Functional Coherence of Molecular Networks in Bioinformatics

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Ananth Grama
Editors

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ISBN 978-1-4614-0319-7 e-ISBN 978-1-4614-0320-3
DOI 10.1007/978-1-4614-0320-3
Springer New York Dordrecht Heidelberg London

Library of Congress Control Number: 2011937231

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Printed on acid-free paper

Springer is part of Springer Science+Business Media (www.springer.com)

Preface

The past decade has seen tremendous advances in our understanding of the basic mechanisms that underlie living organisms. These advances have been motivated by our ability to gather large amounts of data relating to the state of living systems (chemical compositions, dynamic fluxes, binding states, etc.), modeling in ways that lend themselves to powerful analyses techniques, and associated algorithms and software. In contrast to traditional approaches that take a deconstructive view of biological processes (scaling up from atomistic and molecular levels), systems biology studies the organization and emergent properties of interacting units (typically biomolecules). This poses profound challenges, as well as exciting opportunities for new discoveries. This edited volume focuses on the computational challenges associated with systems-level modeling of biological function and explores how functional relationships among biomolecules are manifested in biological networks.

Systems-level (network) models of biological systems typically rely on graphs with nodes corresponding to biological entities and edges corresponding to interrelationships among these entities. Constructing such models from data, reasoning from these models, characterizing their organization and function, and relating them to the genotype/phenotype, pose complex modeling and algorithmic challenges. While one may be tempted to view these as traditional graph algorithms, well studied in computer science literature, the unique characteristics of biological interaction data necessitates development of novel models and methods. These characteristics include: (1) incomplete and noisy datasets, (2) highly skewed distributions, (3) need for establishing statistical validity, (4) incorporating elements of space, time, and scale, and (5) relating across disparate abstractions.

While there is tremendous ongoing research and development activity in this area, there is an established core of results that provides the basis for future development. This book provides a comprehensive overview of the state-of-the-art, as it relates to modeling and analysis of living systems as interacting biological units. By the nature of the underlying processes, the book intersects broad sub-disciplines within biology, statistics, and computer science. It addresses methods for data collection and curation, model inference, statistically grounded analyses,

algorithms, software and frameworks, and validation. It also motivates a number of open problems, which provide excellent avenues for continuing efforts in the area.

The book is the result of significant efforts on part of the contributing authors. The editors would like to thank all of the authors for their outstanding contributions.

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