



Computational Biology and Bioinformatics: Gene Regulation

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The advances in biotechnology such as the next generation sequencing technologies are occurring at breathtaking speed. Advances and breakthroughs give competitive advantages to those who are prepared. However, the driving force behind the positive competition is not only limited to the technological advancement, but also to the companion data analytical skills and computational methods which are collectively called computational biology and bioinformatics. Without them, the biotechnology-output data by itself is raw and perhaps meaningless. To raise such awareness, we have collected the state-of-the-art research works in computational biology and bioinformatics with a thematic focus on gene regulation in this book.

This book is designed to be self-contained and comprehensive, targeting senior undergraduates and junior graduate students in the related disciplines such as bioinformatics, computational biology, biostatistics, genome science, computer science, applied data mining, applied machine learning, life science, biomedical science, and genetics. In addition, we believe that this book will serve as a useful reference for both bioinformaticians and computational biologists in the post-genomic era.

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Editorial Review

Review

This dense book is a collection of peer-reviewed chapters on the subject of bioinformatics and computational biology in the context of gene regulation. Each chapter was written by a unique set of authors, and the editor compiled the totality to fill a perceived information void. Given the multitude of authors, as well as the challenging subject matter, the readability of each chapter varies. The 17 chapters are organized into six sections covering genes; RNAs; proteins; epigenetics; a case study of gene mutations linked to drug resistance; and advanced topics covering quality assurance, computational trends in sequence alignment, state estimation and process monitoring, next-generation sequencing, metabolic engineering, evolutionary conservation, and protein model ranking. All the chapters are annotated well with references, numerous figures (in color, when necessary), equations, graphs, charts, models, and tables that effectively support the text. Many tables include descriptions, remarks, additional references, and databases with website links. According to the editor, this book is intended to be "self-contained and comprehensive" and geared toward upper-level undergraduates and beginning graduate students in the interdisciplinary areas where biology, computer science, and statistics congregate.

--C. L. Iwema, *University of Pittsburgh*, appear in February 2017 issues of CHOICE

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