

been proposed by Henrique Malvar, Meyer, with typical modesty, named these functions Malvar's wavelets.) The last four chapters discuss some applications of wavelets to image analysis, fractals, turbulence, and astronomy, mentioning work in progress and referring the reader to the literature. In many respects the book is a personal view of the field, and others would no doubt have tackled the undertaking quite differently; this actually adds to the book's interest. There are still mathematical formulas on almost every page, so that I would not recommend the book to mathophobes, but I believe it is accessible to any scientifically minded reader with rudimentary knowledge of Fourier analysis; furthermore, the seasoned mathematician will find discussions of many interesting nonmathematical topics, so that the book is by no means superfluous for readers of the other book under review here. The translation is slightly less close to the original lecture notes, but that can be considered a plus, since a very close translation would not have captured the casual style of the notes. Some of the material has been revised and updated by the translator, Robert D. Ryan, in collaboration with Meyer. I noticed a few typos, and I guess Ryan is not a musician, since on page 6 of the English translation the reader is still told that "ré mineur" is a musical note. But these are minor blemishes, and I recommend the book as a delightful introduction to wavelets.

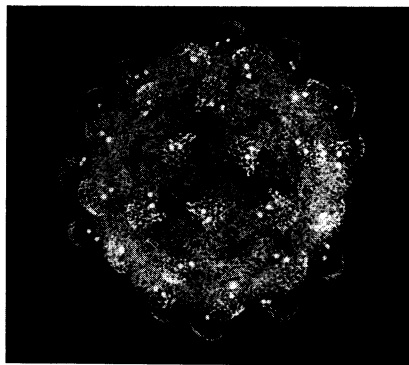
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Cell-Mediated Immunity

Viruses and the Cellular Immune Response.
D. BRIAN THOMAS, Ed. Dekker, New York,
1993. xviii, 524 pp., illus. \$185.

In the past few years fundamental information concerning the recognition of viral antigens by receptors on CD4⁺ and CD8⁺ T lymphocytes has become available. Although much remains to be learned, as exemplified by our ignorance of the basic immunopathogenesis underlying HIV-1 infection, we now have a solid scientific basis for modeling cellular immune responses to virus infections, especially for viruses that induce diseases in mice.

With this book D. Brian Thomas has attempted to unify the current literature on cellular immunity to viruses, which he thinks is "fragmented," with cellular immunologists and virologists focusing on differ-



"Computer graphic representation of the crystal structure of [foot and mouth disease virus] serotype O1. The majority of the protein structure was clearly resolved by X-ray crystallographic techniques. However the G-H loop of VP1 (amino acids 136-159) was too disordered to produce meaningful electron density. The spaces potentially occupied by these 'invisible' regions are represented by clouds of dots." [From Francis and Rowlands's chapter in *Viruses and the Cellular Immune Response*; courtesy of David Stuart, University of Oxford]

ent aspects of the problem. I concur that most virologists are concerned with molecular aspects of antigenicity and viral replication and often consider neutralizing antibody to be the primary (if not the sole) determinant of immune protection. Likewise, as Thomas states, some cellular immunologists have concentrated on using virus systems to address basic questions of antigen processing and positive and negative selection of the T cell repertoire. Other immunologists, however, including some of the contributors to this book, have explored in fine detail the interactions between the infecting virus and the immune system of the host.

The first few chapters provide an overview of some of the complexities of immune responses in the virus-infected host and of developing concepts of the processing of viral antigens for T cell receptor recognition. Following are useful reviews of the roles of dendritic cells and of the roles of cytokines in infectious diseases. The bulk of the book consists of detailed reviews of individual viruses, focusing on cell-mediated immunity. These provide a good beginning for the reader interested in learning about specific cellular immune responses. Particularly interesting are the chapters on the complex interactions of adenoviruses, cytomegalovirus (CMV), and Epstein-Barr virus (EBV) with the T cell responses of the infected host. It is clear that we need to learn more about how T cells control the polyclonal stimulation of B cells by EBV and why CMV causes fatal pneumonias in some transplant recipients and retinitis in AIDS patients. There are three chapters devoted to HIV-1, including a thorough

review by Venet, Gomard, and Lévy of human T cell responses. The book concludes with a brief and insightful review by Allison of current vaccine development efforts incorporating concepts of CD4⁺ and CD8⁺ T cell responses as well as protective antibodies.

