

they held in common "teleomechanism." He views this tradition, however, as separable into three stages, for which he has invented subtitles. "Vital mechanism" was the earliest version of the program. The more powerful versions of von Baer and Müller he names "developmental morphology." The third stage, resulting from the critiques of Hermann Lotze and Justus Liebig and from the work of Carl Bergmann and Rudolph Leuckart in the 1840's, eliminated the concept of a special vital force from the teleological framework; Lenoir calls this phase "functional morphology." The final two chapters of the book focus on the development of the new research programs that collided with and ultimately overshadowed teleomechanism, especially the reductionist approach of Hermann Helmholtz and the Darwinian account of evolution.

The central themes that the teleomechanist biologists maintained remained very similar from the time of Kant to their last echoes in von Baer's criticism of Darwinism in 1874. Adopting the scheme of Imre Lakatos, Lenoir defines these persistent ideas as the "hard core" of their research program. Many variations on these themes appeared, however, as they were applied to particular areas of biological investigation—to embryology, to the advent of the cell theory, to the major developments in physiology and physiological chemistry of the 1840's. In describing this interplay between general principles and specific investigative efforts, Lenoir is especially illuminating. In his summaries of the ways in which observational or experimental approaches to particular biological problems grew out of, sustained, or were interpreted by means of the teleomechanist principles, he provides probing insights into the ways in which general ideas derive new meanings from changing contexts.

This book represents an impressive overall achievement and should stimulate a major change in the way future historians of science treat this formative period in the emergence of modern biology. There are, however, some prominent difficulties. The most serious, I believe, lies in the retrospective labels Lenoir attaches to his group of biologists. Although he makes clear in the introduction that he has himself imposed the terms "teleomechanism" and its subcategories on the thought of his subjects, the regular repetition of these terms soon builds the impression that "vital mechanism," "developmental morphology," and "functional morphology" were clearly delineated schools in their own

time. The risk in these designations is that they impose more definite boundaries between ideas of individuals than actually existed and suppress basic differences between those grouped together.

A lesser flaw, but nevertheless a problem for readers, is that Lenoir's strategy requires him to repeat the same basic ideas over and over in order to demonstrate that all the important German biologists he describes held to them. The result is persuasive but somewhat oppressive. Most superficial, but most distracting, are deficiencies in the style and editing of the book. In his best passages Lenoir expresses his ideas forcefully, vividly, and with originality. In other places, however, he lapses into cumbersome, wooden sentences that more than belabor his arguments. Moreover, typographical errors are blatantly frequent. Most of them are minor, but a few are serious enough that the sense of a whole sentence or paragraph nearly disappears. In the printing of the book the type has been so clumsily aligned at the margins that some adjacent lines appear to be set in different type. A book of the significance of this one deserves more careful final preparation.

FREDERIC L. HOLMES

*Section of History of Medicine,
Yale University School of Medicine,
New Haven, Connecticut 06510*

Molecular Evolution

Macromolecular Sequences in Systematics and Evolutionary Biology. Papers from a symposium, Vancouver, Canada, 1980. MORRIS GOODMAN, Ed. Plenum, New York, 1982. xiv, 418 pp., illus. \$45.

The study of molecular evolution has recently achieved a new level of sophistication as emphasis has shifted from the study and comparison of amino acid sequences of proteins to the direct analysis of the underlying nucleotide sequences. As technological advances in molecular biology make possible the rapid ascertainment of nucleotide sequences of a great variety of genomic regions (the coding regions of which can be inferred and translated into amino acid sequences through knowledge of the genetic code), it is appropriate to review what we have learned so far about mechanisms and phylogenetic patterns of molecular evolution. This appears to have been a goal of Goodman in assembling this group of papers.

Six of the papers originated from a

1980 symposium. Goodman has added three more, providing a volume that selectively spans an admirable breadth of topics in molecular evolutionary biology. The papers have been revised to include references through 1981 and are thus reasonably up-to-date, a difficult task in this fast-paced field. Though the quality, scope, and intended audiences of the contributions vary considerably, the book is a useful summary of some of the important features of macromolecular evolution as revealed by the analysis of protein sequences. It also provides a gentle yet reasonably thorough introduction to new directions in molecular biology and evolution, particularly for evolutionary biologists relatively uninitiated in molecular biology. Molecular biologists might also glean some direction concerning interesting organisms, sequences, or gene families to investigate at the nucleotide sequence level.

The book begins with a chapter by Novacek that reviews anatomical and paleontological interpretations of the phylogeny of eutherian mammals. The phylogenies and dates of divergence proposed for eutherians form the basis of many of the later arguments concerning rates and patterns of molecular evolution. The next four papers focus on several families of proteins. Their structure-function relationships and patterns of phylogeny and evolution are revealed by comparisons of their amino acid sequences from a variety of organisms. Some authors focus on the phylogenetic relationships of the proteins themselves (as in Hunt and Dayhoff's analysis of chromosomal protein families). The implications of the patterns of protein phylogeny for the systematics of the organisms are also discussed (for example by Beintema and Lenstra with respect to ribonucleases, by De Jong with respect to eye lens proteins, and by Goodman *et al.* with respect to globins). Ironically, the instances where sequence and organism phylogenies disagree are the most enlightening. It is from these examples that we often discover significant yet previously overlooked evolutionary mechanisms (for example concerted evolution) and evidence of the frequency with which events such as gene duplication occur. Put in the context of the dates of divergence postulated by paleontologists, molecular phylogenies also provide a rich though potentially unreliable source of information on the frequencies and rates of various modes of sequence evolution. Individual proteins clearly cannot be counted on to provide accurate molecular clocks. In addition, what may be a reasonably accurate clock in

one group of taxa may be an inaccurate one, or tick at a different rate, in another group.

