

# Preface

The field of computational biology and bioinformatics has been rapidly evolving in recent years. It holds tremendous potential to have a good impact on understanding genetics, developing personalized medicine solutions. Hundreds of books have been written on it. In particular, there are only few bioinformatics books with a focus on gene regulation. Therefore, this book has been compiled to fill the void. The book is an open-chapter-called collection of peer-reviewed chapters contributed by international experts who have passed through rigorous blind reviews. Following the central dogma of molecular biology, the book content is divided into six sections: Genes (Chapters 1 to 3), RNAs (Chapters 4 and 5), Proteins (Chapters 6 and 7), Epigenetics (Chapters 8 and 9), Case Study (Chapter 10), and Advanced Topics (Chapters 11 to 17).

(Section 1: Genes) In Chapter 1, Cao and Yip compile a comprehensive survey on enhancers which are central to gene transcription. In Chapter 2, Wei et al. introduce a software package for detecting differential gene expression. In Chapter 3, Fujita et al. describe how Granger causality can be applied to infer gene regulatory networks from gene expression data.

(Section 2: RNAs) In Chapter 4, Keservani et al. present a reader-friendly tutorial on RNA sequencing and its relation to gene regulation. In Chapter 5, Samantarrai et al. focus on non-coding RNAs and its network applications from the view of system biology.

(Section 3: Proteins) In Chapter 6, Mishra et al. compare different algorithms for the annotation of hypothetical proteins. In Chapter 7, Hahn and Muley review the computational protein-protein functional linkage prediction methods. They also propose a gene co-regulation based method for functional linkage prediction.

(Section 4: Epigenetics) In Chapter 8, Wang et al. give us a review on bioinformatics methodologies and tools for performing epigenomic analysis of chromatin organization and DNA methylation. In Chapter 9, Lou focuses on the statistical modeling of DNA methylation with sharp insights into its role in coding regions and gene regulation.

(Section 5: Case Study) In Chapter 10, Wang et al. describe a case study of EGFR-related gene mutations which are linked to drug resistance in non-small-cell lung carcinoma treatments.

(Section 6: Advanced Topics) In Chapter 11, Giannoulatou et al. review contemporary approaches for quality assurance in genome-scale bioinformatics analyses. In Chapter 12, Issa reports the recent trends in biological sequence alignment methods. In Chapter 13, Mansouri et al. introduce a mathematical book chapter on state estimation and process monitoring of nonlinear biological

phenomena. In Chapter 14, Neelapu and Challa provide us a review on metagenomics with an emphasis on gene regulation. In Chapter 15, Thukral and Hasija describe how gene regulation can be altered in the context of metabolic engineering. In Chapter 16, Gupta et al. review general bioinformatics tools for phylogenetic analysis and ortholog identification which can shape gene regulation mechanisms of different species throughout the evolutionary history. In Chapter 17, Shikhin et al. have compiled a book chapter about protein model ranking through topological assessment.

In summary, state-of-the-art computational biology and bioinformatics studies are described and summarized in this book. This book provides updated reviews on the computational biology and bioinformatics studies for gene regulation. I hope that this book can help accelerate the advancement of the scientific community in computational biology and bioinformatics, benefiting the human beings and other species on the earth.

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