

Preface

In the past decade, we have seen mounting evidence of the usefulness of computational approaches to bioinformatics and biomedical research. Semantic computing, machine learning classifiers, clustering algorithms and mathematical methods have been particularly influential in contributing insights in the era of post-genomics research. In the post-genomics era, computational biology will certainly play an increasingly important role in elucidating the underlying features and mechanisms in biological systems.

The use of advanced computational approaches is an effective mean to address difficult problems in bioinformatics and biomedical research. An advantage of applying computational methods is to reduce the cost and time compared to doing real experiments; hence, there are needs for developing and advancing such area of research. As the volume of biomedical data increases, so does demand for establishing and building up more computational methods for solving a wide range of applications.

This book is a collection of 10 chapters written by international researchers with expertise in microarray data analysis, semantic computing, dynamics modelling of biomolecular interactions, fuzzy integral, molecular simulation and machine learning algorithms. In particular, a variety of computational methods are presented to different areas of studies in biomedicine and bioinformatics analysis; such as, time series data analysis, ensemble clustering, protein and nucleic acid interaction, host-pathogen interaction system, RNA network in autoimmune diseases, multiple omics data integration, T-cell epitope and cytometry.

In short, this book presents the use of advanced computational methods for a range of biomedical applications. Instead of focusing on problems in molecular biology, sequence analysis or cancer-related research, the book pay attention to a range of biomedical issues rather than the fundamentals.

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Taichung, 2017