

CONTENTS

Contributors	xi
Preface	xv
1. Principles of Model Building: An Experimentation-Aided Approach to Development of Models for Signaling Networks <i>Ambhigainath Ganesan and Andre Levchenko</i>	
I. Introduction	2
II. Signaling Systems and Mathematical Models	3
III. Experimentation-aided Model Development	4
IV. Conclusion	16
Acknowledgments	16
References	16
2. Integrated Inference and Analysis of Regulatory Networks from Multi-Level Measurements <i>Christopher S. Poultney, Alex Greenfield, and Richard Bonneau</i>	
I. Introduction	20
II. Overview of Model/Algorithm	25
III. Biological Insights	33
IV. Open Challenges	38
V. Computational Methods	40
References	50
3. Swimming Upstream: Identifying Proteomic Signals that Drive Transcriptional Changes using the Interactome and Multiple "-Omics" Datasets <i>Shao-shan Carol Huang and Ernest Fraenkel</i>	
I. Introduction	58
II. Computational Methods	61
III. Biological Insights	70
IV. Open Challenges	74
Acknowledgments	77
References	77

4. A Framework for Modeling the Relationship between Cellular Steady-state and Stimulus-responsiveness

Paul M. Loriaux and Alexander Hoffmann

I. Introduction	82
II. Overview of Algorithm	83
III. Biological Insights	91
IV. Open Challenges	95
V. Computational Methods	96
Further Reading	107
References	108

5. Stochastic Modeling of Cellular Networks

Jacob Stewart-Ornstein and Hana El-Samad

I. Introduction	112
II. The Need for a Stochastic Modeling Framework	114
III. Overview of Computational Approach	115
IV. Biological Insights from Computational Approaches	116
V. Computational Methods	117
VI. Open Challenges	129
VII. Conclusions	134
References	134
Further Reading	137

6. Quantifying Traction Stresses in Adherent Cells

Casey M. Kraning-Rush, Shawn P. Carey, Joseph P. Califano, and Cynthia A. Reinhart-King

I. Introduction	140
II. Overview of Method	142
III. Biological Insights from Traction Methods	155
IV. Open Challenges	159
V. Methods	160
VI. Summary	172
Acknowledgments	172
References	172
Further Reading	177

7. CellOrganizer: Image-Derived Models of Subcellular Organization and Protein Distribution

Robert F. Murphy

I. Introduction	180
II. Components of a Model of Subcellular Organization and Protein Distribution	181
III. Models of Subcellular Organization	181

IV. Protein Distributions Across Subcellular Structures	190
V. Use of Models for Testing Algorithms	191
VI. Conclusion	191
Acknowledgments	192
References	192
8. Spatial Modeling of Cell Signaling Networks	
<i>Ann E. Cowan, Ion I. Moraru, James C. Schaff, Boris M. Slepchenko, and Leslie M. Loew</i>	
I. Introduction	196
II. Overview of Spatial Modeling	197
III. Building a Spatial Model	202
IV. Running Spatial Simulations with VCell: Numerical Method and Simulation Parameters	209
V. Application to a Specific Example: cAMP Signaling in Neuronal Cells	213
Acknowledgments	218
References	218
Further Reading	220
9. Stochastic Models of Cell Protrusion Arising from Spatiotemporal Signaling and Adhesion Dynamics	
<i>Erik S. Welf and Jason M. Haugh</i>	
I. Introduction	224
II. Model Synthesis	224
III. Model Analysis	228
IV. Biological Insights from the Modeling Approach	232
V. Open Challenges	234
VI. Computational Methods	235
Acknowledgments	239
References	239
10. Nonparametric Variable Selection and Modeling for Spatial and Temporal Regulatory Networks	
<i>Anil Aswani, Mark D. Biggin, Peter Bickel, and Claire Tomlin</i>	
I. Introduction	244
II. Overview of the NODE Model	246
III. Biological Insights	252
IV. Open Challenges	256
V. Computational Methods	256
VI. Building a NODE Model	256
VII. Building a Comb Diagram with the NALEDE Extension	258
Further Reading	259
Acknowledgments	259
References	260

