling several middens at one site.) For how long is a midden occupied? (Probably a few years.) Are fossil middens evenly distributed in time? (No, they cluster around 1000 years ago and 10,000 years ago, reflecting the research interests of the investigators.)

The second part of the book deals with the late Quaternary vegetation of different regions. In some respects the authors in this section are themselves like packrats. Each is territorial and pertinacious in how he chooses to quantify and interpret data and how he divides the geologic record. Areas of contention are clear. Van Devender infers a mild, wet glacial climate and fairly dry summers in the early Holocene in the Sonoran and Chihuahuan deserts. Spaulding suggests that the Mohave desert experienced cold, dry glacial conditions and wet summers in the early Holocene. Thompson draws upon an array of paleoenvironmental data to conclude that the Great Basin vegetation was impoverished during glacial times and that conditions were colder and slightly drier than today. In the Grand Canyon region, Cole believes that changes in vegetation at the end of the Pleistocene lagged well behind the triggering climatic warming, a conclusion that is disputed by Spaulding, Van Devender, and others. Betancourt's analysis of the Colorado Plateau focuses on the importance of local geology and physiography in creating associations of plants that today have no modern counterpart. To an outsider these disagreements sound somewhat fratricidal, and one wishes for more effort at conciliation. Indeed, on balance there is more agreement than dissension. All concur that desert communities in the Southwest do not have a long history. Some taxa clearly had their heyday in the glacial period (for example, bristlecone and limber pine in the Great Basin and Mohave region and pinyon pine in the southern desert lowlands) and today are relatively restricted. Other taxa, dominant at present like ponderosa pine, saguaro, and foothills paloverde, are rare in the fossil record, suggesting restricted glacial distributions. The midden record provides evidence of both long-distance dispersal and vicariance in the Holocene. Because the response of communities to past climatic changes is highly individualistic, modern communities appear as transitory associations in time.

The third section of the book presents some case studies in which packrat midden analysis has been used to address specific problems. Mehringer and Wigand examine in detail the late-Holocene spread of juniper in southeastern Oregon. Other components of middens, including grasses, mammals, and insects, are discussed in a series of papers, and in general they show less variability through time than the woody taxa. Likewise, Long and others produced a climate record based on stable isotope ratios in plant cellulose and found that it did not match that developed from the flora.

The last section reminds us that midden analysis is a tool that can extend beyond the range of North American *Neotoma*. Middens of Procaviidae and Petromuridae in the Middle East and Africa and *Leporillus* in Australia contain well-preserved biological remains, and the opportunities to develop a midden data base in other semiarid regions seem promising.

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Suborganismal Analysis

Molecular Systematics. DAVID M. HILLIS and CRAIG MORITZ, Eds. Sinauer, Sunderland, MA, 1990. xvi, 588 pp., illus. $65; paper, $37.95.

Molecular systematics began as an ambitious but relatively modest enterprise in 1904 with G. H. F. Nuttall's application of serology to the problem of relatedness among animal species. In the last decade it has grown to a veritable revolution as systematists have borrowed techniques from molecular genetics to study the distribution of genetic variation across the hierarchy of life. *Molecular Systematics* is a much-needed *how to* and *why* book on the application of molecular techniques in systematic biology. Hillis and Moritz have judiciously adopted a broad definition of systematics that includes comparative studies of biotic diversity at all levels; thus the book addresses intraspecific variation and microevolutionary process, traditionally the substance of population genetics, as well as the expected topics of phylogenetic inference and circumscription of species, the more traditional subject matter of systematic biology. Indeed, the application of molecular techniques to reveal the extent and organization of genetic variation not only between and within species but within the genome seems destined to form new syntheses between evolutionary biology, developmental biology, and genetics.

The book is organized into three sections that correspond to stages of a molecular

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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