scheme the concept of empty three-dimensional space is anomalous because it supposes attributes such as three-dimensionality where there is nothing that has these attributes.

In the late 13th and 14th centuries, it became common to suppose that God might have created another cosmos outside of this one. Had he done so, he would be present there just as he is omnipresent in this cosmos. But he would not *move* there, since he is immutable, so he must already be in every place or space in which he might have created something. It was concluded, therefore, that God is now present outside the cosmos.

Does this imply that there is now infinite space outside the cosmos as the Stoics asserted? It is at this point that scholastic discussions of extracosmic void space become most fascinating by virtue of the intermingling of scientific, logical, and theological reasoning. According to the Aristotelian viewpoint, there will be no extension outside the cosmos unless there is substance there. This follows simply because everything that exists must be a substance or an attribute of a substance and more particularly because extension must be the extension of something. Sometimes the argument appears that for empty space to be extended there must at the very least be a sort of material scaffolding alongside it to provide it with a measure (see p. 124).

Does God's presence outside the cosmos provide a basis for extension there? Might extension be an attribute of God? This seemingly easy solution was generally blocked by the theological doctrines that had been developed to explain God's omnipresence. Although God is present everywhere, it was argued, he is not extended in space in the sense that one part of him is in one place and another part in another place. This would conflict with the Christian understanding of the nature of God. Rather God is totally present in every part of space. If this is so, although God is everywhere, he is not extended, so extension cannot be his attribute. If extracosmic extension is not God's attribute, could it be ascribed to some other entity? No: even if the requirements of strict Aristotelianism are relaxed to suppose that extracosmic space is an independent nonmaterial extended entity, theology bars the door to this solution by declaring that there can be no infinite eternal entity other than God.

Medieval scholastics, then, modified the Aristotelian view by postulating the existence of God and space outside the cosmos, but this did not lead to a concept of extended space outside the cosmos because of the combined requirements of Aristotelianism and scholastic theology. As God's attribute, extracosmic space was infinite but nonextended. The story of how this theoretical bind was eluded or sidestepped to postulate the existence of infinite extended space forms the core of the second and most important section of Grant's book. (The other major section deals with the possibility of empty space within the cosmos.) Almost every possible way out was tried. Grant believes that Henry More and Isaac Newton made three-dimensional space God's attribute and simply accepted the conclusion that God is an extended being. J. E. McGuire, however, has argued that even Newton still accepted the medieval whole-in-every-part view of God's omnipresence (see p. 253 and note 420). For the light it might cast on this problem more attention should be paid to the medieval doctrine that spiritual beings are present in space through their activity, the more powerful being having a larger sphere of activity.

Clearly there is ample material here for still further studies both of the background of Newton's concept of absolute space and with regard to understanding the dynamics of scientific change. Without doubt, in the 16th and 17th centuries metaphysical and theological considerations played an essential role even within nonscholastic physics.

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Gene Duplication

Evolution and Variation of Multigene Families. TOMOKO OHTA. Springer-Verlag, New York, 1980. viii, 132 pp., illus. Paper, $9.80. Lecture Notes in Biomathematics, vol. 37.

Much of the excitement in genetics lately comes from the discovery that a large and important part of eukaryotic genomes is made up of families of homologous genes. This finding opens up an array of new questions in population and quantitative genetics as well as evolutionary theory. In a series of papers Ohta has analyzed several specific problems related to multigene families. In this book she provides a compilation of these papers, with the exception of some of her most recent ones. Some previously unpublished results are also included. The compilation will be useful because it presents the results in a logical order and with a consistent algebraic notation.

Despite the overly general title this is not meant to present a general theory of multigene families, but only a treatment of certain problems. The word "evolution" in the title could have been replaced by "neutral evolution" for most of the work. Such topics as the coexistence of functional and nonfunctional genes in the same family are not considered. The number of genes per family is assumed to be fixed, so that the many important questions dealing with the evolution of multiplicity itself are bypassed. The term "multigene families" is also very narrowly defined to mean genes of high multiplicity arranged in direct, tandem repeats. The prevailing view now is that multigene families of low multiplicity (2 to 10 copies) are much more typical, and many of these are widely dispersed throughout the genome rather than tandemly repeated. Moreover, movable genetic elements have been discovered in several organisms and can occupy as much as 10 to 20 percent of the euchromatic genome. The existence of such elements poses the intriguing possibility that action at the molecular level can be separate from, and even opposed to, selection at the organismal level. No precise theory exists for handling these and many other questions related to multigene families.

The scope of the book can be summarized as follows: Consider a very long sequence of tandemly repeated genes undergoing selectively neutral mutations at a constant rate. Each new mutation is assumed to be unique, thus increasing variability in the sequence. Meanwhile, unequal crossovers between homologous regions shifted by one or more positions tend to decrease variability by creating duplications and deletions. Ohta examines the properties of the equilibrium at which these opposing forces are balanced and presents a description in terms of identity coefficients, correlations between loci, and so on. She then compares this description to existing data on amino acid sequences of immunoglobulins to argue that, with appropriate choice of model parameters, they agree. She also uses this approach to compare opposing mutational hypotheses (somatic versus germ line) for the origin of hypervariable regions. By examining within- and between-species variability, she shows that the data fit her model better under the germ-line hypothesis.

A consistent mathematical strategy is employed throughout the book. We start by defining some variable or set of variables of interest such as the probability of identity between two genes or measures of linkage disequilibrium. These variables can change each generation by a series of steps including mutation, random drift, and intra- and inter-chromosomal crossing-over in that order. After each step the expectations of the variables are written in terms of their values after the previous step. By algebraically combining these equations, we find an approximation (it can no longer be called an expectation) of the change from one generation to the next, from which equilibrium values can be obtained. There is no attempt, except by computer simulations in some cases, to determine the stability or uniqueness of these equilibria or the rate at which they are approached. The number of repeats per chromosome is assumed to be constant, so that each unequal crossover that produces a duplication of one gene must be immediately followed by a deletion of one gene. Unequal crossovers where the two chromosomes are m genes out of register is assumed to be equivalent to m unit cycles as above. The complexity of the theory necessitates these simplifying assumptions.