11. Quantitative Models of the Mechanisms that Control Genome-Wide Patterns of Animal Transcription Factor Binding	
<i>Tommy Kaplan and Mark D. Biggin</i>	
I. Introduction	264
II. Overview of Model/Algorithm	265
III. Biological Insights	270
IV. Open Challenges	275
V. Computational Methods	276
VI. Glossary	279
Further Reading	280
References	280
12. Computational Analysis of Live Cell Images of the <i>Arabidopsis thaliana</i> Plant	
<i>Alexandre Cunha, Paul T. Tarr, Adrienne H.K. Roeder, Alphan Altinok, Eric Mjolsness, and Elliot M. Meyerowitz</i>	
I. Introduction	286
II. Overview of Systems and Methods	288
III. Biological Insights	299
IV. Open Computational Challenges	300
V. Imaging and Computational Methods	302
VI. Further Reading	319
Acknowledgments	320
References	320
13. Multi-Scale Modeling of Tissues Using CompuCell3D	
<i>Maciej H. Swat, Gilberto L. Thomas, Julio M. Belmonte, Abbas Shirinifard, Dimitrij Hmeljak, and James A. Glazier</i>	
I. Introduction	326
II. Glazier–Graner–Hogeweg (GGH) Modeling	326
III. CompuCell3D	331
IV. Building CC3D Models	333
V. Conclusion	362
Acknowledgments	362
References	363
14. Multiscale Model of Fibrin Accumulation on the Blood Clot Surface and Platelet Dynamics	
<i>Zhiliang Xu, Scott Christley, Joshua Lioi, Oleg Kim, Cameron Harvey, Wenzhao Sun, Elliot D. Rosen, and Mark Alber</i>	
I. Introduction	368
II. Biological Background	370
III. Overview of the Modeling Approach	372
IV. Study of the Role of the Fibrin Network	373

V. Multiscale Model of Thrombus Development with Fibrin Network Formation	377
VI. GPU Implementation of the Simulation of the Platelet–Blood Flow Interaction	381
VII. Concluding Remarks	385
Acknowledgments	386
References	386
Index	389
Volumes in Series	401

- Mark Alber (367), Department of Applied and Computational Mathematics, University of Notre Dame, Notre Dame, Indiana, USA; Department of Medicine, Indiana University School of Medicine, Indianapolis, Indiana, USA
- Alphan Altınok (285), Division of Biology, California Institute of Technology, Pasadena, California, USA
- Anil Aswani (243), Department of Electrical Engineering and Computer Sciences, University of California, Berkeley, California, USA
- Julia M. Belmonte (325), Department of Physics, Biocomplexity Institute, Indiana University, Bloomington, Indiana, USA
- Peter Bickel (243), Department of Statistics, University of California, Berkeley, California, USA
- Mark D. Biggin (243, 249), Genomics Division, Lawrence Berkeley National Laboratory, Berkeley, California, USA
- Richard Bonneau (19), Department of Biology, Center for Genomics and Systems Biology, New York University, New York, NY, USA; Computer Science Department, Courant Institute of Mathematical Sciences, New York, NY, USA
- Joseph P. Califano (109), Department of Biomedical Engineering, Cornell University, Ithaca, New York, USA
- Shawn P. Carey (139), Department of Biomedical Engineering, Cornell University, Ithaca, New York, USA
- Scott Christley (347), Department of Surgery, University of Chicago, Chicago, Illinois, USA
- Ann E. Cowan (195), R. D. Berlin Center for Cell Analysis and Modeling, University of Connecticut Health Center, Farmington, CT, USA
- Alexandre Cunha (285), Center for Advanced Computing Research, Division of Engineering and Applied Science, California Institute of Technology, Pasadena, California, USA; Center for Integrative Study of Cell Regulation, California Institute of Technology, Pasadena, California, USA
- Hana El-Samad (111), Department of Biochemistry and Biophysics, California Institute for Quantitative Biosciences, University of California, San Francisco, CA
- Ernest Fraenkel (57), Department of Biological Engineering, Massachusetts Institute of Technology, Cambridge, Massachusetts, USA; Computer Science and Artificial Intelligence Laboratory, Massachusetts Institute of Technology, Cambridge, Massachusetts, USA