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Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	Mitochondrial Haplogroup Assignment for High-Throughput Sequencing Data from Single Individual and Mixed DNA Samples -- Signet Ring Cell Detection with Classification Reinforcement Detection Network -- SPOC: Identification of Drug Targets in Biological Networks via Set Preference Output Control -- Identification of a novel compound heterozygous variant in NBAS causing bone fragility by the type of osteogenesis imperfecta -- Isoform-disease association prediction by data fusion -- EpIntMC: Detecting Epistatic Interactions using Multiple Clusterings -- Improving Metagenomic Classification using discriminative k-mers from sequencing data -- Dilated-DenseNet For Macromolecule Classification In Cryo-electron Tomography -- Ess-NEXG: Predict Essential Proteins by Constructing a Weighted -- Protein Interaction Network based on Node Embedding and XGBoost --

mapAlign: an efficient approach for mapping and aligning long reads to reference genomes -- Functional Evolutionary Modeling Exposes Overlooked Protein-Coding Genes Involved in Cancer -- Testing the Agreement of Trees with Internal Labels -- SVLR: Genome Structure Variant Detection Using Long Read Sequencing Data -- De novo prediction of drug-target interaction via Laplacian regularized Schatten-p norm minimization -- Diagnosis of ASD from rs-fMRIs based on brain dynamic networks -- miRNA-Disease Associations Prediction Based on Negative Sample Selection and Multi-layer Perceptron -- Checking Phylogenetic Decisiveness in Theory and in Practice -- TNet: Phylogeny-Based Inference of Disease Transmission Networks Using Within-Host Strain Diversity -- Cancer breakpoint hotspots versus individual breakpoints prediction by machine learning models -- Integer Linear Programming Formulation for the Unified DuplicationLoss-Coalescence Model -- In silico-guided discovery of potential HIV-1 entry inhibitors mimicking bNAb N6: virtual screening, docking, molecular dynamics, and post-molecular modeling analysis -- Learning Structural Genetic Information via Graph Neural Embedding -- A New Network-based Tool to Analyse Competing Endogenous RNAs -- Deep Ensemble models for 16S Ribosomal Gene Classification -- Search for tandem repeats in the first chromosome from the rice genome -- Deep Learning approach with rotate-shift invariant input to predict protein homodimer structure -- Development of a Neural Network-Based Approach for Prediction of Potential HIV-1 Entry Inhibitors Using Deep Learning and Molecular Modeling Methods -- In Silico Design and Evaluation of Novel Triazole-Based Compounds as Promising Drug Candidates Against Breast Cancer -- Identification of essential genes with NemoProfile and various machine learning models -- NemoLib: Network Motif Libraries for network motif detection and analysis -- Estimating enzyme participation in metabolic pathways for microbial communities from RNA-seq data -- Identification of Virus-Receptor Interactions based on Network Enhancement and Similarity -- Enhanced functional pathway annotations for differentially expressed gene clusters -- Automated Detection of Sleep Apnea from Abdominal Respiratory Signal using Hilbert-Huang Transform -- Na/K-ATPase glutathionylation: in silico modeling of reaction mechanisms -- HiChew: a tool for TAD clustering in embryogenesis -- Generation of Hi-C maps from DNA sequence data using Deep Learning -- SC1: A Tool for Interactive Web-Based Single Cell RNA-Seq Data Analysis -- Quantitative analysis of the dynamics of maternal gradients in the early Drosophila embryo -- Atom Tracking Using Cayley Graphs -- SPOC: Identification of Drug Targets in Biological Networks via Set Preference Output Control -- Identification of a novel compound heterozygous variant in NBAS causing bone fragility by the type of osteogenesis imperfecta. .

Sommario/riassunto

This book constitutes the proceedings of the 16th International Symposium on Bioinformatics Research and Applications, ISBRA 2020, held in Moscow, Russia, in December 2020. The 23 full papers and 18 short papers presented in this book were carefully reviewed and selected from 131 submissions. They were organized in topical sections named: genome analysis; systems biology; computational proteomics; machine and deep learning; and data analysis and methodology.