1.

Record Nr.	UNINA9910455059103321
Titolo	Regulatory genomics [[electronic resource]] : proceedings of the 3rd annual RECOMB workshop : National University of Singapore, Singapore 17-18 July 2006 / / editors, Leong Hon Wai, Sung Wing-Kin, Eleazar Eskin
Pubbl/distr/stampa	London, : Imperial College Press, c2008
ISBN	1-84816-252-9
Descrizione fisica	1 online resource (144 p.)
Collana	Series on advances in bioinformatics and computational biology, , 1751-6404 ; ; 8
Altri autori (Persone)	EskinEleazar LeongHon Wai <1955-> SungWing-Kin
Disciplina	572.865
Soggetti	Genetic regulation Genomics Electronic books.
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	Foreword; RECOMB Regulatory Genomics 2006 Organization; CONTENTS; Keynote Papers; Computational Prediction of Regulatory Elements by Comparative Sequence Analysis M. Tompa; A Tale of Two Topics - Motif Significance and Sensitivity of Spaced Seeds M. Li; Computational Challenges for Top-Down Modeling and Simulation of Biological Pathways S. Miyano; An Improved Gibbs Sampling Method for Motif Discovery via Sequence Weighting T. Jiang; Discovering Motifs with Transcription Factor Domain Knowledge F. Chin; Applications of ILP in Computational Biology A . Dress On the Evolution of Transcription Regulation Networks R. Shamir Systems Pharmacology in Cancer Therapeutics: Iterative Informatics-Experimental Interface E. Liu; Computational Structural Proteomics and Inhibitor Discovery R. Abagyan; Characterization of Transcriptional Responses to Environmental Stress by Differential Location Analysis H. Tang; A Knowledge-based Hybrid Algorithm for Protein Secondary Structure Prediction W. L. Hsu; Monotony and Surprise (Conservative Approaches to Pattern Discovery) A . Apostolic0; Evolution of Bacterial

	Regulatory Systems M. S. Gelfand; Contributed Papers TScan: A Two-step De NOVO Motif Discovery Method 0. Abul, G. K. Sandve, and F. Drabbs1. Introduction; 2. Method; 2.1. Step 1; 2.2. Step 2; 2.2.1, Over-representation Conservation Scoring; 2.2.2. Frith et al. Scoring; 3. Experiments; 4. Conclusion; References; Redundancy Elimination in Motif Discovery Algorithms H. Leung and F. Chin; 1. Introduction; 2. Maximizing Likelihood; 3. The Motif Redundancy Problem; 3.1. The motif redundancy problem; 3.2. Formal definition; 4. Algorithm; 5. Experimental Results; 6. Concluding Remarks; Appendix; References GAMOT: An Efficient Genetic Algorithm for Finding Challenging Motifs in DNA Sequences N. Karaoglu, S. Maurer-Stroh, and B. Manderick1. Introduction; 2. GA for Motif Finding; 3. An Efficient Algorithm (GAMOT); 3.1. Fast motif discovery; 3.2. The genetic algorithm; 4. Experimental Results; 4.1. Comparison with exhaustive search; 4.2. Comparison with GAI and GA2; 4.3. Comparison with other algorithms; 4.3.1. Quality of the solutions; 4.4. GAMOTparameters; 5. Conclusions and Future Work; References; Identification of Spaced Regulatory Sites via Submotif Modeling E. Wijaya and R. Kanagasabai 1. Introduction 2. Related Work; 3. Our Approach; 4. Problem Definition; 5. Algorithm SPACE; 5.1. Generation of candidate motifs; 5.2. Constrained frequent pattern mining; 5.2.1. Generalized gap; 5.2.2. Mining of constrained frequent patterns; 5.3. Significance testing and scoring; 6. Experimental Results; 6.1. Results on Tompa's benchmark data set; 6.2. Results on synthetic data set; 7. Discussion and Conclusions; References; Refining Motif Finders with E-value Calculations N. Nagarajan, P. Ng, and U. Keich; 1. Introduction; 2. Efficiently Computing E-values 3. Optimizing for E-values - Conspv
Sommario/riassunto	Research in the field of gene regulation is evolving rapidly in the ever-changing scientific environment. Advances in microarray techniques and comparative genomics have enabled more comprehensive studies of regulatory genomics. The study of genomic binding locations of transcription factors has enabled a more comprehensive modeling of regulatory networks. In addition, complete genomic sequences and comparison of numerous related species have demonstrated the conservation of non-coding DNA sequences, which often provide evidence for cis-regulatory binding sites. Systematic methods to decipher