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978-0-521-88895-0 - Protein Interaction Networks: Computational Analysis
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Protein Interaction Networks: Computational Analysis

The analysis of protein–protein interactions is fundamental to the understanding of cellular organization, processes, and functions. Proteins seldom act as single isolated species; rather, proteins involved in the same cellular processes often interact with each other. Functions of uncharacterized proteins may be predicted through comparison with the interactions of similar known proteins. Recent large-scale investigations of protein–protein interactions using such techniques as two-hybrid systems, mass spectrometry, and protein microarrays have enriched the available protein interaction data and facilitated the construction of integrated protein–protein interaction networks. The resulting large volume of protein–protein interaction data has posed a challenge to experimental investigation.

This book provides a comprehensive understanding of the computational methods available for the analysis of protein–protein interaction networks. It offers an in-depth survey of a range of approaches, including statistical, topological, data-mining, and ontology-based methods. The author discusses the fundamental principles underlying each of these approaches and their respective benefits and drawbacks, and she offers suggestions for future research.

Aidong Zhang is a professor in the Department of Computer Science and Engineering at the State University of New York at Buffalo and the director of the Buffalo Center for Biomedical Computing (BCBC). She is an author of more than 200 research publications and has served on the editorial boards of the *International Journal of Bioinformatics Research and Applications* (IJBRA), *ACM Multimedia Systems*, the *International Journal of Multimedia Tools and Applications*, the *International Journal of Distributed and Parallel Databases*, and *ACM SIGMOD DiSC* (Digital Symposium Collection). Dr. Zhang is a recipient of the National Science Foundation CAREER Award and SUNY (State University of New York) Chancellor's Research Recognition Award. Dr. Zhang is an IEEE Fellow.

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PROTEIN INTERACTION NETWORKS

Computational Analysis

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State University of New York, Buffalo

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CAMBRIDGE UNIVERSITY PRESS
Cambridge, New York, Melbourne, Madrid, Cape Town, Singapore,
São Paulo, Delhi

Cambridge University Press
32 Avenue of the Americas, New York, NY 10013-2473, USA

www.cambridge.org
Information on this title: www.cambridge.org/9780521888950

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First published 2009

Printed in the United States of America

A catalog record for this publication is available from the British Library.

Library of Congress Cataloging in Publication data
Zhang, Aidong, 1961–
Protein interaction networks : computational analysis / Aidong Zhang.
p. cm.
Includes bibliographical references and index.
ISBN 978-0-521-88895-0 (hardback)
1. Protein-protein interactions – Data processing. 2. Protein-protein interactions – Mathematical models. I. Title.
[DNLM: 1. Protein Binding – physiology. 2. Protein Interaction Mapping – methods. 3. Computational Biology – methods. QU 55 Z625p 2009]
QP551.5.Z53 2009
572′.64–dc22 2009002688

ISBN 978-0-521-88895-0 hardback

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To my daughter, Cathy

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Preface

I am pleased to offer the research community my second book-length contribution to the field of bioinformatics. My first book, *Advanced Analysis of Gene Expression Microarray Data*, was published in 2006 by World Scientific as part of its Science, Engineering, and Biology Informatics (SEBI) series. I first became involved in the study of bioinformatics in 1998 and, over the ensuing decade, have been struck by the enormous quantity of data being generated and the need for effective approaches to its analysis.

The analysis of protein–protein interactions (PPIs) is fundamental to the understanding of cellular organizations, processes, and functions. It has been observed that proteins seldom act as single isolated species in the performance of their functions; rather, proteins involved in the same cellular processes often interact with each other. Therefore, the functions of uncharacterized proteins can be predicted through comparison with the interactions of similar known proteins. A detailed examination of a PPI network can thus yield significant new insights into protein functions. These interactions have traditionally been examined via intensive small-scale investigations of a small set of proteins of interest, each yielding information about a limited number of PPIs. The existing databases of PPIs have been compiled from such small-scale screens, presented in individual research papers. Because these data were subject to stringent controls and evaluation in the peer-review process, they can be considered to be fairly reliable. However, each experiment observes only a few interactions and yields a data set of very limited size. Recent large-scale investigations of PPIs using such techniques as two-hybrid systems, mass spectrometry, and protein microarrays have enriched the available protein interaction data and facilitated the construction of integrated PPI networks. The resulting large volume of PPI data has posed a challenge to experimental investigation. Consequently, computational analysis of the networks has become a necessary tool for the determination of functionally associated proteins.

This book is intended to provide a comprehensive understanding of the computational methods available for the analysis of PPI networks. It offers an in-depth survey of a range of approaches to this analysis, including statistical, topological, data-mining, and ontology-based methods. The fundamental principles underlying each of

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these approaches are discussed, along with their respective benefits and drawbacks. Suggestions for future research are also offered. In total, this book is intended to offer bioinformatics researchers a comprehensive and practical guide to the analysis of PPI networks, which will assist and stimulate their further investigation.

Some knowledge on the part of the reader in the fields of molecular biology, data mining, and statistics is assumed. Apart from this, the book is designed to be self-contained, as it includes introductions to the fundamental concepts underlying data generation and analysis. Thus, this book is expected to be of interest to a variety of researchers. It can be used as a textbook for advanced graduate courses in bioinformatics, and most of its content has been tested in the author's graduate-level course in this field. In addition, it can serve as a resource for graduate students seeking topics for investigation. The book will also be useful to researchers involved in computational biology in universities, organizations, and industry. For this audience, it will provide guidance on the techniques available for analysis of PPI networks. Research professionals interested in expanding their knowledge base can draw upon the material presented here to gain an understanding of principles and methods involved in this growing and highly significant field.

ACKNOWLEDGMENTS

I would like to express my deepest thanks to my doctoral students, Pritam Chanda, Young-rae Cho, Woo-chang Hwang, Taehyong Kim, and Lei Shi, for their excellent technical contributions. I am also highly appreciative of the editorial work of Rachel Ramadhyani.

The inspiration for this book was an invitation from Ms. Lauren Cowles, a senior editor from Cambridge University Press. I would like to express my special thanks to her.

Aidong Zhang
Buffalo, New York

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