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## Preface

Thanks to the large diffusion of bacterial genome analysis, determining the genome sequence of (almost any) organisms has become a routine task. One of the most important drawbacks associated with the booming of genomics resides in the possibility to quickly derive a comprehensive metabolic reconstruction of a cell and to use computational simulations to predict its metabolic landscape.

Metabolic modeling confers to microbiologists the opportunity to further expand the knowledge offered by genome sequence alone. Indeed, despite the analysis of genome sequence *per se* that can provide interesting and fundamental hints on microbial life (e.g., genome structure, presence/absence patterns, and phylogenetic features), many questions may remain unresolved. This may limit the study of microbial genomics to the assembly and the interpretation of gene lists. To provide a system-level picture of cellular life and gain some insights on, for example, the effect of gene deletions and/or nutritional fluctuations, more sophisticated analytic tools have to be exploited. Constraint-based metabolic modeling (CBMM) represents one of these methodologies, combining good predictive abilities with a relatively simple conceptual and practical framework. This latter point probably best explains the success and the recent spreading of this approach as, ultimately, CBMM allows both the generation of testable hypotheses and the reduction of the amount of wet-lab experiments to be performed, saving time, efforts, and costs.

This book is intended to provide the most recent methodologies about the study of cellular metabolism using *in silico* approaches. The volume is ideally divided into three distinct parts. In the first part tools and methodologies for metabolic reconstructions and basic CBMM are presented (Chapters 1–10). The second part of the book (Chapters 11, 12, and 13) contains protocols for the generation of experimental data that can guide metabolic reconstruction and modeling, namely transcriptomics, proteomics, and mutants generation. The final part of the book (Chapters 14–18) covers more advanced methodologies for quantitative modeling of cellular metabolism, including dynamic Flux Balance Analysis, host-pathogen metabolic interactions, and multiobjective optimization. In each of these parts the most up-to-date protocols and procedures for metabolic reconstruction and CBMM will be provided. The aim of the present book is then to serve as a “field guide” both for qualified investigators on cellular metabolism (including computational biologists, microbiologists, physiologists, biochemists) who want to update their technical knowledge and for less-experienced researchers who want to start working with CBMM.

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