1. Record Nr. UNINA9910712615203321

Titolo	Logistic and linear regression model documentation for statistical relations between continuous real-time and discrete water-quality constituents in the Kansas River, Kansas : July 2012 through June 2015
Pubbl/distr/stampa	U.S. Department of the Interior, U.S. Geological Survey Reston, Virginia
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia

2. Record Nr. UNISA996198282803316

Autore	Higgs Paul G
Titolo	Bioinformatics and molecular evolution / / Paul G. Higgs and Teresa K. Attwood
Pubbl/distr/stampa	Malden, MA, : Blackwell Pub., c2005
ISBN	1-118-69706-5 1-118-69707-3 1-282-11744-0 9786612117442 1-4443-1118-2
Edizione	[1st ed.]
Descrizione fisica	1 online resource (398 p.)
Altri autori (Persone)	AttwoodTeresa K
Disciplina	572.8
Soggetti	Molecular evolution - Mathematical models Bioinformatics Evolució molecular Models matemàtics Bioinformàtica Biologia molecular Llibres electrònics
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 and index.
Nota di contenuto	The revolution in biological information -- Nucleic acids, proteins, and amino acids -- Molecular evolution and population genetics -- Models of sequence evolution -- Information resources for genes and proteins -- Sequence alignment algorithms -- Searching sequence databases -- Phylogenetic methods -- Patterns in protein families -- Probabilistic methods and machine learning -- Further topics in molecular evolution and phylogenetics -- Genome evolution -- DNA microarrays and the 'omes.
Sommario/riassunto	In the current era of complete genome sequencing, Bioinformatics and Molecular Evolution provides an up-to-date and comprehensive introduction to bioinformatics in the context of evolutionary biology. This accessible text: provides a thorough examination of sequence analysis, biological databases, pattern recognition, and applications to genomics, microarrays, and proteomics emphasizes the theoretical and statistical methods used in bioinformatics programs in a way that is accessible to biological science students