structed changes in other states' figures, a simple drop in a state's population can never raise its apportionment under a nonmonotonic method like Hamilton's.) Apart from the preposterousness of such subterfuges, it is not obvious in the Table 1 examples that state 4's apportionment and population at t (say, 1970) should have a necessary bearing on its apportionment and population at $t + 1$ (1980) if this means shortchanging state 1 at $t + 1$ for ten years (until 1990) by giving it less than its quota rounded down.

In support of the Webster method, both theoretical reasoning and Monte Carlo simulations show it to be uniquely free of bias against small or large states and much less liable to violate quota than any other methods that satisfy population monotonicity. Since the Hamilton method is also unbiased if this criterion is modified to take account of the minimum requirement of at least one representative per state, the question turns on whether satisfying population monotonicity (Webster) should weigh more heavily than guaranteeing quota (Hamilton), especially given that quota violations seem rare under the Webster method.

Fair Representation is an important book in two respects. First, it should spark an informed debate about reform of the current apportionment system. The authors present cogent reasons for reform in a style that is both lucid and entertaining. Moreover, their arguments can be followed by nonmathematicians since the technical details, including proofs, are confined to an appendix (pp. 95–156). The potential political impact of the book is emphasized in its promotion, which claims that unless the current apportionment method is changed "an excessive number of seats may be shifted from predominantly Democratic states in the Northeast and Midwest to rural, largely Republican ones in the South and West" (jacket cover). The actual effect of reform would be less dramatic. If Webster were substituted for the current method, it would, on the basis of the 1980 census, which was not complete as this book went to press, shift exactly one seat from New Mexico to Indiana. Not surprisingly, the Indiana House delegation is sponsoring a reform bill.

Second, and perhaps more important, Balinski and Young's book is a model of the kind of insight that formal analysis can bring to a problem like the apportionment problem. Its major contribution is to clarify the principles of fair representation and show the fundamental logical conflict among several of these principles. Because, as a result of this conflict, there can be no perfect method of apportionment, the controversy over methods will probably continue. This book sets the logical context for that debate.

STEVEN J. BRAMS
Department of Politics, New York University, New York 10003
PHILIP D. STRAFFIN, JR.
Department of Mathematics, Beloit College, Beloit, Wisconsin 53511

Evolution from the Molecular Viewpoint

Genome Evolution. Papers from a symposium, Cambridge, England. G. A. DOVER and R. B. FLAVELL, Eds. Published for the Systematics Association by Academic Press, New York, 1982. xvi, 382 pp., illus. Cloth, $33.50; paper, $17.50. Special Volume no. 20.

Evolution and Development. Papers from a workshop, Berlin, May 1981. J. T. BONNER, Ed. Springer-Verlag, New York, 1982. x, 358 pp., illus. $22. Dahlem Workshop Reports. Life Sciences Research Report 22.

These books represent the latest in the relentless surge of molecular biology's incorporation of evolution into its mechanistic world. They specifically focus on the continuing and growing quest for a material basis for genomic organization and genomic change, both in the development of individuals and in the origin of species.

The volumes contain 34 papers written by 92 authors (three appearing in both volumes). The papers in *Genome Evolution* are arranged in five parts: on models of genomic evolution (seven papers), on evolution of gene families (five), on nuclear organization and DNA content (three), on genome evolution and species separation (three), and a concluding overview. The great majority of the 48 authors work in laboratories of molecular biology or genetics. The papers in *Evolution and Development* are arranged according to level: molecular (two papers), cellular (five), life cycle (two), and evolution (two). There are in addition four Group Reports, one for each level. Of the 47 authors who contributed to this volume, molecular biologists and geneticists constitute about 40 percent, with more traditional developmental biologists also strongly represented and the remainder being morphologists or paleontologists.