Not covered are class I-restricted CD8⁺ cytolytic T lymphocyte responses to influenza A viruses and lymphocytic choriomeningitis virus, which have been fruitful for the study of cellular immune responses and immunopathology, and vaccinia virus, which was successfully used to eliminate smallpox. It might have been more appropriate to devote space to these important viruses and to omit coverage of some of the less-studied viruses.

Recent breakthroughs in the understanding of T cell receptor recognition of major histocompatibility complex (MHC)-peptide complexes by crystallography and the characterization of natural peptides that serve as epitopes for T cell receptors have been based on studies of virus-specific T cell clones and virus-infected cells. Although some of these accomplishments are carefully reflected in this book, others (for example, the definition of natural peptide epitopes on virus-infected cells) are not. In addition, the inclusion of color figures of some of the structures (for example, the MHC-peptide binding site, the influenza hemagglutinin molecule), would have helped the reader to better understand structure-function relationships. Despite these flaws, this is a useful reference book for anyone interested in learning more about cellular immune responses to viruses.

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Life and Computers

Artificial Intelligence and Molecular Biology.
LAWRENCE HUNTER, Ed. AAAI, Menlo Park, CA, and MIT Press, Cambridge, MA, 1993. x, 470 pp., illus. Paper, \$39.95 or £35.95.

Artificial intelligence (AI) comprises activities ranging from straightforward applied programming to the development of general theories of problem solving. Molecular biology is perhaps less broad, but is arguably equally ambitious as a discipline. In considering a book entitled *Artificial Intelligence and Molecular Biology* it is worth asking just what aspects of these two fields are covered, and for whom. Lawrence Hunter's collection of papers is surprisingly eclectic, both

in the biological problems addressed and in the AI approaches taken. Five chapters review applications in various stages of development, with four (by Steeg, Holbrook *et al.*, Edwards *et al.*, and Glasgow *et al.*) describing symbolic or neural-network approaches to RNA or protein-structure analysis and prediction and the fifth (by Mavrouniotis) outlining a qualitative simulation system for metabolic pathways. Two chapters (one by Hunter, the other by Karp) exemplify the use of molecular biology as a model system to investigate general issues in planning and learning. The remaining four chapters (by Searls, Zhang and Waltz, Lathrop *et al.*, and Galper *et al.*) fall in between these extremes, raising general issues of problem and data representation in the context of biological applications.

This book is written for computer scientists. It begins with a broad survey (by Hunter) of basic molecular biology for the novice and ends with an admonition (by Lederberg) to the AI programmer not to accept all claims made by biological "experts" as unchallengeable truths. The volume is clearly meant as an invitation to AI researchers to join a new, multidisciplinary field, and is likely to succeed as such. Biologists interested in entering this area of research are not so lucky: there is no introductory survey of AI, and the introductory sections of the chapters are unlikely to be comprehensible to a biologist as naïve about AI as the AI audience is assumed to be about biology. The book is worthy reading, however, for theoretically inclined and computationally reasonably sophisticated biologists, both as a window onto new computing techniques and for what it reveals about many computational scientists' view of biology.

One of the defining themes of AI research is that the ways in which data, information, or knowledge is represented have a profound influence on the course and success of problem solving. This is hardly a novel observation; what AI provides, for the first time, are tools that allow a systematic study of how the representation of problems and data affect the efficiency or even the possibility of finding a

solution. Every chapter of *Artificial Intelligence and Molecular Biology* addresses this issue; however, none focuses on it or attempts a comparative analysis of different representation methods for a single problem. It is an interesting synthetic exercise for the reader to compare, for example, the variety of representation methods employed in the five chapters on protein-structure prediction and to see how these methods influence the additional assumptions that are made and the algorithms and computing architectures that are chosen to attack the problem. No approach appears, at this stage, to be a clear winner, and only small advances are made beyond the performance obtainable with traditional statistical methods. The optimal representation for posing and solving the structure-prediction problem is still unknown; the work represented in this book may shed some light on why this is so.

