proves to be a valuable source of information for all life scientists.

Jürgen Sühnel
Biocomputing Group, Institute of Molecular Biotechnology, Jena Centre for Bioinformatics Beutenbergstrasse 11 D-07745 Jena, Germany
E-mail address: jsuehnel@imb-jena.de

Hermann Berg*
Laboratory of Bioelectrochemistry, Campus Beutenberg, Beutenbergstrasse 11, D-07745, Jena, Germany
E-mail address: Hbergjena@hotmail.com

* Corresponding author. Greifbergstrasse 15, Jena D-07749, Germany. Tel./fax: +49-3641448250.

doi:10.1016/j.bioelechem.2003.09.002

Bioinformatik. Methoden zur Vorhersage von RNA- und Proteinstrukturen (Bioinformatics. Methods for RNA and protein structure prediction)
G. Steger, Birkhäuser Verlag, Basel-Boston-Berlin, 2003, ISBN 3-7643-6951-5, € 44.86 + VAT

In the early days of the development of predictive algorithms for molecular biology (when the term bioinformatics was not yet coined), approaches related to either 3D structures or sequences seem to have developed at a comparable speed [see, e.g., the following landmark papers from the 1960s and 1970s: Levitt, *Detailed molecular model for transfer ribonucleic acid*. Nature 224 (1969) 759-763; Needleman, Wunsch, *A general method applicable to the search for similarities in the amino acid sequences*. J. Mol. Biol. 48 (1970) 443-453; Chou, Fasman, *Prediction of protein conformation*. Biochemistry 13 (1974) 222-245; Chothia, *Structural invariants in protein folding*. Nature 254 (1975) 304–308]. Later on, there was a strong shift towards sequence analysis and a preference for informatics methods accompanied by a more or less phenomenological view of the field leading to the notion of bioinformatics and to its emergence as an independent discipline. More recently, the scope of this field has broadened again including constituents such as sequence analysis, structural bioinformatics, network analysis, but also methods from theoretical biophysics and still other fields. From a methodological point, we need a combination of informatics approaches with methods from other fields, making the notion of computational biology very likely more appropriate than bioinformatics. A widely used workaround to this terminology problem is to adopt a relatively broad view of bioinformatics without worrying too much about the precise meaning of the term.

Structural biology has experienced fast developments within recent years. The number of experimentally known 3D structures of proteins and nucleic acids has dramatically increased. Currently (July 15, 2003), we know the 3D structures of 19,631 proteins, 918 protein-nucleic acid complexes and 1205 nucleic acids. The latter two groups comprise 654 structures that contain RNA. Furthermore, various structural genomics projects have been started aimed at the structure determination of all proteins for a given species. Even though the output from these projects in terms of new structures is not yet very impressive, this will certainly change within the next few years. Also, RNA structural biology has come of age, the most recent highlight being the atomic structures of the small and large ribosomal subunits. Moreover, five rounds of the structure prediction contest CASP have been performed. All these developments can be expected to have great impact on structure prediction methods. Hence, a book on structure prediction that describes the current status of this field is highly welcome.

The book by Steger has 16 chapters, with 7 of them devoted to RNA and the remaining 9 to proteins. DNA is not taken into account. Both, the RNA and protein parts of the book start with an introduction to secondary and 3D structures, and then describe algorithms and methods for structure prediction. A methods chapter on structure determination is included in the RNA part. It describes RNA-specific methods such as chemical probing, but also methods, in particular NMR spectroscopy and X-ray crystallography that are relevant to proteins as well. On the other hand, Circular Dichroism and Fourier-Transform Infrared Spectroscopy are not mentioned. There is also a special chapter on cooperative equilibria of RNA.

The major part of the book is devoted to structure prediction methods and here there is a strong focus on secondary structure prediction. This is actually one of the strengths of this book. The algorithms are described in great detail and supplemented with practical examples. On the other hand, RNA or protein secondary structure is of course only one part of the story. Unfortunately, the 3D aspects of structure prediction are not adequately covered. In the RNA part 3D structure prediction is completely missing. For example, the program Mc-Sym should have been mentioned here. There is almost no mentioning of the very influential RNA structure models generated by the Westhof group (except for references in Chapter 1.1.4). Also SCOR, the RNA analogon to the structural classification of proteins (SCOP), is not described.

In the book's protein part, a few 3D structure prediction methods, such as modeling by homology, threading, and folding by molecular dynamics simulations are briefly discussed. However, again as compared to the very detailed secondary structure prediction parts (ca. 60 pages) they are too short (ca. 30 pages) and some topics that are believed to be a must in a protein structure prediction textbook are not mentioned. Examples are statistical potentials, the CASP competition and target selection for structural genomics projects.

In summary, the book provides an in-depth treatment of secondary structure prediction methods both for RNA and proteins. If one is specifically interested in this field the book is really worth buying, but someone interested in 3D structure prediction beyond its secondary structure part will have to resort to other books.

Jürgen Sühnel *
Biocomputing Group,
Institute of Molecular Biotechnology,
Jena Centre for Bioinformatics, Jena, Germany
E-mail address: jsuehnel@imb-jena.de

* Corresponding author. Tel./fax: +49-3641-65-6200/6210.

doi:10.1016/j.bioelechem.2003.09.003