The chapters in part 1 of *Genome Evolution* can be grouped into those that focus largely on processes (DNA transposition by Finnegan *et al.*; gene amplification by Bostock and Tyler-Smith) and those that focus largely on products (transposable elements by W. F. Doolittle; highly repeated DNA's by Miklos, by Roizès and Pagès, and by Jones and Singh; moderately repeated DNA's by Gillespie *et al.*). Doolittle returns to the notion of selfish DNA, which at the DNA sequence level can be considered a selectionist explanation for the occurrence of transposable elements. At the level of the individual organism, little if any evidence exists for the role of transposition as a normal feature in development (Finnegan *et al.*). In whole populations, however, two results of transposition are identifiable, but, as Doolittle argues, it is not yet clear whether these are more than the incidental effects of evolution at the DNA sequence level. One result is the generation of mutant phenotypes. Indeed, at least in *Drosophila*, many if not most one-time "point mutations" are actually the insertion (or deletion) of a few to several kilobases of DNA, indirectly or directly caused by transposable elements. A second plausible result of transposition is the generation of families of middle repetitive DNA. Sequence similarity in a family of repeats is possibly aided by unequal sister strand exchange, or, as Roizès and Pagès emphasize, by mismatch repair followed by replication of the converted sequence after strand transfer (that is, gene conversion). Britten (in a broad-ranging essay in *Evolution and Development*) estimates for vertebrates a change of mobile repetitive elements equivalent to the loss or gain of 60 kilobases per genome in 10^4 years. The time scale could even be shorter. Accordingly the development of families of middle repetitive DNA must serve as the major mechanism of quantitative genomic change over time scales of interest in the process of speciation (10^3 to 10^5 years).

Over the shorter, developmental time, gene amplification may be a significant mechanism of genome alteration (Bostock and Tyler-Smith). But the connection between laboratory work on methotrexate-resistant cells and natural situations involving, for example, insect predation on plants exuding poisonous compounds has yet to be made, even though the amplification that occurs in response to insecticide application provides an analogue.

The five chapters of part 2 include progress reports on the evolution of globin genes (Jeffreys), actin genes (Davidson *et al.*), and antibody genes (Zachau

et al. and Rabbitts *et al.*) and a concluding chapter on polyploid organisms (Leipoldt and Schmidtke), which boldly asserts, "Since, clearly, most eukaryotic organisms are diploid, but because circumstantial evidence suggests that all organisms have experienced one or more rounds of polyploidization in their phylogenetic past, it can be said that probably all eukaryotes are diploidized polyploids."

In globins, replacement sites may diverge at a rate of 0.1 percent per 10^6 years, intergenic regions at a rate of 0.2 percent per 10^6 years, silent sites at a rate of about 1 percent per 10^6 years, and pseudogenes at yet a higher rate. Globin data also excellently illustrate the problem of determining what most DNA is doing. Only about 16 percent of the DNA in globin clusters is reported to occur in precursor messenger RNA (and half of this DNA is spliced out in the mature mRNA), leaving 84 percent of the DNA in the cluster with function unknown. Globins also provide a possible case of a processed gene ("retrogene") as well as a possible case of lateral gene transfer to legumes. Perhaps for reasons of space, Jeffreys in his very nice summary of the globin microcosm uses a sort of shorthand that is misleading when he writes that "birds and mammals diverged about 270 million years ago." In fact, the oldest mammals date from about 210 million years ago and the oldest birds from about 140 million years ago; what Jeffreys means is that the split among the reptilian stocks that subsequently led on one branch to mammals and on another to birds was about 270 million years ago (technically, 320 is more likely). It would be clearer and most accurate to say that birds and mammals last shared a common ancestor 320 million years ago.

The positions of intervening sequences are partially different in actins of different phyla (Davidson *et al.* in *Genome Evolution*), and this leads to the view that the placement of intervening sequences may be of prime phylogenetic use at the level of phylum or higher (Davidson in *Evolution and Development*). Also of interest is the observation that the rate of change is different for coding sequences, 3′ untranslated regions, and intervening sequences, thus providing three potential evolutionary clocks capable of measuring events at different degrees of relationship, but still within one gene family. Actin is much more widely distributed among the 30 or so animal phyla than is hemoglobin, and if for no other reason the study of actin in due course may provide the first DNA-based phylogeny of the animal kingdom.

Part 3 includes what was for me the most stimulating paper in these two books, a presentation by Bennett of a predictive model of chromosomal order within the cell. If he is correct, chromosome alignment in the haploid genome is determined primarily by similarity in the length of the arms. The promise of this simple model is that, for example, it would allow one to understand the order in which genes may transfer from one chromosome to the next by reference to the proximity of arm positions. Bennett's model deserves to be widely tested. The second paper in part 3 is on the intriguing possible structural role of intercalary repetitive DNA's in determining the positional order of interphase chromosomes (Manuelidis).