Defining a problem inevitably involves abstraction. The evident parallels between the process of constructing problem and data representations for an expert system and the process of identifying the key abstractions with which to build a theoretical explanation gave rise to the mid-1970s AI slogan "Programs Are Theories." The chapter by Searls describing the use of grammatical structures and procedures in DNA and protein-sequence analysis epitomizes this way of thinking; here computational linguistics is proposed as lit-

erally a theory of molecular structure and function. Searls's chapter is the longest in the book, and by far the most ambitious; apparently alluding to Kant, he describes it as "a prolegomenon to a formally-based computational linguistics of biological sequences" (p. 48). Searls proposes that DNA is a language, that gene expression is parsing, and that "gene products (i.e. proteins) and their biological activities may be thought of as the *meaning* of the information in genes, and perhaps entire organisms as the meaning of genomes" (p. 97). Evolution itself is presented as a formally specifiable linguistic process acting on sequences. This is heady stuff and belies strongly nativist assumptions. Structures outside the genome, the subtleties of cell-environment interac-

tion, and population-level selection appear to play no role in Searls's vision of molecular biology. The abstraction—the sequence of characters—has hidden these from view.

The power of the sequence abstraction to illuminate and obscure is one of the lessons of *Artificial Intelligence and Molecular Biology*. In his introductory overview of molecular biology Hunter states: "All of an organism's inherited characteristics are contained in a single messenger molecule: deoxyribonucleic acid, or DNA. The characteristics are represented in a simple, linear, four-element code" (p. 3). These are attractive myths, and their seductive power is reinforced by the results flowing from the genome projects. Their power to obscure, to hide the information contained in cytoskeletal and membrane organization or in chromosomal structure and the essential role this information plays in the life of the cell, is seldom explicitly noted. Lederberg warns in the foreword that "we will have to face up to making real sense of [sequences] in the context of a broader frame of biological facts and theory" (p. x). Anyone pursuing the development of cross-disciplinary theory in biology would be well advised to heed this warning.

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Books Received

Alzheimer's Disease and Related Disorders. Selected Communications. M. Nicolini, P. F. Zatta, and B. Corain, Eds. Pergamon, Tarrytown, NY, 1993. I, 474 pp., illus. \$144 or P90. Advances in the Biosciences, vol. 87. From a conference, Padova, Italy, July 1993.

Animal Models of HIV and Other Retroviral Infections. Paul Racz, Norman L. Letvin, and Jean Claude Gluckman, Eds. Karger, New York, 1993. viii, 200 pp., illus. \$158.50 or DM 237 or SwF 198. Based on a workshop, Hamburg, Germany.

Archibald Garrod and the Individuality of Man. Alexander G. Bearn. Oxford University Press, New York, 1993. xviii, 227 pp., illus. \$49.95.

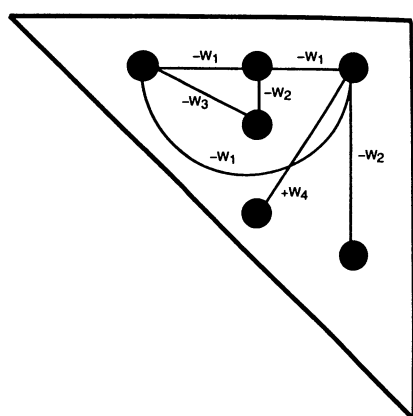
Benign and Malignant Lymphadenopathies. Clinical and Laboratory Diagnosis. Gerassimos A. Pangalis and Aaron Polliack, Eds. Harwood, Langhorne, PA, 1993. xii, 338 pp., illus., + plates. \$76 or P47; to institutions. \$95 or P58.

Berkeley's Philosophy of Mathematics. Douglas M. Jesseph. University of Chicago Press, Chicago, 1993. xii, 322 pp., illus. \$66.25; paper, \$22.95. Science and Its Conceptual Foundations.

Beyond Relativism. Science and Human Values. Roger D. Masters. University Press of New England, Hanover, NH, 1993. xiv, 248 pp., illus. \$24.95.

The Biological Century. Friday Evening Talks at the Marine Biological Laboratory. Robert B. Barlow, Jr., John E. Dowling, and Gerald Weissmann, Eds. Marine Biological Laboratory, Woods Hole, MA, 1993 (distributor, Harvard University Press, Cambridge, MA). xiv, 289 pp., illus. \$45.

Biological Effects and Physics of Solar and Galactic Cosmic Radiation. Part B. Charles E. Swenberg, Gerda Horneck, and E. G. Stassinopoulos, Eds. Plenum, New York, 1993. viii, 939 pp., illus. \$155.



"The structure of the basic network used for RNA secondary structure prediction. W_1 is the inhibitory signal between elements of a row; W_2 is the inhibitory signal between elements of a column; W_3 is the inhibitory signal that prevents knotting; W_4 is the excitatory signal between elements of possible secondary structures." [From Steeg's chapter in *Artificial Intelligence and Molecular Biology*]