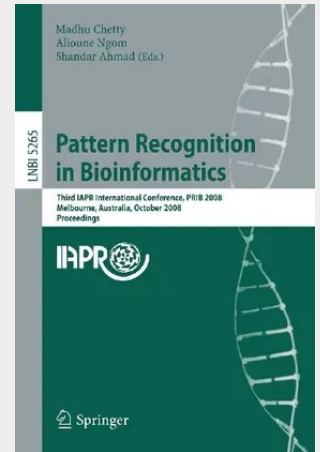


Pattern Recognition in Bioinformatics

Third IAPR International Conference, PRIB 2008, Melbourne, Australia, October 15-17, 2008. Proceedings

In the post-genomic era, a holistic understanding of biological systems and processes, in all their complexity, is critical in comprehending nature's choreography of life. As a result, bioinformatics involving its two main disciplines, namely, the life sciences and the computational sciences, is fast becoming a very promising multidisciplinary research field. With the ever-increasing application of large-scale high-throughput technologies, such as gene or protein microarrays and mass spectrometry methods, the enormous body of information is growing rapidly. Bioinformaticians are posed with a large number of difficult problems to solve, arising not only due to the complexities in acquiring the molecular information but also due to the size and nature of the generated data sets and/or the limitations of the algorithms required for analyzing these data. Although the field of bioinformatics is still in its embryonic stage, the recent advancements in computational and information-theoretic techniques are enabling us to conduct various in silico testing and screening of many lab-based experiments before these are actually performed in vitro or in vivo. These in silico investigations are providing new insights for interpretation and establishing a new direction for a deeper understanding. Among the various advanced computational methods currently being applied to such studies, the pattern recognition techniques are mostly found to be at the core of the whole discovery process for apprehending the underlying biological knowledge. Thus, we can safely surmise that the ongoing bioinformatics revolution may, in future, inevitably play a major role in many aspects of medical practice and/or the discipline of life sciences.

In the post-genomic era, a holistic understanding of biological systems and processes, in all their complexity, is critical in comprehending nature's choreography of life. As a result, bioinformatics involving its two main disciplines, namely, the life sciences and the computational sciences, is fast becoming a very promising multidisciplinary research field. With the ever-increasing application of large-scale high-throughput technologies, such as gene or protein microarrays and mass spectrometry methods, the enormous body of information is growing rapidly. Bioinformaticians are posed with a large number of difficult problems to solve, arising not only due to the complexities in acquiring the molecular information but also due to the size and nature of the generated data sets and/or the limitations of the algorithms required for analyzing these data. Although the field of bioinformatics is still in its embryonic stage, the recent advancements in computational and information-theoretic techniques are enabling us to conduct various in silico testing and screening of many lab-based experiments before these are actually performed in vitro or in vivo. These in silico investigations are providing new insights for interpretation and establishing a new direction for a deeper understanding. Among the various advanced computational methods currently being applied to such studies, the pattern recognition techniques are mostly found to be at the core of the whole discovery process for apprehending the underlying biological knowledge. Thus, we can safely surmise that the ongoing bioinformatics revolution may, in future, inevitably play a major role in many aspects of medical practice and/or the discipline of life sciences.



53,49 €
49,99 € (zzgl. MwSt.)

Lieferfrist: bis zu 10 Tage

Artikelnummer: 9783540884347
Medium: Buch
ISBN: 978-3-540-88434-7
Verlag: Springer
Erscheinungstermin: 29.09.2008
Sprache(n): Englisch
Auflage: Erscheinungsjahr 2008
Serie: Lecture Notes in Computer Science
Produktform: Kartoniert
Gewicht: 739 g
Seiten: 472
Format (B x H): 155 x 235 mm

