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## Preface

The explosion of new technologies in the post-genomic era is allowing the study of biological systems on a genome-wide scale, at the main functional genomic levels: (epi)-genome, transcriptome, proteome, endo- and exometabolome, and their interactions. At the same time that these techniques are being applied and refined, the complexity of biological systems is being rediscovered (1) with thousands of components (e.g., genes, transcripts, proteins, metabolites) participating in finely tuned metabolic and regulatory networks. “Molecular pathways, rather than being linear, independent from or parallel to each other, are instead incredibly intertwined and form very complex biological networks. Phenotypes are probably more directly related to systems properties than they are to DNA and ‘genes’” (Marc Vidal in (2)). The idea that multi-scale dynamic complex systems formed by interacting macromolecules and metabolites, cells, organs, and organisms underlie some of the most fundamental aspects of life was proposed by a few visionaries half a century ago (*see* (3) and references therein). We are witnessing a powerful resurgence of this idea made possible by the availability of genome sequences, ever improving gene annotations and interactome network maps, the development of new informatic and imaging tools, and the use of concepts from engineering and physics. Alongside other fundamental “great ideas” as suggested by Paul Nurse (4), systems-level understanding (i.e., systems biology) may materialize as one of the major ideas of post-genomic biology (2–4).

Systems biology aims at deciphering all of the genotype–phenotype relationships at the levels of genes, transcripts (RNAs), peptides, proteins, metabolites, and environmental factors participating in complex cellular networks. This should reveal the mechanisms and principles governing the behavior of complex biological systems. Systems biology is not so much concerned with inventories of working parts but, rather, with how those parts interact to produce working units of biological organization whose properties are much greater than the sum of their parts (3–5).

The purpose of this book is to present (a) an up-to-date view of the optimal characteristics of the yeast *Saccharomyces cerevisiae* as a model eukaryote for systems biology studies (6, 7), (b) a perspective on the latest experimental and computational techniques for systems biology studies, most of which were first designed for and validated in yeast, and (c) selected examples of yeast systems biology studies and their applications in biotechnology and medicine. The main molecular mechanisms, biological networks, and sub-cellular organization are essentially conserved in all eukaryotes, being derived from a complex common ancestor (8). Thus *S. cerevisiae* will continue to make a huge contribution to our understanding of eukaryotic systems biology. New advanced post-genomic techniques are opening the way to the characterization of the core of interactions, modules, architectures, and network dynamics that are essential to all eukaryotes. Yeast systems biology experiments under controlled conditions can uncover the complexity and interplay of biological networks with their dynamics, basic principles of internal organization, and balanced orchestrated functions between organelles in direct interaction with the environment as well as the characterization of short- and long-term effects of perturbations and dysregulation of networks that may illuminate the origin of complex human diseases. These

approaches can then be reproduced in systems biology studies of more complex organisms, including higher eukaryotes and, ultimately, humans (2, 3).

This book comprises four sections: In Section I (**Chapter 1**), we present an up-to-date view of the optimal characteristics of the yeast *S. cerevisiae* as a model eukaryote for systems biology studies, with selected examples in biotechnology and medicine.

In Section II (**Chapters 2–18**), we present a perspective on the latest high-throughput and molecular techniques and protocols.

In Section III (**Chapters 19–27**), we present a perspective on advanced computational, in silico, systems biology strategies, and studies for quantitative data analysis and integration, as well as modeling approaches toward a holistic quantitative description of the yeast cell as a model for the essential unit of eukaryotic life.

In Section IV (**Chapter 28**), relevant contributions of *S. cerevisiae* as a tool for mammalian studies are presented.

This book is intended for postgraduate students, post-doctoral researchers, and experts in different fields with an interest in (a) comprehensive systems biology strategies in well-defined model systems with specific objectives; (b) a better knowledge of the latest post-genomic strategies at all “omic levels and computational approaches toward analysis, integration, and modeling of biological systems, from single-celled organisms to higher eukaryotes.”

New types of expertise and sustained collaborations between researchers from many different fields both within biology and in the engineering, physical, and computational sciences are essential to advance our knowledge of the exquisite complexity of eukaryotes at the systems level (2–5) (**Chapter 1**). We thank all our authors and advisors; their deep knowledge and expertise in different fields have proven invaluable in this essentially multidisciplinary effort. We are also grateful to our families for their support in enabling us to complete this project.

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<http://www.springer.com/978-1-61779-172-7>

Yeast Systems Biology

Methods and Protocols

Castrillo, J.I.; Oliver, S.G. (Eds.)

2011, XIV, 535 p. 85 illus., 2 illus. in color., Hardcover

ISBN: 978-1-61779-172-7

A product of Humana Press