

# Preface

Bioinformatics is recognized as the science of the 21st century, and a lot of research has been conducted and on-going throughout the world in this field. An updated resource with respect to time is required for a better understanding of the tremendous power of computational approaches and their application in solving complex biological problems. This book covers the basic understanding of the bioinformatics topics as well as focuses on recent developments in the methods, tools, and approaches related to bioinformatics, which includes biological databases and their application, sequence analysis and comparison, phylogeny, NGS data analysis, genome, and transcriptome assembly and annotation, gene ontology, metagenomics studies, SNP and SSR identification and analysis, transcriptome analysis; microarray studies, RNA-Seq data analysis, protein structure prediction, visualization, analysis and validation; pharmacophore modeling, structure-based and ligand-based drug design, molecular docking, molecular dynamics simulation, optimization of lead compounds, pharmacokinetics and pharmacodynamics modeling, in silico vaccine designing, pathway modeling and simulation, network biology, metabolomics, and flux balance analysis, systems biology and big data analysis, machine learning, and data mining approaches.

This book also covers the broad spectrum of computational analysis and case studies and enables the reader to find information about various bioinformatics methods, tools, and their applications in a single resource. Bioinformatics has a very broad range of applications, and this field is upgrading very rapidly as many new resources and approaches are being developed day by day. The chapters of this book have been compiled considering the diverse applications of this field. This book can serve as a very useful learning source for undergraduate, postgraduate, and research students of bioinformatics, biotechnology, life sciences, and agricultural sciences, chemical, pharmaceutical, and medical sciences who have no computational background. Besides, it is also useful for bioinformatics and computer science students, research scientists, and pharmaceutical persons to understand the fundamental concepts of bioinformatics and utilize this knowledge to tackle research projects. However, in spite of the best efforts, the first version of a book always has some opportunities to improve. We will be happy to receive the important suggestions for further improvements in the content coverage.