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Nota di contenuto	Intro -- Preface -- Organization -- Contents -- Computational Advances in Bio and Medical Sciences -- DNA Read Feature Importance Using Machine Learning for Read Alignment Categories -- 1 Introduction -- 2 Related Work and Motivation -- 3 Methods -- 3.1 Data Acquisition and Read Mapping -- 3.2 Feature and Class Extraction -- 3.3 Machine Learning Methods -- 4 Results -- 4.1 Model Accuracy -- 4.2 Feature Importance -- 4.3 Feature Ranking Similarity Across Different Data -- 4.4 Machine Learning Filter Proof-of-Concept -- 5 Conclusions -- References -- MetaProb 2: Improving Unsupervised Metagenomic Binning with Efficient Reads Assembly Using Minimizers -- 1 Introduction -- 2 Method -- 2.1 Phase 1: Unitig Construction -- 2.2 Phase 2: Community Detection -- 2.3 Phase 3: Species Identification -- 3 Results and Discussion -- 3.1 Datasets Description and Performance Evaluation Metrics -- 3.2 Results -- 4 Conclusions and Future Work -- References -- Computational Study of Action Potential Generation in Urethral Smooth Muscle Cell -- 1 Introduction -- 2 Methods -- 3 Results -- 4 Discussion -- References -- Metabolic Pathway Prediction using Non-negative Matrix Factorization with

Improved Precision -- 1 Introduction -- 2 Method -- 2.1 Decomposing the Pathway EC Association Matrix -- 2.2 Community Reconstruction and Multi-label Learning -- 3 Experiments -- 3.1 T1 Golden Data -- 3.2 Three E. coli Data -- 3.3 Mealybug Symbionts Data -- 3.4 CAMI and HOTS Data -- 4 Conclusion -- References -- A Novel Pathway Network Analytics Method Based on Graph Theory -- 1 Introduction -- 2 Methods -- 2.1 Identification of Significantly Enriched Pathways -- 2.2 Construction of a Weighted Network -- 2.3 Identification of Sub-networks -- 2.4 Identification of Important Pathways -- 3 Results and Discussions -- 3.1 Dataset Employed -- 3.2 Outcomes and Relevant Discussions.

4 Conclusions -- References -- Latent Variable Modelling and Variational Inference for scRNA-seq Differential Expression Analysis -- 1 Introduction -- 2 Methods -- 2.1 ext-ZINBayes -- 2.2 SIENA -- 3 Results -- 4 Conclusion -- References -- Computational Advances for Single-Cell Omics Data Analysis -- Computational Cell Cycle Analysis of Single Cell RNA-Seq Data -- 1 Background and Motivation -- 2 Methods -- 2.1 Datasets -- 2.2 The SC1 Cell Cycle (SC1CC) Analysis Tool -- 3 Results and Discussion -- 3.1 Results on the hESC Dataset -- 3.2 Results on the PBMC Dataset -- 3.3 Results on the -CTLA-4 Dataset -- 3.4 Results on the mHSC Dataset -- 4 Conclusion -- References -- Single-Cell Gene Regulatory Network Analysis Reveals Potential Mechanisms of Action of Antimalarials Against SARS-CoV-2 -- 1 Introduction -- 2 Materials and Methods -- 2.1 Data Set -- 2.2 Machine Learning Workflow -- 3 Results and Discussion -- 4 Conclusion -- References -- Computational Advances for Next Generation Sequencing -- RACCROCHE: Ancestral Flowering Plant Chromosomes and Gene Orders Based on Generalized Adjacencies and Chromosomal Gene Co-occurrences -- 1 Introduction -- 2 Methods -- 2.1 Input -- 2.2 The Pipeline -- 2.3 Visualizing and Evaluating the Reconstruction -- 2.4 Ancestral Gene Function -- 3 Reconstruction of Monocot Ancestors -- 3.1 Properties of the Contig Reconstruction -- 3.2 Clustering -- 3.3 Painting the Chromosomes of the Present-Day Genomes -- 3.4 Evaluation -- 3.5 MCScanX Visualization -- 4 Discussions and Conclusions -- A Redistributing Genes from Families Exceeding Upper Size Limits -- B Modes of Contig Construction -- C Matching Contigs to Chromosomes of Extant Genomes -- D Construction of Ancestral Chromosomes -- E Functional Annotation of Ancestral Genes -- References.

A Fast Word Embedding Based Classifier to Profile Target Gene Databases in Metagenomic Samples -- 1 Introduction -- 2 Methods -- 2.1 Indexing Protein Reference Databases -- 2.2 Prediction of Short Reads -- 2.3 Databases -- 2.4 True Positive Dataset -- 2.5 False Positives Dataset -- 2.6 Time and Memory Profiling -- 2.7 Functional Annotation of Metagenomic Datasets -- 3 Results and Discussion -- 3.1 Detection of True Positive Hits -- 3.2 Detection of False Positives Hits -- 3.3 Time and Memory Usage of MetaMLP -- 3.4 Functional Annotation of Different Environments -- 3.5 Observation of MetaMLP Annotations Against an Extensive Metagenomics Study -- 4 Conclusions -- References -- Clustering Based Identification of SARS-CoV-2 Subtypes -- 1 Background -- 2 Clustering Methods -- 2.1 CliqueSNV Based Clustering -- 2.2 k-modes Clustering -- 2.3 MeShClust -- 2.4 Gap Filling -- 3 Assessment of Clustering Viral Subtypes -- 3.1 Cluster Entropy -- 3.2 Fitness -- 4 Results -- 4.1 Analysis of GISAID Data -- 4.2 Analysis of EMBL-EBI Data -- 5 Conclusions -- References -- Author Index.

