



Computational Modeling of Gene Regulatory Networks - A Primer

Hamid Bolouri

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This book serves as an introduction to the myriad computational approaches to gene regulatory modeling and analysis, and is written specifically with experimental biologists in mind. Mathematical jargon is avoided and explanations are given in intuitive terms. In cases where equations are unavoidable, they are derived from first principles or, at the very least, an intuitive description is provided. Extensive examples and a large number of model descriptions are provided for use in both classroom exercises as well as self-guided exploration and learning. As such, the book is ideal for self-learning and also as the basis of a semester-long course for undergraduate and graduate students in molecular biology, bioengineering, genome sciences, or systems biology.

Contents:

- Introduction
- What Is a System, and Why Should We Care?
- What Models Can and Cannot Predict
- Why Make Computational Models of Gene Regulatory Networks?
- Graphical Representations of Gene Regulatory Networks
- Implicit Modeling via Interaction Network Maps
- The Biochemical Basis of Gene Regulation
- A Single-Cell Model of Transcriptional Regulation
- Simplified Models: Mass-Action Kinetics
- Simplified Models: Boolean and Multi-valued Logic
- Simplified Models: Bayesian Networks
- The Relationship between Logic and Bayesian Networks
- Network Inference in Practice
- Searching DNA Sequences for Transcription Factor Binding Sites
- Model Selection Theory
- Simplified Models — GRN State Signatures in Data
- System Dynamics
- Robustness Analysis
- GRN Modules and Building Blocks
- Notes on Data Processing for GRN Modeling
- Applications of Computational GRN Modeling
- Quo Vadis

Readership: Undergraduate- and graduate-level experimental biology students and researchers and practicing biologists; computational biology students and researchers; students and researchers in bioengineering, genome sciences, and related disciplines.

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