Steger, G.: **Bioinformatik. Methoden zur Vorhersage von RNA- und Proteinstrukturen.** – Birkhäuser Basel – Boston - Berlin 2003. ISBN 3-7643-6951-5. 302 pp., CHF 74.00, € 44.86.

Bioinformatics as a discipline is still very young, although its popularity is rapidly increasing in the last few years. Many universities worldwide opened study programs in bioinformatics and a lot of books were published recently. However, there is the still the question: What is bioinformatics ? It seems not yet to be clear, how to define bioinformatics. On the one hand are software engineers writing software that is used in biology and on the other hand are biologists using internet databases. Between these two extreme examples is a wide field that probably is somehow connected to bioinformatics. This lack of definition certainly is the reason, why a large amount of books that claims to treat bioinformatics suffers deeply in quality. Whereas in physical chemistry the content of a compendium is clear, and the several books mainly differ in the way how to present this content, in the case of bioinformatics nearly everything dealing with computers and biology is sold under this label. The book "Bioinformatik" by Gerhard Steger does not claim to cover all bioinformatics, but the subtitle states clearly that it deals with methods for the prediction of RNA and protein structures. These methods make it possible to get a quick impression of possible structure and function for experimentally gained DNA, RNA, or protein sequences. The book reflects an increasing awareness of the potential of these prediction methods to save a lot of time and money in the lab. The book can be separated in two main parts: RNA and proteins. In both parts the book tries to cover all aspects of prediction. In one chapter a biological problem of prediction is introduced including the biophysical basics of the prediction methods. The further chapters explain the computational methods with a short example, explain the mostly complicated algorithm chosen to solve the biological problem and show at least one implementation. Quality of the results are discussed by taking a concrete biological example. The book therefore is not a manual for the different web-based services and programs showing the user where to click on, but explains computational methods using concrete biological examples. The references at the end of the book are covering indeed the most important original literature. The book can be used as a starting point and the reader interested in a particular problem has the possibility to get further literature and a deeper knowledge. However, I would appreciate to have the references at the end of each chapter to gain a quick overview what are the most important papers dealing with this particular problem. Chapters 1, 8, and 9 are dealing with the biochemical and biophysical basics of RNA and protein structures. These introductions seem not to be for an uninformed reader, and cannot substitute basic knowledge in biochemistry and biology, but with its straightforwardness are an excellent repetition. A reader coming from the direction of software engineering certainly will need additional information and may use these introductions as a table of content for what he should learn in advance.

To summarize the content of the book: The RNA part starts with graphs and alignments, equilibrium in double-stranded nucleic acids, primer design, and mutations. Methods using dynamic programing, genetic algorithms, information theory, and simulated annealing are introduced. The RNA part is very detailed and gives the impression to be the main priority of the book. The protein part starts with the prediction of transmembrane-helices per Hidden-Markov-model, introduces prediction of secondary structure *via* neuronal networks, and finishes with protein folding by *ab-initio*-methods, homology modelling, and inverse folding „threading".

However, the last three chapters seem to be more an introduction into the field, making the reader curious for further information. Of course, it is true that only *ab-initio* calculation can easily fill a book and the same is true for homology modelling and molecular dynamics, but I personally would appreciate a little bit more information in these fields. But maybe this should be part of a second book "Bioinformatik II".

My overall view of the book is more than favourable. Despite the fact that the origin of the book can be found in a university lecture for students of biology, the book is valuable not only for biologists but also for biochemists, biophysical chemists, and software engineers that want to step into the fascinating world of structure prediction. It gives an overview of what is state of the art in predicting RNA and protein structures and demonstrates, how informatics can valuable contribute to solving biological programs. The book has to be taken as a basic course in the field of prediction methods and combines in a very solid way theory and practical approach. For the German speaking scientific community the book certainly sets standards and has the potential to become one of the templates used for creating basic university courses in bioinformatics and thus helps to define at least a part of bioinformatics more precisely.

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