The issue of genome evolution as related to species separation, the subject of part 4, provided the chief motivation for the organizers for the meeting. Thus this topic is discussed by both conveners. Flavell's paper utilizes data from cereals, and Dover's is based on information from *Drosophila*. There is a third paper in part 4, by MacGregor, who correlates genome size in amphibians (over a range of 1 to 90 picograms!) with chromosome size and speciation. And Gillespie *et al.* in part 1 present a model of "genome resetting" based on newly amplified repeated DNA. From data presented in these and other papers one can comprehend how genomic differences in amount or type of DNA probably arose in different local populations of a species and thus how geographic differentiation in genome size and composition came about. The crunch comes in relating that observation, via data on chromosome pairing, differences in duration of cell cycle, or another factor, to a significant tendency toward reproductive isolation, a difficulty Rees *et al.* and Miklos forcefully point out. Rees *et al.* (in part 3) state, "Large-scale variation in DNA amount has astonishingly little effect on many aspects of growth and development of the phenotype." And Miklos (in part 1), although supporting the role of highly repeated DNA's in genetic variation, does not find a connection with speciation, and indeed very strongly supports "a plurality of causes for speciation events."

The basic idea that genomic differences in DNA in geographically differentiated populations *ought* to result in reproductive incompatibility, and hence be the basis for speciation, has occurred independently to many authors over the past decade (for example, Yunis and Yasmineh; Corneo; Hatch; Fry and Salser; Craig; Brutlag; Gall and Atherton). Only recently has the process been christened with such names as "molecular drive" and "genome resetting" leading to "accidental speciation." In any event, until a connection with incipient reproductive isolation is mechanistically accounted for, through data on genome organization or sequence specificity or some other genomic feature, the clearly plausible notion of a simple genomically controlled mechanism for spewing out species upon species must remain conjectural. And correlations between satellite DNA, middle repetitive families, or other aspects of the genome and species differentiation will remain simply correlations. However, if a causal connection can be made, then in one step most of the characteristics that morphologists, behaviorists, and others study as isolating mechanisms may come to be seen simply as after the fact—interesting in their own right, but not of fundamental importance in the vast majority of cases of speciation. This is the challenge that molecular biology is bringing to the study of the origin of species. Behaviorists and morphologists may have nothing to fear, however, if Maynard Smith's understanding is correct. In his concluding overview he writes, "There are numerous cases in which two related species of animals are isolated by behavioral differences in courtship but, if interspecific mating is brought about in captivity, the resulting hybrids are perfectly fertile. This commonly happens, for example, in birds, grasshoppers and *Drosophila*. This illustrates the point that, although at the molecular level a single process often turns out to have a single cause, unitary explanations are less commonly true at the organismic level. There are general principles in evolutionary biology, notably the principle of natural selection, but the details of the process are irreducibly complex."

Maynard Smith also states, correctly I feel, that with regard to genome evolution "we are still in the stage of trying to ask sensible questions." As the "null hypothesis" on the relation between the structure of the genome and organism development, he suggests, "There is no structure on a scale larger than the gene family . . . that is developmentally relevant." The alternative position, which he labels "neo-Goldschmidtian," is that "significant morphological evolution requires genomic reorganization, and morphological conservatism will be accompanied by conservation of the genome."

In one way or another the assessment of the null hypothesis is the major focus of argument in most of the papers of *Evolution and Development*. By its in-

tention as a Dahlem workshop, this book is much more speculative than is *Genome Evolution*. At the molecular level are papers by Britten on genomic alterations and by Davidson on genomic regulatory organization, both referred to above. At the cellular level there are contributions by Wessels on the description of processes of metazoan morphogenesis; Freeman on comparative development of embryos, with an additional call for "judicious use of appropriate molecular chronometers" as the "only approach" capable of resolving phylum-phylum phylogenetic relationships; Wolpert on pattern formation; Kaufman and Wakimoto on the larger significance of homeotic and segment patterning loci; and Katz on the as yet rather poorly known "ontogenetic buffer mechanisms." A recurring theme of these four papers at the cellular level (and in the Group Report) is the need in attributing meaning to a pattern (or morphology) to differentiate the specific function of some process from incidental side effects of that process, whose "real" function is quite different, and from mere historical remnants. This problem of sorting out ultimate cause from proximal effect is also raised in the two papers at the level of the life cycle. Thus Stearns discusses life histories and asks, "How much of any particular plastic response in a life history trait has evolved, and how much is inevitable?," and Bonner and Horn in their essay on size, shape, and developmental timing confront the same issue of partitioning out incidental effects. Finally, at the level of evolution, Alberch and Gould respectively focus on developmental constraints in evolutionary processes and on the role of developmental timing in macroevolution.

