METADATA

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Abstract

This book aims to cover a wide range of topics in contemporary biosciences under the unifying lens of computational biology. It focuses on computational approaches to problems in biological data analysis and, from this perspective, its subject matter lies at the intersection of different disciplines, with the main emphasis on biosciences, mathematics, statistics, and computer science. The book is structured in 13 chapters, corresponding to the number of weeks in an academic semester. Of these, the first and last chapters contain the basic introductory concepts and examples of applications of Computational Biology, respectively, while the intermediate 11 chapters are devoted to specific biological problems. More specifically, the book covers topics such as sequence analysis (genomic composition, primary structure, patterns, alignment of primary sequences, Chapters 2–5), the study of the secondary structure of biological sequences (Chapter 6), phylogenetic analysis (Chapter 7), gene expression analysis (Chapters 8–9), biological network analysis (Chapter 10), genetic diversity analysis (Chapter 11), and large-scale biological data processing (Chapter 12). Each chapter is structured in such a way as to cover both the basic biological principles of the problem under study and the mathematical concepts and computational methodologies for its solution. Alongside the development of the topics, there are one or more practical exercises aimed at familiarizing students with the corresponding methodologies, as one of the objectives of this textbook is to serve as a laboratory manual. At the end of each chapter, there are examples of applications and a detailed bibliography with suggestions for the level at which students may wish to deepen their knowledge of specific topics.

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