Jenkins, John B.: Human Genetics. Menlo Park (Cal.), Reading (Mass.), London, Amsterdam, Don Mills (Ont.), Sydney: The Benjamin Cummings Publ. 1983. xv+ 461 pp., several figs., several tabs.

This book is intended as a one-term introduction to human genetics for students who have a background of college-level biology or chemistry.

The first six chapters deal with various aspects of classical genetics. That is, they discuss the basic principles of inheritance as formulated by Mendel and applied to humans – the chromosome theory of inheritance and some of the extensions of those basic principles. The next five chapters focus on the nature and function of genetic material and immunogenetics. Two chapters deal with polygenic inheritance and the genetics of human behavior. The final chapter discusses the genetics of human populations and the biological history of the human species.

The text is written in a simple, understandable manner and contains many illustrations. In some cases the problems are too simplified (the stages of the meiotic prophase, the inheritance of retinoblastoma, the description of eucaryotic gene).

Each chapter has learning aids: key words in boldface within the text, chapter summaries in outline form, lists of key terms and concepts at the ends of chapters, review questions and problems (with answers provided), and references to further reading. At the back of the book is a comprehensive glossary.

Students of biology and medicine will find this book most valuable.

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Bellmann, Klaus (ed.): Molecular Genetic Information Systems. Modelling and Simulation. Berlin: Akademie Verlag 1983. 325 pp., 115 figs., 23 tabs. Hard bound DM 60,–.

Molecular genetics is certainly a very fruitful area of experimental research; the modelling of these bioinformatic systems has lagged behind however. This volume is the first to help amend this omission. It is the result of a decade of work by mainly one research group consisting of members of the institutes of Cybernetics and Information processing, Molecular Biology, Mathematics and Computer techniques of the Academy of Sciences in Berlin, DDR. Instead of using global modelling (as was done previously) this working group has attempted to incorporate in its models detailed hypotheses concerning information processing in (epi)genetic systems. This approach enhances the interest of the models both from a theoretical and from an experimental point of view. The resulting models are research tools for studying the consequences of variation in subprocesses on the overall information processing of the system. Moreover, some of the models presented are the best introductions I know to the fields concerned.

In classical (mostly continuous) modelling formalisms it is not feasible to incorporate detailed information processing in the models. Attention is therefore paid in this volume to discrete, more or less individual-based, modelling formalisms. In such formalisms the model takes the form of a description of the possible subsequent (inter)actions and transformations of the molecules in the system. To this end a special-purpose simulation language, called SIMTRA, is introduced. It is used for modelling prokaryotic and eukaryotic transcription control with emphasis on queueing characteristics and for the modelling of a RNA bacteriophage system from infection until new phage formation with emphasis on differential gene expression. Continuous threshold models are used for modelling multigene control networks (thereby generalising Kaufmann networks), various forms of promotor/operon organisation, and bacteriophage lambda development. Very intriguing is also the last chapter in which insight into evolutionary strategies is used – with very promising results – for parameter estimation in mathematically badly behaved systems e.g. in the eukaryotic transcription model.

The book is a very worth while addition to the literature and it is to be hoped that the rapid progress in experimental research will in future be followed closely by detailed modelling. This will increase our theoretical understanding of existing molecular informatic systems set in a context of conceivable variations.

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