1. Record Nr. UNIBAS000026133

Autore	Barth, Hans
Titolo	Verità e ideologia / Hans Barth
Pubbl/distr/stampa	Bologna : <<Il>> Mulino, c1971
Descrizione fisica	XXV, 372 p. ; 22 cm
Collana	Collezione di testi e di studi , Storiografia
Disciplina	141
Soggetti	Idealismo - Storia
Lingua di pubblicazione	Italiano
Formato	Materiale a stampa
Livello bibliografico	Monografia

2. Record Nr. UNINA9910299230003321

Autore	Ho Kum-p'a
Titolo	Protein Homology Detection Through Alignment of Markov Random Fields : Using MRFalign / / by Jinbo Xu, Sheng Wang, Jianzhu Ma
Pubbl/distr/stampa	Cham : , : Springer International Publishing : , : Imprint : Springer, , 2015
ISBN	3-319-14914-8
Edizione	[1st ed. 2015.]
Descrizione fisica	1 online resource (59 p.)
Collana	SpringerBriefs in Computer Science, , 2191-5768
Disciplina	004 005.55 519.5 570285
Soggetti	Bioinformatics Mathematical statistics Statistics Computational Biology/Bioinformatics Probability and Statistics in Computer Science Statistics for Life Sciences, Medicine, Health Sciences
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	Introduction -- Method -- Software -- Experiments and Results -- Conclusion.
Sommario/riassunto	This work covers sequence-based protein homology detection, a fundamental and challenging bioinformatics problem with a variety of real-world applications. The text first surveys a few popular homology detection methods, such as Position-Specific Scoring Matrix (PSSM) and Hidden Markov Model (HMM) based methods, and then describes a novel Markov Random Fields (MRF) based method developed by the authors. MRF-based methods are much more sensitive than HMM- and PSSM-based methods for remote homolog detection and fold recognition, as MRFs can model long-range residue-residue interaction. The text also describes the installation, usage and result interpretation of programs implementing the MRF-based method.