

# Preface

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Gene and genome sequencing on one hand and protein sequencing on the other hand have generated lots of data which needs to be stored, analyzed and inferences drawn. These developments led to the applications of bioinformatics tools in the field of biology. This book describes the principles underlying the analysis of sequence information from genes, genomes and proteins. Data mining, its principle and applications are discussed. There are two types of analysis. One type of analysis aims at identifying or detecting elements comprising genes and genome whereas other type of analysis aims at predicting these elements. For example, one can have information regarding a gene either through sequence comparison or through *ab initio* prediction methods. Thus all structural and regulatory elements of gene and genome can be studied. Different types of databases in case of nucleic acids and proteins are discussed. The methods of pairwise sequence comparison and multiple sequence comparison and their algorithms are discussed. Methods for visual comparison are also described. The different available software programmes are described and their addresses are given which will help students and researchers in obtaining and using for practical purposes.

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