

Preface

In recent years, *systems biology* has emerged as an interdisciplinary research field combining biology with computer science and mathematics. Computational models for complex biological processes are the general paradigm, predominantly in terms of ordinary differential equations (ODEs). The main scientific tasks are mathematical modelling of biochemical and physiological processes, numerical simulation of the dynamics of biological networks, and identification of model parameters via a comparison with measurement data.

Typical books on systems biology do not go into the necessary detail as far as these topics are concerned. At best, they merely mention algorithmic approaches, but without offering a deeper understanding. On the other hand, books on ODEs or parameter identification are typically written for a mathematical community, nearly unreadable for systems biologists or, more generally, for computational biologists. As authors of the present book, we have worked hard to fill this gap: Our aim has been to make the important mathematical issues readable and to focus on systems biological needs. What came out is *not a book on systems biology, but on computational methods in systems biology*.

Our book is based on *university courses* repeatedly given to students of bioinformatics who only had moderate knowledge of mathematics. The idea of the courses had been to convey mathematical insight as far as it is indispensable for systems biological modelling. Consequently, the book aims at teaching the necessary mathematical prerequisites by means of many examples rather than by theorems. This does not and cannot mean to avoid mathematical formulas as a whole.

Throughout the text, numerical *software* is discussed in terms of its strengths and weaknesses with respect to various systems biological issues. Web addresses are included where the mentioned software can be downloaded.

Acknowledgements First of all, we want to thank our ZIB colleague Thomas Dierkes for his patience and invaluable help in the preparation of the computational results for the GynCycle model (Sect. 3.5.3). We also wish to thank our ZIB colleagues Rainald Ehrig and Claudia Stötzel for their helpful groundwork. Moreover, we are indebted to Matthias König and Hermann-Georg

Holzhütter from Charité Berlin for their support in the example presented in Sect. 2.5.3 (Warburg effect of tumor cells). Finally, we are grateful to Pooja Gupta for her careful reading of earlier drafts of the manuscript.

Berlin, Germany
May 2015

Peter Deufilhard
Susanna Röblitz

A Guide to Numerical Modelling in Systems Biology

Deuflhard, P.; Röblitz, S.

2015, X, 168 p. 42 illus., 33 illus. in color., Hardcover

ISBN: 978-3-319-20058-3