

## Book review

**"Systems Biology: A Textbook"****Edda Klipp, Wolfram Liebermeister, Christoph Wierling,  
Axel Kowald, Hans Lehrach, Ralf Herwig**Wiley, 2009, € 69.–, ISBN-10: 3-527-31874-7, ISBN-13: 978-3-527-31874-2;  
English language

Sci Pharm. 2009; 77: 911–912

doi:10.3797/scipharm.br-09-01

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This book arose from a practical course that was given by the authors at the Max Planck Institute of Molecular Genetics in Berlin-Dahlem.

Systems Biology is a field of science which is presently in rapid evolution and is in part still seeking a clear definition of what it really is. Only four years ago, a book about „Systems Biology: Definitions and Perspectives“ (L. Alberghina, H. V. Westerhoff; Springer Verlag 2005) appeared which quite obviously was dealing and struggling with the scepticism of most colleagues in molecular biology. Many people in the field more or less said „systems biology is just a new name for what we did since many years“. On the other hand, the pioneers of this field, like Westerhoff, Klipp, Alberghina and others, maintained that systems biology was a genuine new science based, of course, on forerunners like mathematical modeling of biological processes, integrative study of cellular metabolism, and, most importantly the new technical possibilities offered by the progress of biological chemistry, genomics, transcriptomics, metabolomics, new DNA sequencing methods and many other high throughput techniques, for which, on the other hand also the rapid progress of computer science and software tools was a prerequisite. In 2009, the situation has completely changed: Among the books that appeared on the market in this year, over 30 have the word „systems biology“ in their title. One of them is the book to be reviewed here.

Systems biology is, or at least attempts to be, much more holistic and integrative than its forerunners. The chapter titles of the textbook by Klipp et al. show that systems biology is a synthesis of biochemistry, computational biology, bioinformatics, mathematical modeling, and rapid data acquisition and analysis from the diverse „omics“ fields. To the present reviewer, one of the greatest challenges of systems biology and of biology in general lies in the unsolved problem of structuring large scale biological knowledge (data, including „text“) into data banks to make it retrievable and comparable, „linkable“, so that new results or predictions can be gained and new hypotheses can be formulated that are testable in the laboratory. There can be no doubt that the development of new algorithms is necessary to reach this aim. It is amazing what can be done using advanced bioinformatic methods with the millions of sequences stored in the sequence databases. But this is only the beginning. In the future, the emphasis is on prediction of function, and function has increasingly to do with complex networks of genes and enzymes.

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Mathematical modeling is central to the field and is presently mainly done to analyse globally cell metabolism and cell signaling, but is by no means restricted to these two applications.

At this moment, even a single cell is by far too complex to be understood in its totality. However, to be useful for physiology and medicine, systems biology must also take into account the interactions between millions of cells. In my view, this field of science is well under way to reach this goal and the book by Klipp et al. is a very helpful guide for those who want more information about the field.

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