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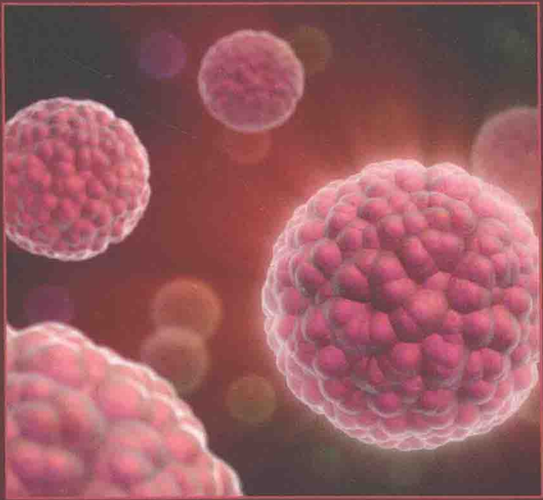
Pattern Recognition in Computational Molecular Biology

TECHNIQUES AND APPROACHES



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WILEY

PATTERN RECOGNITION IN COMPUTATIONAL MOLECULAR BIOLOGY

Techniques and Approaches

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PREFACE

Pattern recognition is the automatic identification of *regularities*, that is, figures, characters, shapes, and forms present in data. Pattern recognition is the core process of many scientific discoveries, whereby researchers detect regularities in large amounts of data in fields as diverse as Geology, Physics, Astronomy, and Molecular Biology. Pattern recognition in biomolecular data is at the core of Molecular Biology research. Indeed, pattern recognition makes a very important contribution to the analysis of biomolecular data. In fact, it can reveal information about shared biological functions of biological macromolecules, that is, DNA, RNA, and proteins, originating from several different organisms, by the identification of patterns that are shared by structures related to these macromolecules. These patterns, which have been conserved during evolution, often play an important structural and/or functional role, and consequently, shed light on the mechanisms and the biological processes in which these macromolecules participate. Pattern recognition in biomolecular data is also used in evolutionary studies, in order to analyze relationships that exist between species and establish whether two, or several, biological macromolecules are *homologous*, that is, have a common biological ancestor, and to reconstruct the phylogenetic tree that links them to this ancestor. On the other hand, with the new sequencing technologies, the number of biological sequences in databases is increasing exponentially. In addition, the lengths of these sequences are large. Hence, the recognition of patterns in such databases requires the development of fast, low-memory requirements and high-performance techniques and approaches. This book provides an up-to-date forum of such techniques and approaches that deal with the most studied, the most important, and/or the newest topics in the field of pattern recognition. Some of these techniques and approaches represent improvements on old ones, while others are completely new. Most of current books on pattern recognition in biomolecular data either lack technical depth or focus on specific, narrow topics. This book is the first overview on techniques and approaches on pattern recognition in biomolecular data with both a broad coverage of this field and enough depth to be of practical use to working professionals. It surveys the most recent developments of techniques and approaches on pattern recognition in biomolecular data, offering enough fundamental and technical information on these techniques and approaches and the related problems, without overloading the reader. This book will thus be invaluable not only for practitioners and professional researchers in Computer Science, Life Science, and Mathematics but also for graduate students and young researchers looking for promising directions in their work. It will certainly point them to new techniques and approaches that may be the key to new and important discoveries in Molecular Biology.

This book is organized into seven parts: *Pattern Recognition in Sequences*, *Pattern Recognition in Secondary Structures*, *Pattern Recognition in Tertiary Structures*, *Pattern Recognition in Quaternary Structures*, *Pattern Recognition in Microarrays*, *Pattern Recognition in Phylogenetic Trees*, and *Pattern Recognition in Biological Networks*. The 29 chapters, which make up the seven parts of this book, were carefully selected to provide a wide scope with minimal overlap between the chapters so as to reduce duplications. Each contributor was asked to cover review material as well as current developments in his/her chapter. In addition, the choice of authors was made by selecting those who are leaders in their respective fields.

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