

Preface

This volume focuses on the modern computational and statistical tools for gene expression and regulation research to improve the understanding prognosis, diagnostics, prediction of severity, and therapies for human diseases. The recent advancements of microarray and next-generation sequencing technologies made it possible to detect gene expression at a genome-wide scale, which has greatly facilitated the identification of pathophysiological changes in various diseases. How are the global gene expression profiles regulated and what are the mechanisms underlying these changes? How are the signaling pathways altered under pathological conditions? How do the various regulatory molecules interact in a network to control disease states? How does the different genetic makeup of individuals affect the disease perceptibility and treatment outcome? These are fundamental questions for finding cures for complex human diseases and developing personalized medicine that is the future of health care. In this volume, we introduce the readers to some of state-of-the-art technologies as well as computational and statistical tools for translational bioinformatics in the areas of gene transcription and regulation, including the tools for next-generation sequencing analyses, alternative splicing, the modeling of signaling pathways, network analyses in predicting disease genes, as well as protein and gene expression data integration in complex human diseases. This volume is particularly suitable for researchers, physicians, or students in the field of molecular, clinical biology and bioinformatics. This exciting volume would not be possible without the expertise and dedication of all the contributing authors. Finally, I would like to dedicate this volume to my family for their unconditional love and support.

Houston, TX

Jiaqian Wu