I had some difficulty with the terminology and definitions and had to rely on the diagrams and equations to determine the meaning of some terms. Thus "family" refers to those related genes on one particular chromosome, with "chromosome" and "family" used interchangeably. The word "lineage" refers to a particular allele. Thus, paradoxically, a gene becomes a different lineage from its ancestors when a mutation occurs. A "family type" identifies a particular group of lineages. Potentially more serious is the ambiguous definition of the fundamental variable, $x_{i,k}$, used throughout the book. In the original paper, this variable was defined as the frequency of the kth lineage in the ith chromosome. However, chromosome labels are ambiguous when crossovers between homologues are considered. Therefore, $x_{i,k}$ has now been redefined (p. 23) as the frequency of the kth lineage in the ith family type. As such, $x_{i,k}$ must be constant through time; only the frequencies of the family types (p_i) are variable. Yet throughout the book $x_{i,k}$ is treated as a variable with quantities such as "$\Delta x_{i,k}$" and the variance of $x_{i,k}$ taking nonzero values. The meaning of this enigmatic variable must be clarified before the theory can be understood.

Finally, it is necessary to ask whether it is advisable to use population genetics as a means of drawing inferences concerning genetic mechanisms, as Ohta does here in comparing the somatic and germ-line hypotheses for immunoglobulins. In most cases, the uncertainties involved in population genetic modeling are so great that it is more efficient to learn the genetic mechanism by other means and then use this information in drawing inferences concerning population genetics. There is also a much broader question along these lines. At what point is our understanding of a given biological situation sufficiently deep to justify the development of such an intricate mathematical theory? This question constantly plagues molecular population geneticists, and it is especially troublesome here with new discoveries concerning multigene families being developed at a breathtaking pace. Theoretical work in this area might be more useful after the experimental facts are better understood.

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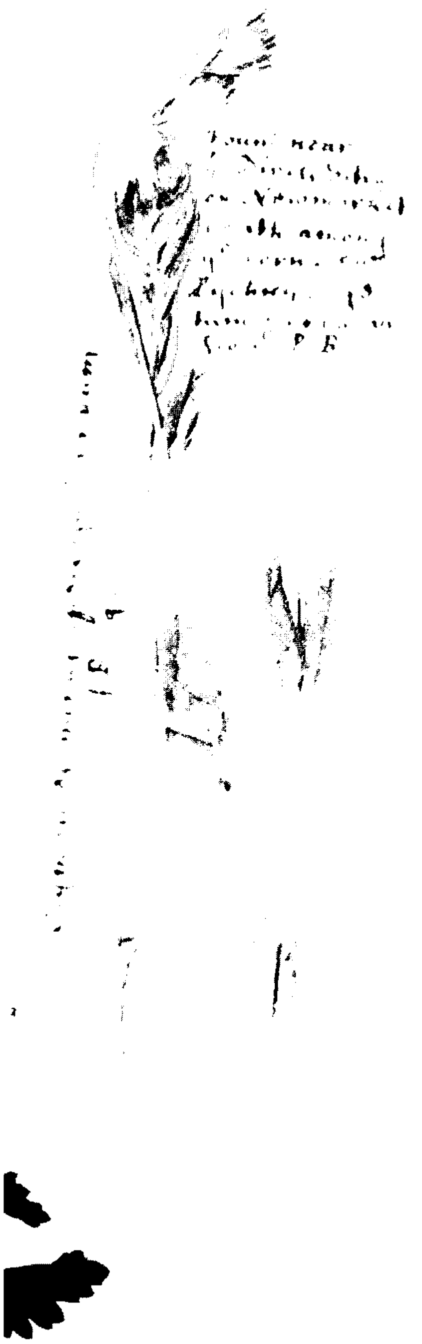
A Botanical Garden

The Shaping of Cambridge Botany. A Short History of Whole-Plant Botany in Cambridge from the Time of Ray into the Present Century. S. M. WALTERS. Cambridge University Press, New York, 1981. xvi, 122 pp., illus. $42.50.

Advice to weary travelers: seek out botanical gardens. They are quiet, beautiful, instructive—and they usually have benches. It is a pity that they so often lack guidebooks. The plants are labeled, but visitors are hard put to find out much about a garden's history or the contributions to science made there. Cambridge University's Botanic Garden is now a happy exception.

Cambridge was late in establishing a botanical garden, though not for want of people willing to try. Most European universities of any note had set up gardens (as part of humanist-inspired reforms of medical teaching) between the mid-16th and mid-17th century; Oxford started its garden in 1621. The first attempt at Cambridge came in 1588 when the herbalist John Gerard recommended himself to the university as a suitable person "for planting of gardens." A century later, the great botanist John Ray lamented the lack of a botanical garden at Cambridge; had he not been forced to leave the university (on religious and political grounds), it is likely that he would have tried to set one up to complement his researches in the fields and gardens around Cambridge. In the 1690's, just when Stephen Hales was pursuing his experiments in plant physiology at Corpus Christi, the university drew up plans for a physic garden, but nothing came of the idea. Three decades later, Richard Bradley sought the new post of professor of botany with the aim of establishing a garden where he would



"Specimen of the cornfield weed *Silene gallica*, found near the Devil's Dyke, the only Cambridgeshire specimen known in Ray's own Herbarium." [From *The Shaping of Cambridge Botany*]