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| | Soggetti | Bioinformatics |
| | | Algorithms |
| | | Computer science - Mathematics |
| | | Discrete mathematics |
| | | Data mining |
| | | Proteins |
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| | | Data Mining and Knowledge Discovery |
| | Lingua di pubblicazione | Inglese |
| | Formato | Materiale a stampa |
| | Livello bibliografico | Monografia |
| | Note generali | Includes index. |
| | Nota di contenuto | Intro -- Preface -- Organization -- Abstracts -- Reference-free Compression of High Throughput Sequencing Data with a Probabilistic de Bruijn Graph -- Genome Scaffolding with PE-Contaminated Mate-Pair Libraries -- Network Properties of the Ensemble of RNA Structures -- Contents -- BicNET: Efficient Biclustering of Biological Networks to Unravel Non-Trivial Modules -- 1 Introduction -- 2 Background -- 3 Solution -- 3.1 Network Modules with Flexible Coherency -- 3.2 BicNET: Efficient Biclustering of Biological Networks -- 4 Results and Discussion -- 4.1 Results on Synthetic Data -- 4.2 Results on Real Data -- 5 Conclusions and Future Work -- References -- Simultaneous Optimization of both Node and Edge Conservation in Network Alignment via WAVE -- 1 Introduction -- 1.1 Motivation -- 1.2 Related Work -- 1.3 Our Contributions and Significance -- 2 Methods -- 2.1 |

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| Sommario/riassunto | This book constitutes the refereed proceedings of the 15th International Workshop on Algorithms in Bioinformatics, WABI 2015, held in Atlanta, GA, USA, in September 2015. The 23 full papers presented were carefully reviewed and selected from 56 submissions. The selected papers cover a wide range of topics from networks to phylogenetic studies, sequence and genome analysis, comparative genomics, and RNA structure. |