

Preface

The book is devoted to the design and analysis of biomolecular circuits as considered in systems biology and synthetic biology – two very dynamic and promising fields of research. Combining expertise and know-how from the biological and physical sciences with computer science, mathematics and engineering, their potential to impact society is only limited by the imagination of those working in the fields.

Synthetic biology promises to introduce new bio-therapeutic, bio-remediation, and bio-sensing applications. For example, synthesizing bacteria to seek out and destroy cancer cells, grass that glows red if planted on top of a land mine, cells that perform arithmetic operations, and small organisms that detect and remove heavy metals from the world's most dangerous drinking water. These systems are all possible by introducing key concepts in the way we abstract and standardize the process by which biological systems are developed. One of the current goals in synthetic biology is showing that, starting with well characterized biological primitives, complex systems can be composed using rules for system composition and automated with algorithms, biophysical models, and liquid handling robotics. A prime example of the synthetic biology community is the exciting International Genetically Engineered Machine competition (iGEM) held every year at MIT in Boston (USA). This event is just the tip of the iceberg. The field is in its infancy much the way the semiconductor industry was in the 1940's. Tremendous advances can be gained by not only furthering our knowledge of the biological phenomenon underlying these systems but also making sure the overall design process is formal, rigorous, and standardized.

Underpinning the advance and application of systems and synthetic biology is the development of appropriate modeling and computational tools for analysis and design purposes. This is an important ongoing research area. The idea is to model biological processes and reactions so as to allow experiments to be carried out *in-silico* before moving to the wet-lab. This is strongly reminiscent of the early days of electronics, where mathematical models had to be formulated to allow, for example, computer aided design (CAD) of integrated circuits and the efficient testing and design of complex devices.

The idea for this book arose during a successful special session on “Design of Biological Circuits and Systems” held at the IEEE International Symposium on Circuits and Systems (ISCAS) in 2009 in Taipei (Taiwan) organized by co-editors Heinz Koepl and Gianluca Setti. The aim of the book is to present in a coherent framework some of the most recent work on the analysis, simulation and design of biomolecular circuits and systems reflecting the interdisciplinary and collaborative nature of the field. The results discussed in the book range from how these systems should be modeled and analyzed to how they should be physically designed and implemented.

The book is organized around four general thematic areas:

- A. Analysis and Simulation
- B. Modularity and Abstraction
- C. Design and Standardization
- D. Enabling Technologies

Drawing parallels to electronic circuit design the chosen organization of the book indicate – what the editors believe – are the important necessary steps to build complex synthetic circuits. Based on an appropriate mathematical formalism of how to describe, analyze and simulate basic cellular processes one can start to abstract away part of this overwhelming complexity (Part A). Abstraction and the clear definition of functional entities or *modules* that can be composed is the crucial step toward large-scale integration (Part B). If well-defined building blocks with well-defined interfaces are in place, standards can be created and the *in silico* design process can be automated (Part C). The concluding theme of the book discusses the experimental feasibility of the corresponding *in vivo* design and analysis process (Part D).

Each of these themes is organized in different chapters that are self-contained so that they can be read individually by experts but also read sequentially by someone wanting to get an overview of the field. The book is intended for computational scientists, e.g. mathematicians, physicists, computer scientist or engineers as well as for researchers from the life sciences. Special efforts have been made to make the chapters accessible for a broad, multi-disciplinary readership. For instance, in the experimental chapters of Part D, care has been taken so that computational researchers can follow the otherwise rather technical expositions on the technologies applied in experimental systems and synthetic biology.

We would like to thank Springer for their help and support in assembling this book together. In particular, we want to thank Charles Glaser for his constant drive behind this book project. The commitment taken and the effort invested by all contributors to deliver the chapter on time is gratefully acknowledged.

We hope the reader will find this book enjoyable and motivating. Systems and synthetic biology are exciting emerging research areas where skills and know-how

from science and engineering are required. We believe this book offers a balanced overview of the many open problems and research challenges in the *design and analysis of biomolecular circuits*.

ETH Zurich, Switzerland
Boston University, USA
University of Ferrara, Italy
University of Bristol, UK and
University of Naples Federico II, Italy
April 29, 2011

Heinz Koeppl
Douglas Densmore
Gianluca Setti
Mario di Bernardo

<http://www.springer.com/978-1-4419-6765-7>

Design and Analysis of Biomolecular Circuits
Engineering Approaches to Systems and Synthetic
Biology

Koepl, H.; Densmore, D.; Setti, G.; di Bernardo, M.
(Eds.)

2011, XIII, 402 p., Hardcover

ISBN: 978-1-4419-6765-7