

Preface

For the field of systems biology to mature, novel statistical and computational analysis methods are needed to deal with the growing amount of high-throughput data from genomics and genetics experiments. This book presents such methods and applications to data from biological and biomedical problems. Nowadays, it is widely recognized that *networks* form a very fruitful representation for studying problems in systems biology [1, 2]. However, many traditional methods do not make explicit use of a network representation of the data. For this reason, the topics treated in this book explore statistical and computational data analysis aspects of *networks* in systems biology [3–6].

Biological phenotypes are mediated by very intricate networks of interactions among biological components. This book covers extensively what we view as two complementary but strongly interrelated challenges in network biology. The first lies in inferring networks from experimental observations of state variables of a system. Interactions among molecular components are traditionally characterized through equilibrium binding or kinetic experiments *in vitro* with dilute solutions of the purified components. However, such experiments are typically low throughput and unable to properly account for the conditions prevailing *in vivo*, where factors such as molecular crowding, spatial heterogeneity, and the presence of ligands might strongly modify the interactions of interest. The possibility of inferring network connectivity and even quantitative interaction parameters from observations of intact living systems is attracting considerable research interest as a way of escaping such shortcomings. The fact that biological networks are complex, that problems are often poorly constrained, and that data are often high dimensional and noisy makes this challenge daunting. The second and perhaps equally difficult challenge lies in deriving results that are both biologically relevant and reliable from incomplete and uncertain information about biological interaction networks. We hope that the contributions in the subsequent chapters will help the reader understand and meet these challenges.

This book is intended for researches and graduate and advanced undergraduate students in the interdisciplinary fields of computational biology, biostatistics, bioinformatics, and systems biology studying problems in biological and biomedical sciences. The book is organized in four main parts: Part One: Modeling, Simulation, and Meaning of Gene Networks; Part Two: Inference of Gene Networks; Part 3: Analysis of Gene Networks; and Part Four: Systems Approach to Diseases. Each part

consists of chapters that emphasize the topic of the corresponding part, however, without being disconnected from the remainder of the book. Overall, to order the different parts we assumed an intuitive – problem-oriented – perspective moving from *Modeling, Simulation, and Meaning of Gene Networks* to *Inference of Gene Networks* and *Analysis of Gene Networks*. The last part presents biomedical applications of various methods in *Systems Approach to Diseases*.

Each chapter is comprehensively presented, accessible not only to researchers from this field but also to advanced undergraduate or graduate students. For this reason, each chapter not only presents technical results but also provides background knowledge necessary to understand the statistical method or the biological problem under consideration. This allows to use this book as a textbook for an interdisciplinary seminar for advanced students not only because of the comprehensiveness of the chapters but also because of its size allowing to fill a complete semester.

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Finally, we hope that this book will help to spread out the enthusiasm and joy we have for this field and inspire people regarding their own practical or theoretical research problems.

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