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	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