Preface

Bioinformatics is playing a significant role in the current revolution in modern biology. It attempts to unfurl the mystery of the biologically meaningful patterns of a sequence string of nucleotides. Teaching bioinformatics is now becoming an integral part of the core curriculum at most universities. We believe that it is only by understanding and wisely using these resources we will be able to push the frontier forward.

In this process we have come up with the following features, which should make this edition particularly helpful to you offering essential, practical answers to the day-to-day problems encountered in a successful career in modern biology. The target audience for this book is the biologists, especially the beginners, who want to learn how to analyze DNA or protein sequences in a simple but meaningful fashion. Readers are not expected to possess special background in statistics, mathematics, or computer science, rather just a basic knowledge of molecular biology and internet is all required.

This manual is expected to serve as a resource guide to some of the web-based analysis packages, including some standalone computing resources that are available free for academics to address some of the basic tasks of bioinformatics. In this manual, we focus on few theoretical aspects and emphasize more on applied concepts on PCR primer designing, sequence retrieval, sequence-similarity searching using BLAST, multiple-sequence alignment, phylogenetic analysis, RNA structure analysis, and protein sequence and structure analysis. Molecular docking is also included in this manual. This could be seen as an enriched task-oriented manual that will direct the reader through step-by-step instructions, completing specific bioinformatics analyses. Every chapter and exercise begins with an overview, followed by specific examples on how to perform and interpret the results, and concludes with exercises to test and explore some of the additional concepts. The manual finally concludes with the authors' recommendations on how to keep current with the ever-increasing information on bioinformatics through the appendix, providing links to the resources discussed and additional resources.

Bioinformatics—A Student's Companion presents a broad overview of the computational resources to help orient those just beginning to use computational

tools to address biological problems. We strongly believe that even a novice can quickly tackle each computational problem and arrive at a satisfying result when guided by this unique step-by-step approach on the collection of software with illustrative examples. Most exercises could be used for practical courses in advanced undergraduate- or graduate-level courses in life sciences.

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