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Altri autori (Persone)	MarksteinPeter XuYing <1960->
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Nota di contenuto	CONTENTS; Preface; Committees; Referees; Keynote Address; Quantitative Aspects of Gene Regulation in Bacteria: Amplification. Threshold, and Combinatorial Control Terry Hwa; Whole-Genome Analysis of Dorsal Gradient Thresholds in the Drosophila Embryo Julia ZeitlingeK Rob Zinzen, Dmitri Papatsenko et al.; Invited Talks; Learning Predictive Models of Gene Regulation Christina Leslie; The Phylofacts Phylogenomic Encyclopedias: Structural Phylogenomic Analysis Across the Tree of Life Kimmen Golander; Mapping and Analysis of the Human Interactome Network Kavitha Venkatesan; 1. INTRODUCTION Gene-Centered Protein-DNA Interactome Mapping A.J. Marian WalhoutProteomics; Algorithm for Peptide Sequencing by Tandem Mass Spectrometry Based on Better Preprocessing and Anti-S ymmetric

Computational Model Kang Ning and Hon Wai Leong; 1. INTRODUCTION; Preprocessing to remove noisy peaks; The anti-symmetric problem; 2. ANALYSIS OF PROBLEMS AND CURRENT ALGORITHMS; 2.1. General Terminologies; 2.2. Datasets; 2.3. Problems Analysis; 3. NEW COMPUTATIONAL MODELS AND ALGORITHM; 3.1. Preprocessing to remove noisy peaks and introduce pseudo peaks; 3.2. The Anti-symmetric Problem
3.3. Novel Peptide Sequencing Algorithm4. EXPERIMENTS; 4.1. Experiment Settings; 4.2. Results; 5. CONCLUSIONS; References; Algorithms for Selecting Breakpoint Locations to Optimize Diversity in Protein Engineering by Site-Directed Protein Recombination Wei Zheng, Xiaoduan Ye, Alan A4 Friedman and Chris Bailey-Kellogg; 1. INTRODUCTION; 2. METHODS; 2.1. Library Diversity; 2.2. Metrics for Breakpoint Selection; 2.3. Dynamic Programming for Breakpoint Selection; 3. RESULTS A N D DISCUSSION; 4. CONCLUSION; ACKNOWLEDGMENTS; References
An Algorithmic Approach to Automated High-Throughput Identification of Disulfide Connectivity in Proteins Using Tandem Mass Spectrometry Timothy Lee, Rahul Singh, Ten-Yang Yen and Bruce Macher1. INTRODUCTION; 1.1. Comparison of the Proposed Approach with Related Works; 2. THE PROPOSED METHOD; 2.1. Problem Formulation; 2.2. Algorithmic Framework; 2.2.1. Finding the MS spectrum match; 2.2.2. Finding the MS/MS spectrum match; 2.2.3. Finding a perfect matching of maximum weight for a fully connected graph; 2.2.4. Consideration of missed proteolytic cleavages and intra-molecular bonded cysteines
2.2.5. Peak finding in the presence of noise2.2.6. Addressing isotopic variation and neutral loss; 2.2.7. Interpretation of peaks given charge state uncertainty; 2.2.8. Overall complexity; 3. EXPERIMENTAL RESULTS; 3.1. Description of the Data and Experimental Procedures; 3.2. Summary of Results; 3.2.1. Analysis of the effect of varying threshold t on results; 3.2.2. Comparison with MS2Assign program; 4. CONCLUSIONS AND DISCUSSION; Acknowledgments; References; Biomedical Application; Cancer Molecular Pattern Discovery by Subspace Consensus Kernel Classification Xiaoxu Hun; 1. INTRODUCTION
1 .1. Nonnegative matrix factorization

Sommario/riassunto

This volume contains about 40 papers covering many of the latest developments in the fast-growing field of bioinformatics. The contributions span a wide range of topics, including computational genomics and genetics, protein function and computational proteomics, the transcriptome, structural bioinformatics, microarray data analysis, motif identification, biological pathways and systems, and biomedical applications. Abstracts from the keynote addresses and invited talks are also included. The papers not only cover theoretical aspects of bioinformatics but also delve into the application of n