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	Altri autori (Persone)	AzuajeFrancisco DopazoJoaquin
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	- EMPHASIS ON COMBINATION OF MULTIPLE DATA TYPES; 4 Applications of Text Mining in Molecular Biology, from Name Recognition to Protein Interaction Maps; 4.1 Introduction 4.2 Introduction to Text Mining and NLP4.3 Databases and Resources for Biomedical Text Mining; 4.4 Text Mining and Protein-Protein Interactions; 4.5 Other Text-Mining Applications in Genomics; 4.6 The Future of NLP in Biomedicine; Acknowledgements; References; 5 Protein Interaction Prediction by Integrating Genomic Features and Protein Interaction Network Analysis; 5.1 Introduction; 5.2 Genomic Features in Protein Interaction Predictions; 5.3 Machine Learning on Protein-Protein Interactions; 5.4 The Missing Value Problem; 5.5 Network Analysis of Protein Interactions; 5.6 Discussion References6 Integration of Genomic and Phenotypic Data; 6.1 Phenotype; 6.2 Forward Genetics and QTL Analysis; 6.3 Reverse Genetics; 6.4 Prediction of Phenotype from Other Sources of Data; 6.5 Integrating Phenotype Data with Systems Biology; 6.6 Integration of Phenotype Data in Databases; 6.7 Conclusions; References; 7 Ontologies and Functional Genomics; 7.1 Information Mining in Genome-Wide Functional Analysis; 7.2 Sources of Information: Free Text Versus Curated Repositories; 7.3 Bio-Ontologies and the Gene Ontology in Functional Genomics 7.4 Using GO to Translate the Results of Functional Genomic Experiments into Biological Knowledge7.5 Statistical Approaches to Test Significant Biological Differences; 7.6 Using FatiGO to Find Significant Functional Associations in Clusters of Genes; 7.7 Other Tools; 7.8 Examples of Functional Analysis of Clusters of Genes; 7.9 Future Prospects; References; 8 The C. elegans Interactome: its Generation and Visualization; 8.1 Introduction; 8.2 The ORFeome: the first step toward the interactome of C. elegans 8.3 Large-Scale High-Throughput Yeast Two-Hybrid Screens to Map the C. elegans Protein-Protein Interaction (Interactome) Network: Technical Aspects
Sommario/riassunto	Data Analysis and Visualization in Genomics and Proteomics is the first book addressing integrative data analysis and visualization in this field. It addresses important techniques for the interpretation of data originating from multiple sources, encoded in different formats or protocols, and processed by multiple systems. One of the first systematic overviews of the problem of biological data integration using computational approachesThis book provides scientists and students with the basis for the development and application of integrative computational met

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