
Preface

This book describes current research from around the world on studies involving bioinformatics and computational biology tools. Bioinformatics is the field of science in which computer science, information technology and biology, merge to form a single discipline. It is the application of information technology and computer science to the field of biology and biological systems. It is a new science which is very helpful in understanding most of the biological processes. In the last few years the use of bioinformatics has increased tremendously and it has aided in developing new methods to understand the complex biological systems. Bioinformatics, which is the melding of molecular biology with computer science, is essential to the use of genomic information in understanding human diseases and in the identification of new molecular targets for drug discovery. Bioinformatics has wide applications and its major uses in this field are gene finding, genome assembly, drug design and discovery and genome wide association studies. The field of bioinformatics has developed in a way that the critical tasks involve the detailed analysis and interpretation of the variety of data, including nucleotide and amino acid sequences, protein domains, and protein structures. This real process of analyzing and interpreting data is commonly known as computational biology. This book describes the use of bioinformatics and computational biology in a variety of processes. Some of these are biobanking, application of next-generation DNA sequencing in medical discovery, microRNA profiling involved in human tumorigenesis and cancer phylogenetics.

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