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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