Book review

Mirkin, B.G.; Rodin, S.N.: Graphs and Genes, Vol. 11. Biomathematics. Berlin, Heidelberg, New York, Tokyo: Springer 1984. xiv + 197 pp., 46 figs. Hard bound DM 69,–.

This book is written by two Soviet scientists, a mathematician and a theoretical biologist, attempting to unite graph theory with the theories concerning genes and genetic control systems. The fruitfulness of a mutual interaction of these two sciences results from the fact that, on the one hand, "geneticists are gradually beginning to understand that, unknowingly, they have been speaking in the language of cybernetics" (Ratner, Editor) and, on the other side, "mathematicians are unexpectedly discovering that many past and present problems and methods of genetics can be naturally formulated in the language of graph theory" (Ratner), which had been developed as an abstract mathematical theory in pure mathematics without having in view any application.

The formalization given here embraces not only such older genetical problems as the construction of genetic maps, the analysis of complementation, etc. but also new problems as the construction of partial complementation maps, phylogenetic trees of proteins etc. and, additionally, problems not treated by the theory up to this time: uniqueness of genetic mapping, search for a best approximation to a map, problems of invariants etc. Furthermore, the methods of graph theory lead to more fundamental problems, such as determining fine internal gene structure, studying the 'semantics' of the genetic language, the genetic organization of ontogenesis, the 'non-adaptive' evolution of macromolecules, etc.

First, some comments concerning the classification and content of this book. It has been divided into 3 chapters and their content may be sufficiently characterized in this review by restricting the description to the chapter-headings (together with an enumeration of the different sub-chapters). Chap. 1: "Graphs in the Analysis of Gene Structure" (Gene systems and their maps; The mathematical theory of linear maps: interval graphs; The mathematical theory of linear maps: interval hypergraphs; Linear mapping algorithms; Examples of structural analysis of genetic systems). Chap. 2: "Graphs in the Analysis of Gene Semantics" (Interallelic complementation and the functioning of protein multimers; The approximation of graphs; Analyzing the spatio-functional organization of specific genetic systems). Chap. 3: "Graphs in the Analysis of Gene Evolution" (Trees and phylogenetic trees; The evolution of families of synonymous proteins). An Epilogue: Cryptographic Problems in Genetics, an appendix: Some Notions about Graphs, an extensive list of references and two indices (index of genetic terms, index of mathematical terms) complete the book.

In a very abbreviated manner one can characterize the content with the authors' own words from the 'Preface to the Russian Edition': "In Chapter one, following the presentation of the basic ideas about genetic control systems, we show how genetic data can be used in studying the organization of chromosomes. In the second chapter some highly controversial questions are discussed, dealing with the description of the functional organization of protein macromolecules. In the third chapter data about the structures of the proteins of a hemoglobin family are used in analyzing its evolution. Qualitative analysis of the evolutionary tree produced by this process leads to a number of important conclusions about the course of evolution."

The original Russian version of this book was published in 1976. Since this time there have been a number of changes in theories about genes due to the improved possibilities of direct biochemical 'reading' of deoxyribonucleic genetic texts. In this context, the authors ask the following question in the 'Preface to the English Edition' (1982): "And since this book is devoted to basic problems in deciphering genetic texts, one might think that its material has become significantly outdated." The main intention of the authors' 'Preface to the English Edition' is to deny this question: "The fact is that biochemists are deciphering only the 'passive' information contained in DNA. The activation, the allocation of this information according to meaning, can only be achieved (at least, presently) by the application of independent genetic data about the interactions of different variants of some genome fragments or other. But for such an 'indirect' approach the language and methods of graph theory turn out to be extremely useful. For this reason the contents of the book are practically invariant under the accumulation of new information about the structure of molecular-genetic systems."

There is no doubt that such an attempt to unite results about graphs and results about genes is very meritorious – yet, surely, only for the few specialists who work themselves in this field. For a nonmathematician, the book may turn out to be only readable with extreme difficulties. Moreover, the book is written in the usual in mathematics concise manner, and also in its presentation it follows in major parts the accepted layout of a mathematical textbook (definition → theorem → proof).

These comments, however, should in no way narrow the value of this excellent progressive step in mathematical biology. The book is greatly welcome for the specialists and can be effectively used in courses on graph theory, applied mathematics, discrete mathematics, mathematical biology, molecular genetics and biological control systems.

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