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	Nota di contenuto	A Classification of de Bruijn Graph approaches for De Novo Fragment Assembly -- Redundancy Treatment of NGS Contigs in Microbial Genome Finishing with Hashing-Based Approach -- Efficient Out-of-core Contig Generation -- In silico Pathogenomic Analysis of Corynebacterium pseudotuberculosis biovar ovis -- Assessing the sex-related genomic composition diffeerence using a K-mer-based approach: a case of study in Arapaima gigas (Pirarucu) -- COVID-19 X-ray Image Diagnostic with Deep Neural Networks -- Classification of Musculoskeletal Abnormalities with Convolutional Neural Networks -- Combining mutation and gene network data in a machine learning approach for false-positive cancer driver gene discovery -- Unraveling the role of Nanobodies Tetrad on their Folding and Stability Assisted by Machine and Deep Learning Algorithms -- Experiencing DfAnalyzer for Runtime Analysis of Phylogenomic Dataflows -- Sorting by Reversals and Transpositions with Proportion Restriction -- Heuristics for Breakpoint Graph Decomposition with Applications in Genome Rearrangement Problems -- Center Genome With Respect to the Rank Distance -- ImTeNet: Image-Text Classification Network for Abnormality Detection and Automatic Reporting on Musculoskeletal Radiographs -- A scientometric overview of bioinformatics tools in the Pseudomonas putida genome study -- Polysome-seq as a Measure of Translational

	Profile from Deoxyhypusine Synthase Mutant in Saccharomyces cerevisiae -- Anti-CD3 stimulated T cell transcriptome reveals novel ncRNAs and correlates with a suppressive profile -- A simplified complex network-based approach to mRNA and ncRNA transcript classification -- A systems biology driven approach to map the EP300 interactors using comprehensive protein interaction network -- Analyzing switch regions of human Rab10 by molecular dynamics simulations -- Importance of meta-analysis in studies involving plant responses to climate change in Brazil -- A brief history of Bioinformatics told by data visualization -- Computational Simulations for Cyclizations Catalyzed by Plant Monoterpene Synthases -- Oncogenic signaling pathways in Mucopolysaccharidoses -- Natural products as potential inhibitors for SARS-CoV-2 papain-like protease: an in silico study.
Sommario/riassunto	This book constitutes the refereed proceedings of the Brazilian Symposium on Bioinformatics, BSB 2020, held in São Paulo, Brazil, in November 2020. Due to COVID-19 pandemic the conference was held virtually The 20 revised full papers and 5 short papers were carefully reviewed and selected from 45 submissions. The papers address a broad range of current topics in computational biology and bioinformatics.