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Zvelebil, M., Baum, J.O.: **Understanding Bioinformatics.** - Garland Science, Taylor & Francis Group, New York - London 2008. 772 pp. ISBN 0-8153-4024-9.

Marketa Zvelebil is the team leader of cancer informatics at The Breakthrough Toby Robins Breast Cancer Research Centre in UK and Jeremy O. Baum is an Honorary Teaching Fellow in the School of Crystallography in Birkbeck College, UK. This comprehensive (more than 700 pp.) book originated as an authors' textbook for teaching bioinformatics at both undergraduate and postgraduate levels, because of the need to bridge the gap between the simplistic introduction and the very detailed monographs.

The book begins with the introduction to the structure of nucleic acids and their roles in living systems, including a brief description of translation of DNA to mRNA and subsequently into proteins. The structure and organization of proteins is also discussed. This information is very basic, but for the people without any biological knowledge as mathematicians or statisticians it can be useful. The further text is divided into seven parts devoted to individual topics. These parts contain both, "Application chapters", which provides a fast and straightforward route to understanding the main concept and "Theory chapters", which gives more details and presents the underlying mathematics. In the second part the readers are introduced into the principles of sequence alignments, variety of analyses of sequences, searching with nucleic acid or protein sequences and the most widely used appropriate databases (*FASTA*, *BLAST*, *BLOCKS*, *PROSITE*, *PHI-BLAST*, *PRATT*, etc.). The part 3 deals with evolutionary processes, it presents the method to obtain phylogenetic trees from sequence dataset. The part 4 leads us through the utilization of the special programs for gene prediction, prediction of promoter region and other steps in genome analysis. The following part 5 provides the

methods of predicting the secondary structure on sequence. The specialized prediction methods for transmembrane proteins are mentioned. The next part 6 deals with protein tertiary structure, and focuses on principles of homology modelling. The structure-function relationships are also discussed. The last part helps us to analyzed large-scale experiments with large numbers of data (microarrays, 2D electrophoreses, SAGE). The text is accompanied with three appendices: a) probability, information and Bayesian analysis; b) molecular energy functions and c) function optimization.

Book has very good graphic arrangement. Within each chapter every section is introduced with a flow diagram to help the student to visualize and remember the topics covered in that section. The text is supplemented with many illustrative colour figures and schemes, colouring boxes with samples of applications or additional information. It was not possible to summarize all current knowledge in this book and therefore at the end of each chapter there are references to original papers and specialized monographs to help reader to widen their knowledge and skills.

"Understanding bioinformatics" is written for advanced undergraduate and graduate students, but in my opinion this book is very useful for many scientist utilizing new progressive methods based on analyzing of large datasets, because all research workers in the areas of biomolecular science are now expected to be competent in several areas of sequence analysis and often, additionally, in protein structure analysis and other more advanced bioinformatics techniques. I could recommend this book to all laboratory bookcases.

R. PODLIPNÁ (*Praha*)