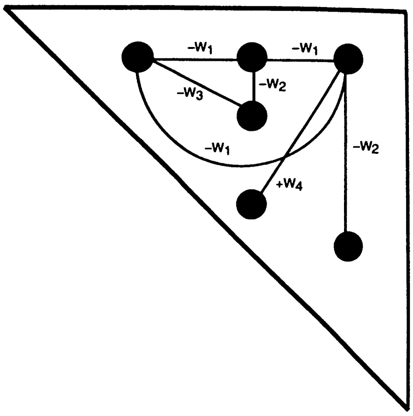
in the biological problems addressed and in the AI approaches taken. Five chapters review applications in various stages of development, with four (by Steeg, Holbrook *et al.*, Edwards *et al.*, and Glasgow *et al.*) describing symbolic or neural-network approaches to RNA or protein-structure analysis and prediction and the fifth (by Mavrovouniotis) 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.



"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*]

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 literally 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 interaction, 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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