Preface

As a special class of noncoding RNAs, microRNAs (miRNAs or miRs for short) have been reported to perform important roles in various biological and pathological processes by regulating respective target genes. To completely understand and fully delineate miR functions, besides performing biological experiments and querying PubMed and TarBase for biologically validated miR targets, biologists can also query various miR target prediction databases/websites for computationally predicted targets. More often than not, biologists need to extract additional information for each and every miR target, either validated or putative, with regard to its related information such as protein functions and affiliated signaling pathways. In short, biologists are facing significant barriers in fully delineating miR functions and the following effective bio-curation. Therefore, there is an urgent need for a comprehensive book focusing on miR target genes, miR regulation mechanisms, miR functions performed in various human diseases, and miR databases/knowledge bases.

This book is intended to give an in-depth introduction to and discussion of miRs and their targets, miR functions, and computational techniques applied in miR research. The primary audience includes, but is not limited to, computational biologists, computer scientists, bioinformaticians, bench biologists, and clinical investigators. No prior knowledge of computer science, databases, semantic technologies, or molecular biology is assumed. But we do assume that readers have some biology background knowledge at the high-school level.

A brief overview of the book structure is as follows. Chapter 1 introduces the concepts of miRs and long noncoding RNAs (lncRNAs) as well as some recent advances in miR/lncRNA biology. Chapters 2, 3, and 4 discuss protein participants in miR regulation; viral microRNAs, host miRs regulating viruses, and bacterial miR-like RNAs; and biomarkers, diagnostics, and therapeutics aspects of miRs, respectively. Chapter 5 introduces basic concepts of relational databases and biomedical big data. Chapter 6 provides an overview of semantic technologies and bio-ontologies. Chapter 7 discusses genome-wide analysis of miR-regulated transcripts. Chapters 8 and 9 describe in detail computational prediction of miR target genes, regulatory interactions between miRs and their targets, as well as an introduction of various miR target prediction databases and relevant Web resources. Chapter 10 discusses some limitations of existing approaches that aim to improve miR target prediction accuracy. Chapters 11 and 12 introduce genomic regulation of miR expression in disease development and next generation sequencing for miR expression profile. Chapters 13 through 16 discuss advanced topics in computational/bioinformatics approaches in miR research, including the handling of high-dimension data, identification and removal of noisy data, logical reasoning, and machine learning techniques. Finally, Chapters 17–19 introduce some advances of miR research in three human diseases: diabetes, obesity, and thyroid carcinoma.

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