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	Nota di contenuto	Molecular computing: From conformational pattern recognition to complex processing networks -- A look at the visual modeling of plants using L-systems -- Bioinformatics and cheminformatics in the drug discovery cycle -- New developments in linking of biological databases and computer-generation of annotation: SWISS-PROT and its computer-annotated supplement TREMBL -- EpoDB: An erythropoiesis gene expression database in progress -- Recent advances in molecular distance geometry -- Three models of gene regulation in E. coli -- A new method to develop highly specific models for regulatory DNA regions -- Towards an object-oriented framework for the modeling of

	integrated metabolic processes -- TRRD and COMPEL databases on transcription linked to TRANSFACAS as tools for analysis and recognition of regulatory sequences -- Integrating heterogeneous datasets in genomic mapping: Radiation hybrids, YACs, genes and STS markers over the entire human chromosome X -- A clustering approach to Generalized Tree Alignment with application to Alu repeats -- Simple folding model for HP lattice proteins -- Fast protein fold recognition and accurate sequence-structure alignment -- Carbohydrates: Second-class citizens in biomedicine and in bioinformatics? -- Structural constraints and neutrality in RNA -- A systematic approach to finding new lead structures having biological activity -- Visualization and analysis of the complete yeast genome -- Virtual reality modeling for structural biology -- Evolutionary grammars: A grammatical model for genome evolution -- From DNA recombination to DNA computing via formal languages.
Sommario/riassunto	This book constitutes the strictly refereed post-workshop proceedings of the German Conference on Bioinformatics, GCB'96, held in Leipzig, Germany, in September/October 1996. The volume presents 18 revised full papers together with three invited papers; these contributions were selected after a second round of reviewing from the 91 conference presentations. The book addresses current issues in computational biology and biologically inspired computing. The papers are organized in sections on biological and metabolic pathways, sequence analysis, molecular modeling, visualization, and formal languages, and DNA.