Book Reviews

Ohta, T.: Evolution and Variation of Multigene Families. Lecture Notes in Biomathematics, Vol. 37, 131 pp., 25 figs., 14 tabs. Berlin, Heidelberg, New York: Springer 1980. Soft bound $ 11.50.

Molecular biologists are studying many genes that have a more complex structure or organization than the genes usually modeled by population geneticists. Many important genes, such as those for immunoglobulins and transfer RNA, occur in multigene families, sets of closely linked repeated genes with homologous nucleotide sequences. The evolution of multigene families is affected by forces that influence the evolution of all genes, such as recombination and genetic drift, and by forces that result from the sequence homology of repeated genes, such as unequal crossing-over. In this book Ohta uses the tools of theoretical population genetics to study how these kinds of forces influence the evolution of multigene families.

One of the book's main subjects is the sequence heterogeneity among the genes in a multigene family. For a single chromosome line, Ohta analyzes how genetic drift and intrachromosomal unequal crossing-over at mitosis result in homogeneity of the genes in a family. In organisms with sexual reproduction, descriptions of single chromosome lines are not sufficient for the description of evolution in a multigene family. In the rest of the models Ohta includes the effects of gene exchange between individuals in a population. The diversity in a multigene family is analyzed at three levels: genes on the same chromosome, genes on different chromosomes in a population, and genes on chromosomes in separate populations. The other main subject of the book is the nonrandom associations between members of a multigene family. Ohta analyzes how the correlation between genes declines as their positions become farther apart, both for genes on the same and on different chromosomes. Taking the level of analysis a step down, she studies the associations between amino acid sites in the genes of a family.

The models include mutation, intrachromosomal unequal crossing-over, interchromosomal equal and unequal crossing-over, the number of genes in a family, population size, and genetic drift. Extensions of the neutral theory of population genetics, the models predict how these forces influence the means and variances of variables describing the heterogeneity and associations of genes in a family. In addition, some models with selection on gene diversity are partly analyzed.

The models apply to multigene families such as the immunoglobulins, satellite DNA's, ribosomal RNA's, transfer RNA's, histones, and ones as small as the hemoglobins. The first chapter defines multigene families and discusses their organization and variability, going into detail about I_gG immunoglobulins. The kinds of information that can be gained from using the models are illustrated throughout the book, but the potential applications go beyond the examples. The analysis of associations between amino acid sites, for instance, could equally well be applied to nucleotide sites. Immunoglobulins are used as examples, but one's favorite multigene family could also be studied this way.

The models can help to distinguish between alternative explanations. To study the origin of antibody diversity, Ohta constructs models for both the germ line theory and the somatic mutation theory. Data on immunoglobulin κ, λ, and heavy chain hypervariable and framework regions turn out to agree with the predictions of the germ line theory models. When studying separate populations that originally were one, Ohta finds that the rate of differentiation of an initially uniform gene family has a large variance. Just by chance, the rates of evolution may be quite different in various populations, even though they have the same parameters. For example, the rates of differentiation of α satellite DNA differ among some rodent species. This result is not surprising because of the high variance of the process; there is no need to invoke an adaptive explanation. By predicting the amount of variation expected from random causes, the models provide null hypotheses that should be rejected before non-random hypotheses can be accepted.

Ohta clearly states the assumptions of each model and also discusses the effects of deviations from some assumptions. The analyses are mostly done using difference equations and diffusion approximations. Less mathematically inclined readers may be intimidated by the derivations, but these do not need to be understood for application of the results. Since variation and associations of genes are the major topics, variances and covariances must be understood. The less mathematical can still benefit from the analyses by noting the assumptions, the definitions of variables, and the results, and by studying the examples.

For workers interested in population genetics, this book extends theory to deal with many important sets of genes. For workers interested in multigene families or molecular evolution, this book is essential for making quantitative explanations about the evolution and heterogeneity of multigene families.

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