

1. Record Nr.	UNINA9910619277503321
Titolo	Computational advances in bio and medical sciences : 11th international conference, ICCABS 2021, virtual event, December 16-18, 2021, revised selected papers // edited by Mukul S. Bansal
Pubbl/distr/stampa	Cham, Switzerland : , : Springer, , [2022] ©2022
ISBN	3-031-17531-X
Descrizione fisica	1 online resource (184 pages)
Collana	Lecture Notes in Computer Science ; ; v.13254
Disciplina	570.285
Soggetti	Bioinformatics
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Includes index.
Nota di contenuto	Intro -- Preface -- Organization -- Contents -- Computational Advances in Bio and Medical Sciences -- Single Model Quality Estimation of Protein Structures via Non-negative Tensor Factorization -- 1 Introduction -- 2 Related Works -- 3 Methodology -- 3.1 Stage I: From Structures to Groups -- 3.2 Stage II: Ranking Groups -- 3.3 Stage III: Partitioning Groups into Subgroups -- 3.4 Stage IV: Scoring Each Structure -- 3.5 Experimental Setup -- 3.6 Dataset -- 3.7 Evaluation Metrics -- 4 Results -- 4.1 Comparative Evaluation on Correlation with TM-Score -- 4.2 Loss-Based Comparison -- 4.3 Statistical Significance Analysis -- 5 Conclusion -- References -- Graph Representation Learning for Protein Conformation Sampling -- 1 Introduction -- 1.1 Related Work -- 2 Methods -- 3 Results -- 3.1 Experimental Setup -- 3.2 Evaluation of Models on Fixed-Length Chains -- 3.3 Evaluation of Models on Variable-Length Chains -- 4 Conclusion -- References -- Excerno: Filtering Mutations Caused by the Clinical Archival Process in Sequencing Data -- 1 Introduction -- 2 Excerno: A Bayes Classifier Using Mutational Signatures -- 3 Simulation and Evaluation Approach -- 4 Simulation Results -- 4.1 Performance Characteristics Across Different COSMIC Baseline Signatures -- 4.2 Performance Characteristics Across Different Percentages of FFPE -- 5 Conclusions -- References -- Relabeling Metabolic Pathway Data with Groups to Improve Prediction Outcomes -- 1 Introduction -- 2 Method -- 2.1