In comparing these two books with regard to ease of use, one notes that Dover and Flavell write in their introduction that "we have not exercised editorial control over [the] contributions." Nor has an index been provided. The papers also lack abstracts, and titles of articles are not included in the references. The Dahlem volume has an index, its references include titles, and seven of its papers have abstracts. *Evolution and Development* has the spark of disciplined originality. The subject matter of *Genome Evolution* is equally fascinating, but the topic deserves a presentation more attentive to the needs of the reader. Together, the two books would make a superb basis for a seminar on evolution.

THOMAS J. M. SCHOPF
Committee on Evolutionary Biology, University of Chicago, Chicago, Illinois 60637

Plasma Physics

Plasma Physics and Nuclear Fusion Research. RICHARD D. GILL, Ed. Academic Press, New York, 1981. xx, 688 pp., illus. $66.50.

The Culham Summer School on Plasma Physics has been held annually for 17 years and is recognized as having provided an excellent introduction to the field for many. This collection, which is based on lectures delivered in the course between 1978 and 1980, should be well received. Although one of the standard textbooks would be better for an introductory course, the book should interest anyone entering or wishing to get an overview of the field. I was pleased to see that on some subjects it is already slightly dated.

The authors have achieved their goal of providing a high-level introduction to a capable student who has little or no background in plasma physics. An attempt is made to treat simple models with enough detail and rigor to impart an understanding of the problems and techniques of each field, and the authors have provided a broad understanding of the organization of each and of what is being accomplished in it. Some of the chapters contain considerable detail and could serve as useful references. The cross-referencing in the early part of the book is well done, but more effort could have been expended in other places. There are many typographical errors throughout the book. They cause no problem but are annoying.

The first three sections of the book provide an introduction and foundation and cover theoretical developments. The first paper, by B. J. Green, is an excellent overview of the field. The next two sections cover experimental devices and heating and diagnostics. Though the discussions of tokamaks, pinches, stellarators, and mirrors in the section on experimental devices are clear and accurate, they are something of a disappointment. The authors of the five papers in the section were too careful in their efforts to delineate the problems and fail to convey the sense of accomplishment and optimism that now exists. The high temperatures achieved on the Princeton Large Torus in 1978 are reported almost in passing. Similar results with higher densities have since been obtained on the Poloidal Divertor Experiment. Recent developments have also introduced new enthusiasm into the program. These include the confinement of a 350 eV plasma for 10 msec in the ZT-40 reversed-field pinch, the achievement of current-free stellarator plasmas with 700 eV temperature, 10^{14} cm^{-3} density, and 35 msec confinement time with neutral injection on Wendelstein VII-A and 200 eV temperature, 5×10^{12} cm^{-3} density, and 40 msec confinement time with electron cyclotron resonance heating on Heliotron E, and the conception of a thermal barrier for the tandem mirror.

The final section covers inertial confinement, charged-particle beams, astrophysical plasmas, and computational plasma physics. The editor has limited the amount of material on these subjects, and though he was correct in doing so it makes one hunger for more.

JOHN L. JOHNSON*
Westinghouse Research and Development Center, Pittsburgh, Pennsylvania 15235

*Present address: Plasma Physics Laboratory, Princeton University, Princeton, New Jersey 08544.

Processes of Cell Division

Mitosis/Cytokinesis. ARTHUR M. ZIMMERMAN and ARTHUR FORER, Eds. Academic Press, New York, 1981. xvi, 482 pp., illus. $55. Cell Biology.

The eukaryotic cell cycle culminates in a radical reordering of cellular contents. The restructured cytoskeleton and condensed chromosomes then follow an ancient choreography that is designed to ensure the precisely equal segregation of genetic information into the forming daughter cells. Because of the importance and the scale of these events in the cell, the subject of mitotic mechanism has captured the imagination of cell biologists since the 19th century. A great deal is known about the basic processes of mitosis and cytokinesis, but some fundamental questions remain unanswered and there is controversy about the nature of the mechanism of mitosis. In this collection, one will find described a wealth of experimental approaches and a wealth of results. Firm conclusions are harder to pin down.

The pace of research in this field is quickening. Many important and, one hopes, conclusive results have recently been published. Thus, some of the arguments of authors in this volume must now be tempered by more recent evidence, particularly with respect to the involvement of actin in the mitotic spindle and to the orientation of spindle microtubules. Nevertheless, the book is timely and broadly representative of the more established research approaches. It serves a valuable purpose in bringing