

Preface

Formal modeling of biological systems is becoming a fundamental step in designing experiments and interpreting their outcome. Omics technologies produce data that challenge standard analytical approaches, thus calling for new methods to analyze and interpret the overwhelming mass of data produced. Simultaneously, the outcome of static omic analysis often provides knowledge to build dynamic models that can uncover the mechanistic details governing the biological system being studied. Many techniques have been developed in the last decade for dynamic simulation of biological systems and the emerging field of language-based modeling is becoming well established in the community. We felt the lack of a comprehensive textbook unifying the static and dynamic approaches that define systems biology, as well as the foundational knowledge in molecular biology that is essential to adequately analyze biological systems.

This book is intended for practitioners of the systems biology field, both with a biological and mathematical/computing background, who want to understand algorithmic modeling and algorithmic systems biology. Some knowledge of basic molecular biology and basic computer science can help, but the aim of the book is to be a self-contained approach to the field. The second chapter introduces some basic molecular biology and experimental techniques to understand how data are produced. The Appendices report basic mathematics and computing needed to understand fully the material in the book. All chapters propose further reading about the topics introduced, to drive the reader to deeper treatments of the topics in the book. All of these references are collected in the bibliography reported at the end of the book.

The book can also be used in advanced undergraduate courses on modeling and analysis of biological systems. It contains many examples that

can help students gain a practical grasp of the main concepts throughout the book. These examples are also templates for approaching exercises and problems that may be encountered outside of the book. The organization of the material is the result of ten years teaching a modeling course at the University of Trento.

The book collects classical material on analysis, modeling and simulation, acting as a unique source of reference. Additionally, it expands on language-based modeling with recent research advances, and therefore can also be considered a research text introducing both the state of the art and recent developments. Therefore, it can also be useful in graduate programs and for researchers that want to approach systems biology from a well-rounded standpoint.

As a final remark, we stress that we were forced to choose among many different formalisms and methods to constrain the book to a reasonable size. The choice was driven by our experience both as researchers and teachers working in the field. We are aware that there are many other excellent solutions to the problems addressed in the book that we were not able to include. The references are intended to manage this issue at least partially.