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Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	Intro -- Preface -- Organization -- Contents -- Applied Bioinformatics and Computational Biology -- Comparative Transcriptome Profiling of <i>Maytenus ilicifolia</i> Root and Leaf -- 1 Introduction -- 2 Methods -- 2.1 Plant Material and Total RNA Isolation -- 2.2 Library Preparation and Sequencing -- 2.3 Quality Control and de novo Assembly -- 2.4 Functional Annotation -- 2.5 Differential Expression Analysis -- 2.6 Gene Ontology Enrichment and KEGG Analysis -- 3 Results and Discussion -- 3.1 De novo Assembly and Functional Annotation of <i>M. ilicifolia</i> -- 3.2 Identification of Differentially Expressed Transcripts in Both Tissues -- References -- Hypusine Plays a Role in the Translation of Short mRNAs and Mediates the Polyamine and Autophagy Pathways in <i>Saccharomyces Cerevisiae</i> -- 1 Introduction -- 2 Materials and Methods -- 2.1 RNA-seq Data Analysis -- 2.2 Strain and Growth Conditions -- 2.3 RNA Isolation and qRT-PCR -- 2.4 Protein Extraction and Western Blot Analysis -- 3 Results and Discussion -- 3.1 Translation of Short ORFs is Impaired in <i>dys1-1</i> Mutant -- 3.2 Hypusination Modulates Autophagy -- References -- Topological Characterization of Cancer Driver Genes Using Reactome Super Pathways Networks -- 1 Introduction -- 2 Method -- 2.1 Reactome Functional Iteration -- 2.2 Super Pathways as Reactome FI Sub-networks -- 2.3 Super Pathways Sub-networks Enriched with Drivers Information -- 3 Results -- 3.1 Centrality Measures -- 3.2 Network Attack -- 4 Discussion and Conclusion -- References -- Bioinformatics and Computational Biology -- CellHeap: A Workflow for Optimizing COVID-19 Single-Cell RNA-Seq Data Processing in the Santos Dumont Supercomputer -- 1 Introduction -- 2 Description of the CellHeap Workflow -- 3 Results -- 3.1 Input Data and Experiment Setup -- 3.2 Environmental Setup -- 3.3 Results Discussion -- 4 Conclusion -- References. Combining Orthology and Xenology Data in a Common Phylogenetic Tree -- 1 Introduction -- 2 Preliminaries -- 3 Tree-Like Pairs of Maps -- 4 Tree-Like Pairs of Maps with Constraints -- 5 Concluding Remark -- References -- ContFree-NGS: Removing Reads from Contaminating Organisms in Next Generation Sequencing Data -- 1 Introduction -- 2 Implementation -- 3 Evaluation -- 4 Conclusion -- References -- Deep Learning-Based COVID-19 Diagnostics of Low-Quality CT Images -- 1 Introduction -- 2 Dataset -- 3 Methodology -- 3.1 Data Preprocessing -- 3.2 Deep Neural Network Architectures -- 4 Experimental Evaluation -- 4.1 Data Preprocessing -- 4.2 Transfer Learning with ResNet50 -- 4.3 Image- and Exam-Level Classification of the Test Set -- 4.4 Interpreting Model Decisions -- 5 Conclusion -- References -- Feature Importance Analysis of Non-coding DNA/RNA Sequences Based on Machine Learning Approaches -- 1 Background -- 2 Pipeline for Machine Learning Classification Task -- 2.1 Prediction of sRNAs -- 2.2 Prediction of CircRNA -- 3 Results and Discussion -- 3.1 Case Study 1: sRNAs in Bacteria -- 3.2 Case Study 2: CircRNA in Humans -- 4 Conclusion -- References -- Heuristics for Cycle Packing of Adjacency Graphs for Genomes with Repeated Genes -- 1 Introduction -- 2 Definitions -- 3 Random Packings -- 4 Genetic Algorithm -- 5 Experimental Results -- 5.1 Applications with the Reversal Distance -- 5.2 Experiments with Real Biological Data -- 6 Conclusion -- References -- PIMBA: A Pipeline for MetaBarcoding Analysis -- 1 Introduction -- 2 Implementation -- 2.1 Preprocessing -- 2.2

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3.3 Metazoan COI Mock Community -- 4 Conclusion -- References --
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-- 4.2 Proteomics Guide -- 4.3 FluxPRT Interface -- 5 Concluding
Remarks -- 6 Availability -- References -- MathPIP: Classification of
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Feature Engineering -- 2.3 Experimental Setting -- 3 Results and
Discussion -- 4 Conclusion -- References -- Metagenomic Insights
of the Microbial Community from a Polluted River in Brazil 2020 -- 1
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Primer-Target Hybridisation to Detect SARS-CoV-2 Variants of Concern
-- 1 Introduction -- 2 Materials and Methods -- 3 Results and
Discussion -- 4 Conclusion -- References -- Author Index.

Sommario/riassunto

This book constitutes the refereed proceedings of the Brazilian Symposium on Bioinformatics, BSB 2021, held in November 2021. Due to COVID-19 pandemic the conference was held virtually The 10 revised full papers and 5 short papers were carefully reviewed and selected from 28 submissions. The papers address a broad range of current topics in computational biology and bioinformatics.
