

**Wiley Series on Bioinformatics:
Computational Techniques and Engineering**

Yi Pan and Albert Y. Zomaya, Series Editors

Multiple Biological Sequence Alignment

SCORING FUNCTIONS, ALGORITHMS AND APPLICATIONS



KEN NGUYEN • XUAN GUO • YI PAN

WILEY

Resumo de Multiple Biological Sequence Alignment: Scoring Functions, Algorithms and Evaluation

Covers the fundamentals and techniques of multiple biological sequence alignment and analysis, and shows readers how to choose the appropriate sequence analysis tools for their tasks. This book describes the traditional and modern approaches in biological sequence alignment and homology search.

This book contains 11 chapters, with Chapter 1 providing basic information on biological sequences. Next, Chapter 2 contains fundamentals in pairwise sequence alignment, while Chapters 3 and 4 examine popular existing quantitative models and practical clustering techniques that have been used in multiple sequence alignment.

Chapter 5 describes, characterizes and relates many multiple sequence alignment models. Chapter 6 describes how traditionally phylogenetic trees have been constructed, and available sequence knowledge bases can be used to improve the accuracy of reconstructing phylogeny trees.

Chapter 7 covers the latest methods developed to improve the run-time efficiency of multiple sequence alignment. Next, Chapter 8 covers several popular existing multiple sequence alignment server and services, and Chapter 9 examines several multiple sequence alignment techniques that have been developed to handle short sequences (reads) produced by the Next Generation Sequencing technique (NSG).

Chapter 10 describes a Bioinformatics application using multiple sequence alignment of short reads or whole genomes as input. Lastly, Chapter 11 provides a review of RNA and protein secondary structure prediction using the evolution information inferred from multiple sequence alignments.

- Covers the full spectrum of the field, from alignment algorithms to scoring methods, practical techniques, and alignment tools and their evaluations -
- Describes theories and developments of scoring functions and scoring

matrices -Examines phylogeny estimation and large-scale homology search "Multiple Biological Sequence Alignment: Scoring Functions, Algorithms and Applications" is a reference for researchers, engineers, graduate and post-graduate students in bioinformatics, and system biology and molecular biologists.

Ken Nguyen, PhD, is an associate professor at Clayton State University, GA, USA. He received his PhD, MSc and BSc degrees in computer science all from Georgia State University. His research interests are in databases, parallel and distribute computing and bioinformatics.

He was a Molecular Basis of Disease fellow at Georgia State and is the recipient of the highest graduate honor at Georgia State, the William M. Suttles Graduate Fellowship. Xuan Guo, PhD, is a postdoctoral associate at Oak Ridge National Lab, USA.

He received his PhD degree in computer science from Georgia State University in 2015. His research interests are in bioinformatics, machine leaning, and cloud computing. He is an editorial assistant of "International Journal of Bioinformatics Research and Applications." Yi Pan, PhD, is a Regents' Professor of Computer Science and an Interim Associate Dean and Chair of Biology at Georgia State University.

He received his BE and ME in computer engineering from Tsinghua University in China and his PhD in computer science from the University of Pittsburgh. Dr. Pan's research interests include parallel and distributed computing, optical networks, wireless networks and bioinformatics.

He has published more than 180 journal papers with about 60 papers published in various IEEE/ACM journals. He is co-editor along with Albert Y. Zomaya of the Wiley Series in Bioinformatics.

[Acesse aqui a versão completa deste livro](#)