The Apportionment Problem

Fair Representation. Meeting the Ideal of One Man, One Vote. MICHEL L. BALINSKI and H. PEYTON YOUNG. Yale University Press, New Haven, Conn., 1982. xii, 192 pp. $27.50.

This is a tour de force of mathematical analysis applied to an interesting, if somewhat technical, political problem: how to assign seats to states in the U.S. House of Representatives to conform with the constitutional edict that "representatives shall be apportioned . . . according to [the states'] respective numbers" (article I, section 2, of the U.S. Constitution). The same problem arises in apportioning parliamentary seats to political parties in proportion to their popular vote, or instructors to university departments in proportion to departmental enrollments. Balinski and Young not only develop a mathematical theory of apportionment but also skillfully weave constitutional history, congressional debates, and political philosophy into their discussion.

The apportionment problem arises from the fact that, unlike taxes, which the Constitution also prescribes must be equitably apportioned among the states, representatives cannot be fractionalized to yield a perfect alignment of state populations and state representation. Integer assignments are further complicated by the constitutional stipulation that each state is entitled to at least one representative.

How to handle the fractions fairly has been a subject of major disagreement, with different solutions proposed by, among others, Alexander Hamilton, Thomas Jefferson, and Daniel Webster. George Washington favored Secretary of State Jefferson's method over Treasury Secretary Hamilton's, casting the first presidential veto against the latter's bill in 1792. Webster's method—the one Balinski and Young advocate—was adopted following the 1840 census, after which a switch was made to the Hamilton method; the Webster method was resurrected after the 1900 census, and still another method is used today.

Hamilton's method is the simplest conceptually. One first computes the exact number of seats, fractions included, to which each state is entitled. This is called the state's quota. Next, one assigns to each state the integer part of its quota. Seats that are left over are then assigned to states whose quotas have the largest fractional parts. Thus, for the hypothetical House with 7 seats shown in Table 1, state 1 gets 5 seats at time $t + 1$, and the remaining 2 seats go to states 2 and 3, which have the two largest fractional parts in their quota.

In contrast to the Hamilton method, the Webster method focuses on the population of a representative's district. The goal is to choose the size so that the number of seats to which each state is entitled, when rounded to the nearest integer, sums to the House size. Thus, in the example in Table 1 at $t + 1$, if we set the district size at 170, states 1 through 4 will be entitled to 4.424, 0.594, 0.582, and 0.576 seats, respectively. These figures, which round to 4, 1, 1, and 1, respectively, sum to the desired House size of 7. Jefferson's method, and a method championed by the mathematician E. V. Huntington that is in use today, are based on the same idea but differ in how they do the rounding, with the former tending to favor larger states, the latter smaller states.

Reasonable as these apportionment methods may seem, they can produce anomalous results, as illustrated by the apportionments in Table 1 at the two different times t and $t + 1$:

1) The Webster method violates quota. If a state's quota is 5.013 (state 1 at $t + 1$), it seems sensible that an apportionment method should give it either this number rounded down or rounded up (5 or 6 seats); yet Webster at $t + 1$ gives state 1 only 4 seats.

2) The Hamilton method violates population monotonicity. Between t and $t + 1$, state 4's population increases by 27 percent (from 77 to 98) but it loses a seat, whereas state 1, whose population increases by only 26 percent (from 598 to 752), gains a seat.

The Hamilton method is also subject to other difficulties, such as the "Alabama paradox," whereby increasing the House size can decrease the representation of some states. Alabama was threatened with such a decrease after the 1880 census, but this seems not a problem today because, since 1912, the House size has remained fixed at 435 members (except for a temporary increase to 437 when Alaska and Hawaii were admitted as states in 1959).

Can we find apportionment methods that do not behave in these paradoxical ways? Balinski and Young, in a theorem of signal importance, prove that the answer is no: there can be no apportionment method that both always satisfies quota and is monotonic in population. In fact, the general argument is already implicit in the examples in Table 1. The only apportionments that satisfy quota and do not give larger states fewer seats than smaller states are (4,2,0,1), (4,1,1,1), and (3,2,1,1) at t and (5,1,1,0) and (6,1,0,0) at $t + 1$. If we are to satisfy quota, state 4 must lose its seat at $t + 1$.

Having proven this elegant impossibility theorem, the authors opt for the population-monotonicity condition over the quota condition, strongly arguing for Webster as the preferred apportionment method. It is at this point that some readers may balk. Violations of quota are salient and could be politically disturbing. By comparison, population monotonicity, as formulated by Balinski and Young, is quite subtle. It is, for instance, highly misleading to claim that under a method that does not satisfy this kind of population-apportionment consistency over time "a state could deliberately undercount its population or encourage emigration to obtain an increase in its representation" (p. 68). Not only would the state have to fabricate new lower figures for itself, it would have to arrange for crucial miscounts in other states as well. (Without carefully con-

Table 1. Apportionments of Webster and Hamilton methods.

State	t				$t + 1$			
	Population	Quota	Webster	Hamilton	Population	Quota	Webster	Hamilton
1	598	3.987	4	4	752	5.013	4	5
2	299	1.993	2	2	101	0.673	1	1
3	76	0.507	0	0	99	0.660	1	1
4	77	0.513	1	1	98	0.653	1	0
Total	1050	7.000	7	7	1050	7.000	7	7

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.

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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