

1.	Record Nr.	UNINA990005475880403321
	Titolo	ROMAN portraits : A loan exhibition of Roman sculpture and coins from the first century b. C. through the fourth century a. D. , Worcester Art Museum, April 6-May 14, 1961 / by Michael Milkovich
	Pubbl/distr/stampa	[s.l.] , : [s.n.], 1961
	Descrizione fisica	87 p. : ill. ; 23 cm
	Locazione	FLFBC
	Collocazione	ARCH. DM 004 8
	Lingua di pubblicazione	Italiano
	Formato	Materiale a stampa
	Livello bibliografico	Monografia
2.	Record Nr.	UNINA990000795670403321
	Titolo	Scienza in pubblico : musei e divulgazione del sapere / a cura di John Durant
	Pubbl/distr/stampa	Bologna, : CLUEB, c1998
	ISBN	88-491-1062-6
	Descrizione fisica	XV, 196 p, [12] p. di tav. : ill. ; 22 cm
	Collana	Lexis ; 4 , Museo Poli : luoghi per il sapere ; 7
	Disciplina	508.074 069
	Locazione	FARBC FLFBC
	Collocazione	GEN B 402 706 DURJ 01
	Lingua di pubblicazione	Italiano
	Formato	Materiale a stampa
	Livello bibliografico	Monografia

3. Record Nr.	UNINA9910800117303321
Autore	Yau Stephen S. -T
Titolo	Mathematical Principles in Bioinformatics // by Stephen S.-T. Yau, Xin Zhao, Kun Tian, Hongyu Yu
Pubbl/distr/stampa	Cham : , : Springer Nature Switzerland : , : Imprint : Springer, , 2023
ISBN	3-031-48295-6
Edizione	[1st ed. 2023.]
Descrizione fisica	1 online resource (177 pages)
Collana	Interdisciplinary Applied Mathematics, , 2196-9973 ; ; 58
Altri autori (Persone)	ZhaoXin TianKun YuHongyu
Disciplina	570.285
Soggetti	Bioinformatics Mathematics Applications of Mathematics
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di contenuto	Preface -- 1 Biological Overview -- 2 Bioinformatics Databases -- 3 Sequence Alignment -- 4 The Time-Frequency Spectral Analysis and Applications in Bioinformatics -- 5 Graphical Representation of Sequences and Its Application -- 6 The Development and Applications of the Natural Vector Method -- 7 Convex Hull Principle and Distinguishing Proteins from Arbitrary Amino Acid Sequences -- 8 New Features or Metric on Sequence Comparison -- References.
Sommario/riassunto	This textbook introduces bioinformatics to students in mathematics with no biology background assumed and it provides solid mathematical tools for biology students along with an understanding of how to implement them in bioinformatics problems. In addition to the basics, the text offers new approaches to understanding biological sequences. The concise presentation distinguishes itself from others on the subject, discussing and providing principles that relate to current open problems in bioinformatics as well as considering a variety of models. The convex hull principle is highlighted, opening a new interdisciplinary research area at the intersection of biology, mathematics, and computer science. Prerequisites include first courses in linear algebra, probability and statistics, and mathematical analysis.

Researchers in mathematics, biology, and math-biology, will also find aspects of this text useful. This textbook is written based on the authors' research works that have been published in various journals along with the lecture notes used when teaching bioinformatics courses at the University of Illinois at Chicago and at Tsinghua University. The content may be divided into two parts. The first part includes three chapters, introducing some basic concepts. Chapter 1 provides biological background in molecular biology for mathematicians. Chapter 2 describes biological databases that are commonly used. Chapter 3 is concerned with alignment methods including global/local alignment, heuristic alignment, and multiple alignment. The second part consisting of five chapters, describes several bioinformatics principles using a rigorous mathematical formulation. Chapter 4 introduces the time-frequency spectral principle and its applications in bioinformatics. In Chapters 5 and 6, two strategies are used, the graphical representation and the natural vector method, to represent biological sequences, and conduct sequence comparison and phylogenetic analysis without alignment. Chapter 7 presents the convex hull principle and shows how it can be used to mathematically determine whether a certain amino acid sequence can be a protein. The last chapter summarizes additional mathematical ideas relating to sequence comparisons, such as new feature vectors and metrics. This part focuses on the governing principle in biology and provides plenty of alignment-free methods, which cannot be found in any other book.
