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Figs. 2, 3 at the end of the issue.

BOOK REVIEW

HAYASHI, K., SAKAMOTO, N.: DYNAMIC ANALYSIS OF ENZYME SYSTEMS. AN INTRODUCTION. — Japan Scientific Societies Press Tokyo, Springer-Verlag, Berlin—Heidelberg—New York—Tokyo 1986. 370 pp. Hard cover DM 98.—.

The monograph written by K. Hayashi (Faculty of Agriculture, Kyushu University, Japan) and N. Sakamoto (Institute of Information Sciences and Electronics, University of Tsukuba, Japan) concerns the quantitative analysis of dynamic behavior of various enzymatic reaction systems by computer simulation. The writers have employed an approach called "enzyme dynamics" rather than "enzyme kinetics" generally known in enzymology. They concentrate on an exact schematic representation of the actual reaction mechanism, derivation of rate equation on the basis of the scheme, and computer simulation of its dynamic behavior.

The monograph consists of nine chapters: Derivation of rate equations for enzymatic reactions (1), Approximation methods for analysis of rate equations (2), Numerical methods for solution of rate equations (3), Analysis of enzymatic reactions in closed system (4), Microscopic and macroscopic analysis of enzyme systems (5,6), Analysis of reaction-diffusion systems (7), Determination of reaction scheme and kinetic parameters (8), and Related topics in dynamic analysis (9). The introductory chapters deal with the derivation and approximation methods for rate equations of enzymatic reactions. The major part is devoted to the dynamic simulation and ana lysis of some fundamental systems such as reactions of the Michaelis-Menten-type and allosteric enzymes, linear chain systems with feedback loops, branched reaction system, and complex systems with particular characteristics. The dynamic simulation is performed by numerical integration of the rate equations with the computer procedures and their principle and applicability are described in detail. The analysis emphasizes the dynamic aspects of the closed and open systems as well as reaction-diffusion system functioning under various conditions. The simulation is further applied to the determination of reaction schemes and parameters for some enzyme systems.

A new approach to the analysis of dynamic behavior of actual enzyme systems is desired and has been developed as enzyme dynamics in conjunction with the progress in molecular description of biochemical processes and simulation techniques using computers. Quantitative analysis of the dynamic behavior of biochemical reactions in the cellular environments leads to elucidation of the relationship between the structure and function of biological systems on the molecular basis, which is one of the most important goals in biology. Dynamic analysis by computer simulation will now furnish the biochemical research in this direction with a potent and quantitative means for understanding the *in vivo* behavior of enzymatic reaction and its regulation at the molecular level. The dynamic simulation can readily be extended to the systems exploited in biochemical and biomedical engineering.

L. ŠINDELÁŘ (*Praha*)