Feed-Forward Phase -- 2.2 Feed-Backward Phase -- 2.3 Closing the Loop -- 3 Experiments -- 3.1 Accumulated History Probability Analysis -- 3.2 Metabolic Pathway Prediction -- 4 Conclusion -- References -- MELEPS: Multiple Expert Linear Epitope Prediction System -- 1 Introduction -- 2 Materials and Methods -- 2.1 Data Collection -- 2.2 The System Flow of MELEPS. 2.3 Integrated Multi-expert Recommendation Methodology -- 2.4 The Weighted Recommendation Score -- 2.5 Performance Measurement of Recommendation -- 3 Results and Discussion -- 3.1 The Weight Parameter Table -- 3.2 Performance of MELEPS -- 3.3 The MELEPS Platform -- 4 Conclusion -- References -- Encoder-Decoder Architectures for Clinically Relevant Coronary Artery Segmentation -- 1 Introduction -- 2 Related Work -- 2.1 Major Vessel Segmentation -- 2.2 Full Coronary Tree Segmentation -- 2.3 Catheter and Full Coronary Tree Segmentation -- 2.4 Other Segmentation Criteria -- 3 Model Evaluation Metrics -- 4 Loss Function -- 5 Architecture -- 5.1 Encoder Comparison -- 5.2 Decoder Comparison -- 5.3 EfficientUNet++ Architecture -- 5.4 Performance vs. Computation Trade-Off -- 6 Experimental Results -- 7 Implementation Details -- 7.1 Training Methodology -- 7.2 Dataset -- 7.3 Data Augmentation -- 8 Discussion and Future Work -- References -- Unified SAT-Solving for Hard Problems of Phylogenetic Network Construction -- 1 Introduction: Evolutionary Trees and Phylogenetic Networks -- 2 Definitions and Problem Statements -- 3 The CNF Formula for the TFP -- 3.1 Identifying, Counting and Limiting Reticulation Nodes in D -- 4 Hybridization Networks: Reticulation Networks When Input Trees Are Specified -- 5 Some Empirical Results -- 5.1 Summary of the Empirical Conclusions -- References -- Feature Selection for Identification of Risk Factors Associated with Infant Mortality -- 1 Introduction -- 2 Method -- 2.1 Study Design and Casuistic -- 2.2 Database Integration -- 2.3 Data Analysis, Cleaning and Preparation -- 2.4 Identification of Main Variables -- 2.5 Tools, Techniques and Software Used -- 3 Results -- 3.1 Data Description -- 3.2 Feature Selection -- 4 Discussion -- 5 Final Considerations -- References. Addressing Classification on Highly Imbalanced Clinical Datasets -- 1 Introduction -- 2 Related Works -- 3 Materials and Methods -- 3.1 Method Overview -- 3.2 Avocado Dataset and Data Cleaning -- 3.3 Performance Metrics -- 4 Results -- 4.1 Techniques Comparison for Demographics Data Section -- 4.2 Classifiers and Techniques Comparison for Demographics Section -- 4.3 All Data Sections Comparisons -- 5 Conclusion -- References -- mcPBWT: Space-Efficient Multi-column PBWT Scanning Algorithm for Composite Haplotype Matching -- 1 Introduction -- 2 Preliminaries -- 2.1 PBWT Overview -- 2.2 Composite Haplotype Matching -- 3 Multi-column PBWT -- 3.1 Divergence Value Properties -- 3.2 Finding Blocks of Starting Matches -- 3.3 double-PBWT -- 3.4 double-PBWT: Comparing Block of Matches -- 3.5 triple-PBWT -- 4 Discussion -- References -- Computational Advances in Molecular Epidemiology -- Clustering SARS-CoV-2 Variants from Raw High-Throughput Sequencing Reads Data -- 1 Introduction -- 2 Related Work -- 3 Proposed Approach -- 3.1 Producing Consensus Sequences -- 3.2 Embedding Approaches -- 3.3 Clustering Algorithms -- 4 Experimental Evaluation -- 4.1 Dataset Statistics and Visualization -- 4.2 Evaluation Metrics -- 4.3 Clustering Comparison Metrics -- 5 Results and Discussion -- 5.1 Clustering Evaluation -- 5.2 Comparing Different Clusterings -- 5.3 Information Gain -- 5.4 Statistical Analysis -- 6 Conclusion -- References -- Analysis of SARS-CoV-2 Temporal Molecular Networks Using Global and Local Topological Characteristics -- 1 Introduction -- 2 Data

and Methods -- 2.1 Data and Preprocessing -- 2.2 Construction of Temporal Networks -- 2.3 Global Network Analysis -- 2.4 Local Topological Analysis -- 2.5 Quantification of Nucleotide Variation -- 2.6 Spectral Network Partitioning -- 2.7 Phylogenetic Analysis -- 3 Results and Analysis.
 3.1 Genetic Characterization of the Viral Population -- 3.2 Changes in Global Properties -- 3.3 Association Between RGF Distance and Genetic Variation -- 3.4 Laplacian Network Partitioning Versus Phylogenetic Analysis -- 4 Conclusions -- References -- An SVM Based Approach to Study the Racial Disparity in Triple-Negative Breast Cancer -- 1 Introduction -- 2 Data and Methods -- 2.1 Data and Preprocessing -- 2.2 Construction of SVM Based Model for Feature Selection -- 2.3 Estimation of Feature/Gene -- 2.4 Feature/Gene Validation Analysis -- 3 Results and Discussion -- 3.1 Selection of Final Features -- 3.2 Expression Status of the Features/Gene -- 3.3 Association of High Expression of KLK10 and Survival Outcome of TNBC -- 4 Conclusion -- References -- Author Index.

2. Record Nr.	UNISA996417611203316
Titolo	Energie & Management Jahresmagazin
Pubbl/distr/stampa	Herrsching, : Energie & Management Verlagsgesellschaft mbH
Descrizione fisica	1 online resource
Soggetti	Energy industries - Germany Power resources - Germany Energy industries Power resources
Lingua di pubblicazione	Tedesco
Formato	Materiale a stampa
Livello bibliografico	Periodico

