

1. Record Nr.	UNINA9911092435503321
Titolo	Selected topics in post-genome knowledge discovery // editor[s], Limsoon Wong, Louxin Zhang
Pubbl/distr/stampa	Singapore, : Singapore University Press Singapore ; ; River Edge, NJ, : World Scientific Pub. Co., c2004
ISBN	9786611934736 9781281934734 1281934739 9789812794840 9812794840
Edizione	[1st ed.]
Descrizione fisica	1 online resource (176 p.)
Collana	Lecture notes series ; ; vol. 3
Altri autori (Persone)	WongLimsoon <1965-> ZhangLouxin
Disciplina	572.8 572.80285
Soggetti	Genetics - Mathematics Genetics
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references.
Nota di contenuto	Contents ; Foreword ; Preface ; Dynamic Programming Strategies for Analyzing Biomolecular Sequences ; 1. Introduction ; 2. Elementary Dynamic-Programming Algorithms ; 2.1. Fibonacci numbers ; 2.2. The maximum-sum substring problem ; 2.3. Longest increasing subsequence 2.4. Longest common subsequence 3. Sequence Alignment ; 3.1. Global alignment ; 3.2. Local alignment ; 3.3. Affine gap penalties ; 3.4. Space-saving strategies ; 3.5. Multiple sequence alignment ; The Representation Comparison and Prediction of Protein Pathways ; 1. Introduction 2. Online Pathway Resources 3. Pathway Representation ; 3.1. Pathway Space

; 3.2. SLIPR Format ; 4. Pathway Comparison
 ; 4.1. Comparing Individual Components ;
 4.2. Aligning Two Pathways Using Dynamic Programming
 ; 4.3. Pathway Database Comparison
 4.4. One Implementation: PM_search Documentation
 5. Orthologous Pathway Prediction ; 6.
 Discussion ; 6.1. Theoretical Issues on Evolutionary Study
 of Pathways ; 6.2. Establishing
 a Relational Pathway Database and its Web Interfaces
 ; 6.3. Pathway Prediction and Beyond
 Gene Network Inference and Biopathway Modeling
 1. Introduction ; 2. Gene Network Inference from
 Microarray Data ; 2.1. Boolean
 Network Model ; 2.2. Bayesian Network Model
 ; 3. Modeling and Simulation ; 3.1. Architecture for
 Biopathway Modeling ; 3.2. How to
 Model Biopathways
 3.3. Genomic Object Net and Biopathway Databases Towards
 Simulation

Sommario/riassunto

The Institute for Mathematical Sciences at the National University of Singapore organized a program on "Post-Genome Knowledge Discovery" from January to June 2002. The program focused on the computational and statistical analysis of sequences and genetics, and the mathematical modeling of complex biological interactions, which are critical to the accurate annotation of genomic sequences, the study of the interplay between genes and proteins, and the study of the genetic variability of species. As part of the program, tutorials for graduate students and newcomers to this transdisciplinary area