The difficulties and ambiguities revealed, more candidly by some authors than others, in attempts to infer distant phylogenetic relationships from protein sequences illustrate a common problem faced by paleontologists and molecular eutherian systematists. The radiations leading to the diverse array of extant mammals occurred over an interval of time that is short relative to that during which they have subsequently evolved. We need sequences that evolved rapidly enough for several substitutions to have occurred between speciation events in order to confidently delineate the branching order of the early mammalian orders over the period of radiation. Yet the rapid change characterizing such a sequence means that multiple (undetected) substitutions at the same site are likely to have occurred since the speciation events. With increased multiple substitutions, deducing the correct phylogeny becomes increasingly difficult, since many alternative phylogenies differ by only a small total number of substitutions. Compound these problems with the difficulties that the degeneracy of the genetic code presents for estimating extant, let alone ancestral, nucleotide sequences from amino acid sequences and there is little wonder so much controversy exists in this field.

Controversy also continues over the adequacy of various approaches for adjusting estimates of sequence divergence for undetected multiple substitutions that have occurred since the divergence of two homologous sequences. Two papers in this volume focus on portions of this controversy and discuss efforts to model the process of nucleotide and amino acid sequence evolution (Coates and Stone, Holmquist *et al.*). They discuss evidence for and the implications of significant nonrandomness in macromolecular evolution, including variable selective constraints on amino acid sequence and the nonuniformity of substitutional events. The extent to which natural selection exerts a driving relative to a restraining force in molecular evolution remains unresolved. However, the ability we now have to examine directly amino acid-changing versus silent nucleotide substitutions and those occurring in noncoding regions promises a rich source of potential clues.

Though simple and rapid DNA cloning and sequencing methods have technically replaced protein sequencing efforts, the protein is a phenotype that will never lose its significance. Rather than make

this realm of evolutionary biology obsolete, the results of direct analyses of nucleotide sequences (nicely reviewed in the final two chapters by Scott and Smith and by Hewett-Emmett *et al.*) are bringing a new level of precision to our understanding of the dynamic structure of the genome and of the processes and events that have resulted in the present diversity of proteins and other macromolecules. It is clear from this volume that comparative molecular studies will play an increasingly significant role, not only in systematics but in molecular and evolutionary biology as a tool for understanding the selective value, if any, of different patterns of nucleotide sequence organization and for understanding mechanisms of change.

CHARLES F. AQUADRO

Laboratory of Genetics, National Institute of Environmental Health Sciences, Research Triangle Park, North Carolina 27709

The Effectiveness of Threat

Detering the Drinking Driver. Legal Policy and Social Control. H. LAURENCE ROSS. Lexington (Heath), Lexington, Mass., 1982. xxviii, 132 pp. \$22.95.

In one form or another the idea that threatening or imposing punishment will inhibit illegal or otherwise undesirable behavior has been embraced by most people in most societies for a long time, and it has found particular expression in modern legal codes. But only within the past 15 or 20 years have serious and concerted efforts been made to test the idea of deterrence scientifically. As a result of these efforts a huge body of evidence involving a variety of threats and punishments, kinds of offenses, types of data, and diverse contexts has already accumulated. It is difficult to draw meaningful conclusions from this mass of work, partly because the research has highlighted methodological barriers preventing confident inference, and partly because of the increasingly recognized complexity of the problem. Most scholars now acknowledge that deterrence is probably a highly contingent phenomenon. Whether it operates or not depends on many variables, one of the more important of which is the kind of offense in question.

The prime virtue of Ross's work is that he focuses on one specific offense and attempts to assemble, synthesize, and interpret the evidence without trying to draw conclusions about deterrence gen-

erally. The focus is specifically upon the effect of legal threats designed to deter drunken driving. Since the overwhelming bulk of evidence concerning this issue derives from investigation of the impact of actual changes in drunk driving laws or in enforcement practices, most of the book describes and interprets interrupted-time-series studies of the effect of modifications of drunk driving laws or their enforcement around the world over the past 50 years. The interrupted-time-series method involves analysis of trends in a dependent variable tracked over a long period of time (so as to take into account seasonal variations) in comparison to the period immediately following the implementation of some discrete change in the independent variable.

Ross concludes that increases in the potency of legal threat, particularly enhancement of the perceived certainty of apprehension among the population, does produce a significant decline in drunk driving, but that such effects are temporary. He suggests that this evanescence is due to the erosion after a short time of perceived certainty of punishment, since efforts at enforcement can rarely achieve or maintain the level that is initially assumed or mandated.

In surveying the evidence, Ross nicely lays out the importance of studying drunk driving and efforts to control it. The offense not only produces monumental social costs, therefore being of wide practical import, but it lends itself especially well to investigation of the deterrence question. Drunken driving happens to be an offense that generally lacks moral prohibition, so that its control falls almost exclusively upon the threat of sanction; there are many instances of naturally occurring discrete changes in legislation or enforcement efforts that can be monitored for effect; it involves outcome measures that are precise, reasonably valid, independent of law enforcement efforts, and routinely collected and usually available over considerable periods of time (such as blood alcohol content of drivers involved in crashes and the relative rates of single-vehicle and multiple-vehicle crashes during various hours of the day and days of the week), and it concerns real behavior rather than that which might be generated in laboratory experiments or reported upon in surveys. Nevertheless Ross carefully points out the problems in drawing strong conclusions about drunk driving and deterrence, focusing systematically upon various possible methodologies and their weaknesses. Although he favors the interrupted-time-series design (which conveniently happens to be