

Foreword to *Theoretical and Applied Aspects of Systems Biology*

A central challenge of medicine is to understand how health and disease emerge from the myriad of molecular interactions among our genes and our environment. Over the past 30 years, researchers have invented a wide array of methods to measure our genes and our environment and numerous computational methods to analyze such molecular data. To date, these methods have been used to collect a wealth of data about a broad range of cellular processes, organisms, patients, and diseases. This has led to numerous insights into the functions of individual genes and the mechanisms of individual diseases, as well as diagnostic tests and treatments for several specific diseases. For example, cell-free fetal DNA sequencing can now be used to diagnose Down syndrome as early as 4 weeks after conception, breast cancers driven by mutations in HER2 are now frequently treated with anti-HER2 antibodies such as trastuzumab, and cytochrome P450 is now routinely genotyped to personalize the dosage of drugs metabolized by cytochrome P450 such as atorvastatin and tamoxifen.

However, despite this progress, we still do not have a comprehensive understanding of how our genes and our environment interact to determine our health. As a result, we still do not understand the genetics of most diseases, we still cannot tailor therapy to individual patients, and many patients continue to suffer from potentially treatable diseases. To better understand and treat disease, we must develop computational models of the molecular systems responsible for our health and disease. In particular, we must develop models that help researchers integrate complementary datasets, predict phenotype from genotype, design new drugs, and personalize medicine.

Overcoming the numerous technical challenges to achieve this vision will likely require the coordinated effort of an international community of modelers, experimentalists, software engineers, clinicians, and research sponsors. To prepare young scientists to address these challenges and to begin to form a community that can tackle them, Fabricio Alves Barbosa da Silva, Nicolas Carels, and Floriano Paes Silva Junior from the Oswaldo Cruz Foundation organized the International Course on Theoretical and Applied Aspects of Systems Biology in Rio de Janeiro, Brazil, in July 2017. The meeting featured ten lectures from scientists from Brazil, Canada,

Luxembourg, the Netherlands, Portugal, and the USA. The lectures taught students how to use multi-omics data and a wide variety of mathematical formalisms, including network modeling, Bayesian modeling, Petri Nets, flux balance analysis, ordinary differential equations, and hybrid modeling, to gain insights into cellular processes such as metabolism, transcriptional regulation, and signal transduction and advance infectious disease medicine, precision oncology, drug development, and synthetic biology. The meeting also featured a poster session for students to share their research.

This book edited by Fabricio Alves Barbosa da Silva, Nicolas Carels, and Floriano Paes Silva Junior summarizes the computational systems biology methods and applications that were presented at the course. The book includes eight chapters that summarize eight of the lectures, as well as five additional chapters contributed by other researchers who participated in the course on applications of systems biology to metagenomics and neuroscience.

Computational systems biology has great potential to transform biological science and medicine and numerous opportunities for young, ambitious scientists to make fundamental contributions to science and medicine. We invite you to use this book to learn about the state of the art and potential of systems biology, and we hope that you join our efforts to use systems biology to advance human health.

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