

Networks of Networks in Biology

Concepts, Tools and Applications

Biological systems are extremely complex and have emergent properties that cannot be explained or even predicted by studying their individual parts in isolation. The reductionist approach, although successful in the early days of molecular biology, underestimates this complexity. As the amount of available data grows, so it will become increasingly important to be able to analyse and integrate these large data sets. This book introduces novel approaches and solutions to the big data problem in biomedicine, and presents new techniques in the field of graph theory for handling and processing multi-type large data sets. By discussing cutting-edge problems and techniques, researchers from a wide range of fields will gain insights into how to exploit big, heterogeneous data in the life sciences through the concept of ‘network of networks’.

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Edited by Narsis A. Kiani , David Gomez-Cabrero , Ginestra Bianconi

Frontmatter

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Contents

List of Contributors page vii
Preface ix

Part I Networks in Biology 1

- 1 An Introduction to Biological Networks 3**
 Nuria Planell, Xabier Martinez de Morentin and David Gomez-Cabrero
- 2 Graph Theory 18**
 Akram Dehnokhalaji and Nasim Nasrabadi

Part II Network Analysis 33

- 3 Structural Analysis of Biological Networks 35**
 Narsis A. Kiani and Mikko Kivelä
- 4 Networks from an Information-Theoretic and Algorithmic Complexity Perspective 56**
 Hector Zenil and Narsis A. Kiani
- 5 Integration and Feature Identification in Multi-layer Networks using a Heat Diffusion Approach 71**
 Gordon Ball and Jesper Tegnér

Part III Multi-layer Networks 83

- 6 Multiplex Networks 85**
 Ginestra Bianconi
- 7 Existing Tools for Analysis of Multi-layer Networks 105**
 Massimo Stella and Manlio De Domenico
- 8 Dynamics on Multi-layer Networks 121**
 Manlio De Domenico and Massimo Stella

Part IV Applications 145

- 9 The Network of Networks Involved in Human Disease 147**
 Celine Sin and Jörg Menche
- 10 Towards a Multi-layer Network Analysis of Disease: Challenges and Opportunities Through the Lens of Multiple Sclerosis 172**
 Jesper Tegnér, Ingrid Kockum, Mika Gustafsson and David Gomez-Cabrero

vi CONTENTS

11 Microbiome: A Multi-layer Network View is Required 183

Rodrigo Bacigalupe, Saeed Shoaie and David Gomez-Cabrero

Part V Conclusion 195**12 Concluding Remarks: Open Questions and Challenges 197**Ginestra Bianconi, David Gomez-Cabrero, Jesper Tegnér
and Narsis A. Kiani*Index* 201

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Preface

Network Science is transforming research in different areas of living sciences, ranging from evolutionary biology to medicine. This book aims to introduce the most recent developments of Network Science and its biological applications. In particular, the architecture of biological systems will be characterized using both single networks (monoplexes) and networks of networks (multi-layer networks). Graph theory and social network analysis are classic subjects of mathematics and sociology that have been widely investigated in the twentieth century. However, only since the late 1990s, when several papers on the fundamental design principles of various kinds of large-scale networks were published, was Network Science established as a novel framework to analyse interacting systems, which led to the expansion of the research field of network analysis, with great impact in biology.

After 20 years, this field is still proliferating, and it has become increasingly clear that the challenge of integrating and modelling heterogeneity and complexity of living systems cannot be addressed by using a single-layer network (monoplex).

Instead, the complexity of living systems – such as the interactions between proteins and the microbiome – is captured by a multi-layer network approach. Multi-layer networks are formed by nodes and interactions of different natures, and connotations, forming different networks that interact with each other, creating a network of networks. The investigation of multi-layer networks is a very active research area in Network Science, which in the last ten years has led to the development of several methodologies to extract information for analysing large data sets and integrating the results from different experiments.

With contributions from key leaders, this book discusses topics in Network Science that are increasingly foundational for the quantitative understanding of living systems. Furthermore, it consolidates existing practical and theoretical knowledge of both monoplexes and multi-layer networks. The book balances application and theory to give a unified overview of this interdisciplinary science. It is intended to serve as an introductory text for graduate students and researchers in physics, biology, and biochemistry, and presents ideas and techniques from fields outside the reader's own area of specialization.

Aims of this Book

This book focuses on network-inspired approaches for the analysis and integration of the large data sets currently prevalent in life sciences. The principal aim of this work is to give a comprehensive overview of new techniques in the field of graph theory for handling and processing multi-type large data sets. By discussing state-of-the-art problems and techniques, this book offers researchers from a wide range of areas the unique opportunity to gain insights for exploiting the richness of life sciences data sets through the concept of 'networks of networks'. It presents a timely, multi-authored compendium representing a diverse set of backgrounds and methods developed in

this area. Contributions have been selected and compiled to introduce the concept and cover different methods in a way that is accessible to people from diverse backgrounds. We hope that researchers from different areas of network analysis will learn new aspects and future directions of this emerging field.

How to Read this Book

In order to reach a broad spectrum of readers – biologists, biochemists, computer scientists, bioinformaticians – the book does not require a deep knowledge of computer science or biology. Instead, the reader will learn about graph theory, graph algorithms, and network analysis, as well as biology.

This book consists of five parts: Part I provides a brief overview of biological networks and graph theory; Part II includes chapters discussing network analysis; Part III presents chapters introducing multiplex and multi-layer networks and tools to extract relevant information from these networks of networks; Part 4 includes chapters presenting the application to real biological case studies and the initial insights gained in this relatively new field of research; finally, Part V provides concluding remarks and an outline of the future directions of the field. The book builds upon the introductory chapters and ends by addressing emerging trends in this growing, vibrant research area. Each chapter can be studied independently.