Four chapters each cover a different, more specialized topic. Searls discusses application of computational linguistic techniques to many problems in nucleic acid and protein sequence analysis. Steeg applies neural networks to RNA structure prediction. Edwards et al. interpret NMR spectra of proteins, and Glasgow et al. apply scene analysis to the phase-shift problem in protein x-ray crystallography.

As mentioned at the beginning of this review, the book is a snapshot of a moving target. Joshua Lederberg predicts that it will be viewed from the future as providing a "pivotal beginning" for understanding of the complete genome. Be that as it may, it would be worthy of purchase by those physical scientists desiring an introduction to AI applications to molecular biology, but it would be of slightly lesser use to the biologist desiring the same. At the end of the first chapter Hunter states: "In order to work with biologists, AI researchers must understand a good deal about the domain and find ways to bridge the gap between these rather different scientific cultures." This may be the most important concept a computer scientist could gain from this book.

Thermodynamics of Membrane Receptors and Channels by Meyer B. Jackson, Editor

CRC Press, Boca Raton, Florida, 1993. 439 pages. $95.00

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The title is intriguing and, as such, must inevitably, at this stage of the game, contain some disappointment. Nevertheless, this is a very creditable and wide ranging collection of reviews on membrane thermodynamics, channels, and receptors. Only in a restricted number of cases, understandably in the chapters by the editor, is there an attempt at a real marriage of thermodynamics with channel and receptor function.

The book opens with a short general chapter by Yeates on the structure of membrane proteins and the thermodynamic factors affecting their stability. This is followed by a treatment by Jordan of the interactions of ions with channel proteins that concentrates on model channel potential profiles and the effects of membrane surface potential. Roise contributes a chapter on the incorporation of peptides into membranes, mostly the electrostatics and binding, with consideration of channel-forming toxins, peptide hormone-mediated activation, and targeting sequences in protein translocation. Thermodynamic models for lipid-protein interactions, based principally on hydrophobic mismatch, are covered extensively by Mouritsen and Sperotto, with summary examples ranging from amphiphilic polypeptides to both receptors and other membrane proteins. Abney and Scalettar deal with statistical mechanical models and simulations of protein-protein interactions; protein crowding is a fascinating aspect of membranes and is particularly relevant to the formation of gap junctions.

At this point, we are approximately halfway through the book, and there is a change of gear with the three chapters authored by the editor. The first of these chapters considers the energetics of membrane receptor activation, based on allosteric models, and ends with a short section: "If Not Allostery, Then What?" (fractals, of course!). The two following chapters then deal with examples, taking separately receptors directly gating channels (mostly nicotinic acetylcholine, but also GABA, glutamate, and cyclic nucleotide), and those coupled to G-proteins and protein kinases. These chapters are necessarily more descriptive, but the first contains sections on the energetics of ACh binding and its transduction, and each chapter ends with a consideration of the appropriateness of allosteric models (directly ligand-gated: very; G-protein and kinase-coupled: maybe).

Then follows a chapter on mechanosensitive channels by Martinac, including simple thermodynamic models for the tension-induced activation. Ebrey gives a detailed and critical account of the photocycle of bacteriorhodopsin with reference also to structure and proton pumping, but relatively brief mention of the energetics of transduction. Parsegian and Zimmerberg discuss the thermodynamics of channels under osmotic stress, which they have shown can be used to measure the change in aqueous channel volume on opening. The VDAC channel, for instance, can be gated by osmotic pressure. Finally, the book closes with a chapter by Heinemann and Sigworth on the study of channel fluctuations by high resolution analysis of open channel noise. This illuminating account is unashamedly kinetic and illustrates the unique information that can be obtained by single channel recordings.

This is not a book to be read at a single sitting. No one individual is familiar on a daily basis with the whole of pair distribution functions, Landau theory, picosecond spectroscopy, power spectra, site-specific mutations, the intricacies of receptor pharmacology, and even perhaps thermodynamics. However, each chapter brings its rewards. The book is well produced (my favorite misprint is "which should stronglycine favor", but this is not representative) by a wide range of experts, contains a mine of information, is actually very readable, and provokes the imagination. Not least, one is prompted to ask what is the thermodynamic basis of receptor and channel function? Maybe this book is just the beginning and a good indication of how complex the question really is.