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Nota di contenuto	<p>BDDBlast A Memory Efficient Architecture for Pairwise Alignments -- Cancer gene graphs on interactive scientific workflow -- Accuracy of RNA Structure Prediction Depends on the Pseudoknot Grammar -- Comparison of machine learning pipelines for gene expression matrices -- Evaluating Machine Learning Models for Essential Protein Identification -- Study on the complexity of omics data: an analysis for cancer survival prediction -- Identifying large scale conformational changes in proteins through distance maps and convolutional networks -- Clustering analysis indicates genes involved in progesterone-induced oxidative stress in pancreatic beta cells: insights to understanding gestational diabetes -- An External Memory Approach for Large Genome De Novo Assembly -- Computational methodology for discovery of potential inhibitory peptides -- A non Exhaustive search of Exhaustiveness -- Search for Zinc complexes with high affinity in Pyrazinamidase from Mycobacterium Tuberculosis resistant to Pyrazinamide -- How bioinformatics can aid biodiversity description: the case of a probable new species of Orthonychiurus (Collembola, Hexapoda) -- Phylogeny trees as a tool to compare inference algorithms of orthologs -- Water pollution shifts the soil and fish gut microbiomes increasing the circulation of antibiotic resistance genes in the environment -- A 1.375-Approximation Algorithm for Sorting by Transpositions with Faster Running Time -- In silico analysis of the genomic potential for the production of specialized metabolites of ten strains of the Bacillales order isolated from the soil of the Federal District, Brazil.</p>
Sommaro/riassunto	<p>This book constitutes the proceedings of the 15th Brazilian Symposium on Bioinformatics on Advances in Bioinformatics and Computational Biology, BSB 2022, which took place in Buzios, Brazil, in September 2022. The 10 full papers and 7 short papers presented in this volume were carefully reviewed and selected from 23 submissions. The papers focus on bioinformatics, computational biology, Biological Databases, Biological Networks, Cheminformatics, Evolutionary Genomics, Computational Proteomics, Systems Biology, Drug Design, Genomics, Machine Learning applications in Bioinformatics, Metagenomics, Molecular Docking and Modeling, Molecular Evolution and Phylogenetics, Protein Structure and Modeling, Proteomics, Transcriptomics, Single-Cell Analysis, Workflows in Bioinformatics. .</p>