

# Preface

Biology has progressed tremendously in the last decade due in part to the increased automation in the generation of data from sequences to genotypes to phenotypes. Biology is now very much an information science, and bioinformatics provides the means to connect biological data to hypotheses. Within this volume, we have collated chapters describing various areas of applied bioinformatics, from the analysis of sequence, literature, and functional data to the function and evolution of organisms. The ability to process and interpret large volumes of data is essential with the application of new high throughput DNA sequencers providing an overload of sequence data. Initial chapters provide an introduction to the analysis of DNA and protein sequences, from motif detection to gene prediction and annotation, with specific chapters on DNA and protein databases as well as data visualization. Additional chapters focus on gene expression analysis from the perspective of traditional microarrays and more recent sequence-based approaches, followed by an introduction to the evolving field of phenomics, with specific chapters detailing advances in plant and microbial phenome analysis and a chapter dealing with the important issue of standards for functional genomics. Further chapters present the area of literature databases and associated mining tools which are becoming increasingly essential to interpret the vast volume of published biological information, while the final chapters present bioinformatics purely from a developer's point of view, describing the various data and databases as well as common programming languages used for bioinformatics applications. These chapters provide an introduction and motivation to further avenues for implementation. Together, this volume aims to provide a resource for biology students wanting a greater understanding of the encroaching area of bioinformatics, as well as computer scientists who are interested learning more about the field of applied bioinformatics.

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